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TO: Jeffrey Parkin

Location: rem/3D39/3C18

Art Unit: 1648

Friday, February 17, 2006

Case Serial Number: 09/669187

From: Toby Port

Location: Biotech-Chem Library

REM-1A59

Phone: 571-272-2523

toby.port@uspto.gov

Searen Notes

Examiner Parkin,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port X22523



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STIC-Biotech/ChemLib

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From:

Parkin, Jeffrey

Sent:

Friday, February 03, 2006 6:25 PM

To: Subject:

STIC-Biotech/ChemLib U.S. Serial No. 09/669,187

Aloha!

Please search **SEQ ID NOS.: 73, 80, 81, 148, and 906** from U.S. Serial No. **09/669,187** v. all relevant databases, including interference. Please limit search results to oligonucleotides less than 50 nt in length, if possible. Place results on both paper and electronic format (i.e., disk, e-mail, etc.). Thanks!

Jeffrey S. Parkin, Ph.D. Primary Examiner Art Unit 1648 REM 3D39 2-0908

3C/8

Searcher:
Searcher Phone:
Date Searcher Picked up:
Date completed:
Searcher Prep Time:
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Type of Search

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Vendors and cost where applicable STN:

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1 Bates,P.J., Miller,D.M., Trent,J.O. and Xu,X. A method for the treatment of malignant diseases by inhibiting nucleolin

REFERENCE AUTHORS TITLE

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Brown-Driver, V.L., Ecker, D.J., Vickers, T.A., Wyatt, J.R. and
Imbach, J.Louis.
Oligonucleotides having a conserved G4 core sequence
Patent: US 5552490-A 121 14-SEP-1999;
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Oxytricha fallax right end of linear DNA fragments in macronucleus.
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repetitive sequence.
Oxytricha fallax
Oxytricha fallax
Stichotrichida; Oxytricha.
Stichotrichida; Oxytricha.
Stichotrichida; Oxytrichidae; Oxytricha.

Micronuclear DNA sequences of Oxytricha fallax homologous to the macronuclear inverted terminal repeat
Nucleic Acids Res. 10 (9), 2911-2924 (1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bates, P.J., Girvan, A.C. and Barve, S.S.
Method for inhibiting nf-kappa b signaling and use to treat or prevent human diseases
Patent: WO 200503733-A 29 28-APR-2005;
University of Louisville Research Foundation, Inc. (US)
Location/Qualifiers
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/organism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"
/noTe="Description of Artificial Sequence: Synthetic polynucleotide sequence"
                                                                                                                            /note="Description of Artificial Sequence: Synthetic polynucleotide sequence"
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 Patent: WO 2005035579-A 28 21-APR-2005;
University of Louisville Research Foundation (US)
Location/Qualifiers
                                                                         /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                      CS097991 28 bp DNA Sequence 29 from Patent WO2005037323. CS097991
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synthetic construct
other sequences; artificial sequences.
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TITLE JOURNAL FEATURES

REFERENCE AUTHORS

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C12Q1/02,
C12Q1/48,C12Q1/68,G01N33/15,G01N33/48,G01N33/50//C07K14/47, PC
C07K16/40,
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C12N15/09,A61K31/70,A61K38/55,A61K39/395,A61K39/395,A61K48/00,
                                                                                                                                                                                                                                                                                                                                                                                                                                      08/844.419, PR
            Thomas, R.S., Jochimu, R., Toru, N., Karen, B.C., Greg, B.M.,
Calvin, B.H. and William, H.A.
Human telomerase catalytic subunit promoter
Human telomerase catalytic subunit promoter
Patent: JP 1992533177-A 226 21-SEP-1999;
JERON CORP, UNIVERSITY TECHNOLOGY CORP
OS Unidentified
PN 21-SEP-1999
PP 19-CST-1999 JP 1998320169
PP 15-OCT-1998 JP 1998320169
PP 15-OCT-1998 JP 1998320169
PR 16-OCT-1998 JP 1998320169
PR 16-OCT-1997 US 08/846.017,06-MAY-1997 US 08/851.843, PR 25-APR-1997 US 08/854.050,14-AUG-1997 US 08/912.951,14-AUG-1997 US 08/912.503 PI THAUG-1997 US 08/912.951,14-AUG-1997 US 08/912.503 PI THAUG-1997 US 08/912.503 PI THAUG-1997 US 08/912.951,14-AUG-1997 US 08/912.503 PI THAUG-1997 US 08/912.951,14-AUG-1997 US 08/912.951,14-AUG-1997 US 08/912.951,14-AUG-1997 US 08/912.951,14-AUG-1997 US 08/912
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Patent: US 6610839-A 568 26-AUG-2003;
Geron Corporation; Menlo Park, CA
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Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0;
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Sequence 568 from patent US 6610839.
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/organism="unknown"
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1 (bases 1 to 44)

Morin, G.B. and Andrews, W.H.
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       1 (bases 1 to 44)
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Matches 20; Conservative 0; Mismatches 0; Indels
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Human telomerase catalytic subunit promoter.
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Patent: US 6093809-A 42 25-JUL-2000;
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Patent: US 6309867-A 42 30-OCT-2001;
Location/Qualifiers
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Sequence 42 from patent US 6093809.
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/organism="unknown"
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Cech, T.R. and Nakamura, T.
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Cech, T.R. and Lingner, J.
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DEFINITION ACCESSION VERSION KEYWORDS

RESULT 9 AR175791 LOCUS

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SOURCE ORGANISM

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TITLE JOURNAL FEATURES

REFERENCE AUTHORS

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E37018 LOCUS DEFINITION ACCESSION VERSION VERSION SOURCE ORGANISM

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PAT 31-JAN-2002

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CALVIN B HARLEY, WILLIAM H ANDREWS
A61K38/00, A61K31/7088, A61K39/00, A61K48/00, A61P35/00, A61P43/00,
                                                                                                     Cech, T.R., Lingner, J., Nakamura, T., Chapman, K.B., Morin, G.B., Harley, C.B. and Andrews, W.H.
Human telomerase catalytic subunit
Patent: EP 1331094-A 568 06-AUG-2003;
Geron Corporation (US); University Technology Corporation (US)
Location/Qualifiers
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C07K5/107, C07K5/117, C07K7/06, C07K7/08, C07K16/40, C12N9/12,
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Sechi, T.R., Lingner, J., Nakamura, T., Chapman, K.B., Mori, G.B.,
Harley, C.B. and Andrews, W.H.
Human telomerase catalytic subunit
Patent: JP 2001081042-A 226 27-MAR-2001;
GERON CORP, UNIVERSITY TECHNOLOGY CORP
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PN JP 2001081042-A/226
PN JP 2001081042-A/226
PD 27-MAR-2001
PP 27-JUL-22000 JP 2000227474
PR 01-OCT-1996 US 08/724643,18-APR-1997 US 08/851843 PR 02-APR-1997 US 08/854650,14-AUG-1997 US 08/851312 PR 14-AUG-1997 US 08/91551,14-AUG-1997 US 08/915503 PI R SECHI,JOACHIM LINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI MORIN,
                                                                                                                                                                                                                                                                                                                              Length 44;
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100.0%; Pred. No. 1.8e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                    /organism="unidentified"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human telomerase catalytic subunit.
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/organism="unidentified"
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/organism='Unidentified'
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JP 2001081042-A/226.
unidentified
unidentified
unclassified.
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CC Topology: Linear;
FH Key
FT source 1.
FT /organism='Unident
 AX810603.1 GI:38524092
                                  unidentified
unidentified
unclassified sequences.
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Best Local Similarity 100.
Matches 20; Conservative
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PC A61K3
PC C07K5
PC C07K5
C12N15/09,
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G01N33/53,
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Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
Cells immortalized with telomerase reverse transcriptase for use in
drug screening
Patent: US 6617110-A 568 09-SEP-2003;
Geron Corporation and University Technology Corporation; Menlo
Park, CA
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Cech, T.R., Lingner, J., Nakamura, T., Chapman, K.B., Morin, G.B.,
Harley, C. and Andrews, W.H.
Method for detecting polymucleotides encoding telomerase
Patent: US 6808880-A 42 26-OCT-2004;
Geron Corporation and Regents of the University of Colorado; Menlo
Park, CA
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100.0%; Score 20; DB 6; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
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                                                                                    44 bp Di Sequence 568 from patent US 6617110. AR393309.1 GI:40118689
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Sequence 42 from patent US 6808880.
AR592667
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Sequence 568 from Patent EP1333094.
AX810603
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/mol_type="genomic DNA"
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AR592667
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KEYWORDS
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ORIGIN

THOMAS GREG B

08/844419

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THOMAS GREG B

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C1201/02,
C1201/48, C1201/68, G01N33/15, G01N33/48, G01N33/50//C07K14/47, PC
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C12N15/09, A61K31/70, A61K38/55, A61K39/395, A61K39/395, A61K48/00,
                                                                                                                                                                                                                 7 US 08/844.419, PR
08/851.843, PR
08/911.312, PR
08/915.503 PI THOMA
                                                                                                                                                                                                                                                                                                                                      CC Topology: Linear;
FT source
FT source
                                                                            Lakun CORP, Lossitt A 225 21-SEP-1999;

OS Unidentified PN JP 199523177-A 225 21-SEP-1999;

OS Unidentified PN JP 199923177-A/225

PD 21-SEP-1999

PF 15-OCT-1996 US 08/324.643.18-APR-1997 US 08/844.419

PR 01-OCT-1996 US 08/346.017,06-MAY-1997 US 08/851.843, PR 09-MAY-1997 US 08/861.843, PR 09-MAY-1997 US 08/846.017,06-MAY-1997 US 08/912.951,14-AUG-1997 US 08/915.503 PI R SECHI,JOCHIMU RINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI GR MORIN,

PI CALVIN B HAREI,WILLIAM H ANDREWS

PC C12015/09,A61K31/70,A61K38/FE **-
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100.0%; Score 20; DB 6; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
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Morin,G.B. and Andrews,W.H.
Promoter for telomerase reverse transcriptase
Patent: US 6610839-A 567 26-AUG-2003;
Geron Corporation, Menlo Park, CA
Location/Qualifiers
                                                                          Toru, N., Karen, B.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ce 1. .46
/organism='Unidentified'
Location/Qualifiers
                                                                       Thomas.R.S., Jochimu,R., Toru,N., Karen,B.C Calvin,B.H. and William,H.A. Human telomerase caralytic subunit promoter Patent: JP 199253177-A 225 21-SEP-1999; JERON CORP, UNIVERSITY TECHNOLOGY CORP
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Sequence 567 from patent US 6610839.
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/organism="unidentified"
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JP 1999253177-A/225
                                           unclassified.
1 (bases 1 to 46)
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Unclassified.
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100.0%; Score 20; DB 6; Length 44; 100.0%; Pred. No. 1.8e+02; ive 0; Mismatches 0; Indels
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Human telomerase catalytic subunit promoter.
E37017.1 GI:13022980
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llarity 100.0%; Pred. No. 1.8e+02;
Conservative 0; Mismatches 0;
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1 (bases 1 to 46)
Cech,T.R. and Nakamura,T.
Telomerase
Telomerase 10S 6309867-A 41 30-OCT-2001;
                                                                                                                                                                                                                                                                                                                                              Patent: US 6093809-A 41 25-JUL-2000;
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                                                                                                                                                                       46 bp
Sequence 41 from patent US 6093809.
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Sequence 41 from patent US 6309867.
AR175790 AR175790.1 GI:17917089
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Cech, T.R. and Lingner, J.
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AR104529.1 GI:12817237
                              20; Conservative
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Best Local Similarity
Matches 20; Conserv
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Matches 20, Conserv
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Matches 20; Conser
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E37017
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AR104529
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inclassified.

unclassified.

l (bases 1 to 46)

Sechi,T.R., Lingmer,J., Nakamura,T., Chapman,K.B., Mori,G.B.,
Harley,C.B. and Andrews,W.H.
Human telomerase catalytic subunit
Human telomerase catalytic subunit
Fatent: JP 2001081042-A.225 27-MAR-2001;
GERON CORP,UNIVERSITY TECHNOLOGY CORP
ON Unidentified
PN JP 2001081042-A/225
PD 27-MAR-2001
PF 27-UTL-2000 JP 2000227474
PR 01-OCT-1996 US 08/84643,18-APR-1997 US 08/844419 PR 25-APR-1997 US 08/846050,14-AUG-1997 US 08/854050,14-AUG-1997 US 08/813132 PR R SECHI, JOACHIM LINGNER, TORU NAKAMURA, KAREN B CHAPMAN, PI GREG
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Human telomerase catalytic subunit
Patent: EP 133994-A 567 06-AUG-2003;
Geron Corporation (US); University Technology Corporation (US)
Location/Qualifiers
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                linear
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100.0%; Pred. No. 1.8e+02;
iive 0; Mismatches 0;
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          46 bp | Sequence 567 from Patent EP1333094. AX810602
                                                                                                                                                                                                                                                                             1. .46
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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Human telomerase catalytic subunit.
BD011268
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                                                                  AX810602.1 GI:38524091
                                                                                                   unidentified
unidentified
unclassified sequences.
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Matches 20; Conservative
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PC C07K5
PC C07K5
C12N15/09,
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BD011268
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Cechh.T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
Cells immortalized with telomerase reverse transcriptase for use in
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1 (bases 1 to 46)

Cech,T.R., Lingmer,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C. and Andrews,W.H.
Method for detecting polynucleotides encoding telomerase
Patent: US 6808880-A 41 26-OCT-2004;

Geron Corporation and Regents of the University of Colorado; Menlo
                                                                                                                                                                                                                                                                                                                                                                  drug screening
Patent: US 6617110-A 567 09-SEP-2003;
Geron Corporation and University Technology Corporation; Menlo
Park, CA
 Gaps
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100.0%; Score 20; DB 6; I
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0;
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                                                                                                                                                    Sequence 567 from patent US 6617110.
AR393308
 Mismatches
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 41 from patent US 6808880.
AR592666
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/mol_type="genomic DNA"
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Best Local Similarity 100.0%;
Matches 20; Conservative 0;
 Conservative
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AR592666
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AR393308
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JP 1999253177-A/222.
unidentified
unidentified
unclassified.

E 1 (bases I to 48)
S Thomas, R.S., Jochimu, R., Toru, N., Karen, B.C., Greg, B.M.,
Calvin, B.H. and William, H.A.
Human telomerase catalytic subunit promoter
Datent: JP 1999253177-A 222 21-SEP-1999;
OS Unidentified
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Human telomerase catalytic subunit promoter.
E37014
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100.0%; Score 20; DB 6; I
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0;
      DNA
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Telomerase
Patent: US 6309867-A 37 30-OCT-2001;
Location/Qualifiers
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Telomerase
Patent: US 6308867-A 40 30-OCT-2001;
Location/Qualifiers
48 bp 1
Sequence 37 from patent US 6309867.
AR175786
AR175786.1 GI:17917085
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Sequence 40 from patent US 6309867.
AR175789 1G1:17917088
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Cech, T.R. and Nakamura, T.
                                                                                              Unclassified.
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AR175789
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                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
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100.0%; Score 20; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
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Patent: US 6093809-A 37 25-JUL-2000;
Location/Qualifiers
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Patent: US 6093809-A 40 25-JUL-2000;
Location/Qualifiers
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AR104528
AR104528.1 GI:12817236
                                                                                                                                                                                                 AR104525 48 bp I
Sequence 37 from patent US 6093809.
AR104525
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/mol_type="unassigned DNA"
      /mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                        Unclassified.
1 (bases 1 to 48)
Cech, T.R. and Lingner, J.
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Cech, T.R. and Lingner, J.
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Unclassified.
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AR104528
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PAT 15-DEC-2004
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Cech, T.R., Lingner, J., Nakamura, T., Chapman, K.B., Morin, G.B.,
Harley, C. and Andrews, W.H.
Method for detecting polynucleotides encoding telomerase
Patent: US 6808880-A 37 26-OCT-2004;
Geron Corporation and Regents of the University of Colorado; Menlo Park, CA
                                                                           Unclassified.

1 (bases 1 to 48)

1 (chapman, K.B., Morin, G.B.,
Harley, C.B. and Andrews, W.H.
Cells immortalized with telomerase reverse transcriptase for use
                                                                                                                                                      drug screening
Patent: US 6617110-A 564 09-SEP-2003;
Geron Corporation and University Technology Corporation; Menlo
Park, CA
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1 (bases 1 to 48)
Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
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                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Sequence 37 from patent US 6808880.
AR592662
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/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                     /organism="unknown"
/mol_type="genomic DNA"
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                GI:40118681
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Best Local Similarity 100.0%;
Matches 20; Conservative 0
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AR393305
AR393305.1
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AR592665
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AR592662
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                                                                                                                                             CALVIN B HAREI,WILLIAM H ANDREWS
C12N15/09,A61K31/70,A61K38/55,A61K39/395,A61K39/395,A61K48/00,
                                                                                                                                                                                                                                                          PC (C12N1/21,C12R1:19), (C12N9/12,C12R1:19), (C12N9/12,C12R1:84), PC (C12N9/12,C12R1:91),C12N15/00,A61K37/64,C12N5/00 CC Strandedness: Single;
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CO2N1/19,C12N1/21,C12N5/10,C12N9/12,C12P21/08,(C12N1/19,
PN JP 1999253177-A/222
PD 21-SEP-1999
PF 15-00-1998 JP 1998320169
PR 01-0CT-1996 JP 1998320169
PR 01-0CT-1997 US 08/844.419
25-APR-1997 US 08/854.017,06-MAY-1997 US 08/851.843, PR 09-MAY-1997 US 08/854.050,14-AUG-1997 US 08/911.312, PR 14-AUG-1997 US 08/912.951,14-AUG-1997 US 08/915.503 PI MAY-1097 US 08/912.951,14-AUG-1997 US 08/915.503 PI MORIN,
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Morin,G.B. and Andrews,W.H.
Promoter for telomerase reverse transcriptase
Patent: US 6610839-A 564 26-AUG-2003;
Geron Corporation; Menlo Park, CA
Location/Qualifiers
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Location/Qualifiers
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Sequence 564 from patent US 6617110.
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Sequence 564 from patent US 6610839.
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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/organism="unknown"
/mol_type="genomic DNA"
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AR390691.1 GI:40112625
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AR390691
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PI CALVIN B HARLEY, WILLIAM H ANDREWS
PC AG1K38/00,A61K31/7088,A61K39/00,A61R48/00,A61P43/00,
PC CO7K5/10,
PC CO7K5/10,
PC CO7K5/107,CO7K5/117,CO7K7/06,CO7K1/08,CO7K16/40,C12N9/12, PC C12N15/09,
PC C12O1/02,C12Q1/48,C12Q1/68,G01N33/15,G01N33/50,G01N33/53, PC G01N33/53,
PC G01N33/56,G01N33/573//C12P21/08,A61K37/02,C12N15/00 CC Strandedness: Single,
CC Topology: Linear;
FH Key Location/Qualifiers
FT Acy Linear;
FT Acy Linear;
FT Acy Linear;
FT Acy Linearin/Qualifiers
FT Acy Linearin/Qualifiers
                                                 THOMAS
GREG B
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                                                                                                 CALVIN B HARLEY, WILLIAM H ANDREWS
AGIXSB/00, AGIX31/7088, AGIX39/00, AGIR48/00, AGIP35/00, AGIP43/00,
CO7K5/10,
CO7K5/107, CO7K5/117, CO7K7/06, CO7K7/08, CO7K16/40, C12N9/12, PC
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25-APR-1997 US 08/846017,06-MAY-1997 US 08/851843 PR 09-MAY-1997 US 08/854050,14-AUG-1997 US 08/911312 PR 14-AUG-1997 US 08/91551,14-AUG-1997 US 08/91553 PI R SECHI,JOACHIM LINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI MORIN,
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100.0%; Score 20; DB 6; I
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0;
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100.0%; Score 20; DB 6; I
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0;
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Patent: US 6093809-A 39 25-JUL-2000;
Location/Qualifiers
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Sequence 39 from patent US 6309867.
AR175788.1 GI:17917087
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/wol_type="unassigned DNA"
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Sequence 39 from patent US 6093809.
AR104527 GI:12817235
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Cech, T.R. and Lingner, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unclassified.
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Unclassified.
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AR104527
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AR175788
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           Harley, C. and Andrews, W.H.
Method for detecting polynucleotides encoding telomerase
Patent: US 6808880-A 40 26-OCT-2004;
Geron Corporation and Regents of the University of Colorado; Menlo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
Human telomerase catalytic subunit
Patent: EP 1331094-A 564 06-AUG-2003;
Geron Corporation (US); University Technology Corporation (US)
Location/Qualifiers
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Human telomerase catalytic subunit
Patent: JP 2001081042-A 222 27-MAR-2001;
GERON CORP, UNIVERSITY TECHNOLOGY CORP
OS Unidentified
PN JP 2001081042-A/222
PP 37-MAR-2001
PP 27-UIL-2000 JP 2000227474
PP 77-UIL-2000 JP 2000227474
PR 01-OCT-1996 US 08/724643, 18-APR-1997 US 08/844419 PP
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BD011265
BD011265.1 GI:18639638
JP 2001081042-A/222.
unidentified
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Sequence 564 from Patent EP1333094.
AX810599
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
                                                                                                                                                      /mol_type="unassigned DNA"
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                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unidentified unclassified sequences.
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Matches 20; Conservative
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AX810599
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us-09-669-187a-73.szlm50.rge

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Unclassified.
1 (bases 1 to 50)
Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
Cells immortalized with telomerase reverse transcriptase for use in
                                                                  PAT 18-DEC-2003
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Patent: US 6617110-A 566 09-SEP-2003;
Geron Corporation and University Technology Corporation; Menlo Park, CA
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Patent: US 6610839-A 566 26-AUG-2003;
Geron Corporation; Menlo Park, CA
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0;
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Sequence 566 from patent US 6610839.
AR390693
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Sequence 39 from patent US 6808880.
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/mol_type="genomic DNA"
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Morin, G.B. and Andrews, W.H.
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AR390693
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AR592664
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C1201/48, C1201/68, G01N33/15, G01N33/48, G01N33/50//C07K14/47, PC
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C12N15/09, A61K31/70, A61K38/55, A61K39/395, A61K39/395, A61K48/00,
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COTRIN/19,C12N1/21,C12N5/10,C12N9/12,C12P21/08,(C12N1/19, PC
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PR 01-OCT-1996 US 08/724.643,18-APR-1997 US 08/844.419,
25-APR-1997 US 08/846.017,06-MAY-1997 US 08/851.843, PR
09-MAY-1997 US 08/854.050,14-AUG-1997 US 08/911.312, PR
14-AUG-1997 US 08/912.551,14-AUG-1997 US 08/915.503 PI TR
R SECHI,JOCHIMU RINGNER, TORU NAKAMURA, KAREN B CHAPMAN, PI GRI
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1 (bases 1 to 50)
Thomas,R.S., Jochimu,R., Toru,N., Karen,B.C., Greg,B.M., Calvin,B.H. and William,H.A.
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Human telomerase catalytic subunit promoter.
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Patent: JP 1999253177-A 224 21-SEP-1999;
JERON CORP,UNIVERSITY TECHNOLOGY CORP
                                                                                                                                                                       Query Match 100.0%; Score 20; DB 6; I
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0;
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100.0%; Score 20; DB 6; I
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0;
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1 (bases 1 to 50)
Cech, T.R. and Nakamura, T.
Telomerase Patent: US 6309867-A 39 30-OCT-2001;
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JP 1999253177-A/224
21-SEP-1999
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JP 1999253177-A/224.
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PAT 14-FEB-2001
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C07KS/10,
C07KS/107,C07K5/117,C07K7/06,C07K1/08,C07K16/40,C12N9/12, PC
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PN JP 2001081042-A/224
PD 27-MAR-2001
PP 27-MAR-2001
PP 27-JUL-2000 JP 200227474
PR 01-OCT-1996 US 08/724643,18-APR-1997 US 08/844419 PR 25-APR-1997 US 08/846105,06-MAY-1997 US 08/81843 PR 09-MAY-1997 US 08/81533 PR 14-AUG-1997 US 08/913132 PR 14-AUG-1997 US 08/913132 PR 14-AUG-1997 US 08/913132 PR SECHI,JOACHIM LINGNER,TORU NAKAMURA,KAREN B CHAEMAN, PI GREG B NORIN, COTKS/10, AGIRS/10708,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIRS/107,AGIR
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ilarity 100.0%; Pred. No. 1.8e+02;
Conservative 0; Mismatches 0;
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Patent: US 6093809-A 39 25-JUL-2000;
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Sequence 39 from patent US 6309867.
AR175788. GI:17917087
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Seguence 39 from patent US 6093809.
AR104527
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/organism="unknown"
/mol_type="unassigned DNA"
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/organism="unidentified"
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/db_xref="taxon:32644"
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1 (bases 1 to 50)
Cech, T.R. and Lingner, J.
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CC Topology: Linear;
FH Key Love
FT Source 1 1
FT /organism='Unidenti
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nes 18; Conserv
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Matches 20; Conserv
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AR104527/c
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DEFINITION
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KEYWORDS
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AUTHORS
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JOURNAL
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  Unclassified.
Unclassified.
Classes I to 50)
Cech, T.R., Lingner, J., Nakamura, T., Chapman, K.B., Morin, G.B.,
Harley, C. and Andrews, W.H.
Method for detecting polynucleotides encoding telomerase
Patent: US 6808880-A 39 26-OCT-2004;
Geron Corporation and Regents of the University of Colorado; Menlo
Park, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAT 25-NOV-2003
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Human telomerase catalytic subunit
Patent: EP 1331094-A 566 06-AUG-2003;
Geron Corporation (US); University Technology Corporation (US)
Location/Qualifiers
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Sechi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Mori,G.B.,
Harley,C.B. and Andrews,W.H.
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100.0%; Pred. No. 1.8e+02;
iive 0; Mismatches 0;
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patent: JP 2001081042-A 224 27-MAR-2001;
GERON CORP UNIVERSITY TECHNOLOGY CORP
OS Unidentified
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                       /organism="unknown"
/wol_type="unassigned DNA"
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JP 2001081042-A/224.
unidentified
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Best Local Similarity 100.8
Matches 20, Conservative
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REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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1 (bases 1 to 50)
Cechh.T.R., Lingmer,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
Cells immortalized with telomerase reverse transcriptase for use in
                                                                                                                                      PAT 18-DEC-2003
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Geron Corporation and University Technology Corporation; Menlo
Park, CA
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Morin, G.B. and Andrews, W.H.
Promoter for telomerase reverse transcriptase
Brante 1 US 6610839-A 566 26-AUG-2003;
Geron Corporation; Menlo Park, CA
Location/Qualifiers
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90.0%; Score 18; DB 6; Le
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 0;
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                                                                                                                                    AR390693 566 from patent US 6610839.
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Sequence 39 from patent US 6808880.
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/organism="unknown"
/mol_type="genomic DNA"
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/organism="unknown"
/mol_type="genomic DNA"
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C12Q1/48, C12Q1/68, G01N33/15, G01N33/48, G01N33/50//C07K14/47, PC
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C12N15/09, A61K31/70, A61K38/55, A61K39/395, A61K39/395, A61K48/00,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PP 21-SEP-1999
PP 15-OCT-1998 JP 1998320169
PR 01-OCT-1996 UB 08/72463,18-APR-1997 US 08/844.419, PR 25-APR-1997 US 08/846.017,06-MAY-1997 US 08/854.050,14-AUG-1997 US 08/813.312, PR 09-MAY-1997 US 08/813.312, PR 09-MAY-1997 US 08/912.951,14-AUG-1997 US 08/911.312, PR R SECHI, JOCHIMU RINGNER, TORU NAKAMURA, KAREN B CHAPMAN, PI GREG MORIN,
                                                                                                                                                                                                                                                                                     Gaps
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JP 1999253177-A/224.
unidentified
SW unidentified
unclassified.
E 1 (bases 1 to 50)
S Thomas,R.S., Jochimu,R., Toru,N., Karen,B.C., Greg,B.M.,
Calvin,B.H. and William,H.A.
Human telomerase catalytic subunit promoter
Patent: JP 1999253177-A 224 21-SEP-1999;
OS Unidentified
PN UP 1999253177-A/224
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Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 0; Indels
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Location/Qualifiers
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Human telomerase catalytic subunit promoter.
E37016
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Cech,T.R. and Nakamura,T.
Telomerase
Patent: US 6309867-A 39 30-OCT-2001;
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                                                                                               1 (bases 1 to 50)
Cech,T.K., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C. and Andrews,W.H.
Method for detecting polynucleotides encoding telomerase
Patent: US 6808880-A 39 26-OCT-2004;
Geron Corporation and Regents of the University of Colorado; Menlo
Park, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cech, T.R., Lingner, J., Nakamura, T., Chapman, K.B., Morin, G.B., Harley, C.B. and Andrews, W.H.
Human telomerase catalyric subunit
Human telomerase catalyric subunit
Patent: EP A.566 06-AUG-2003;
Geron Corporation (US); University Technology Corporation (US)
Location/Qualifiers
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1 (Dases 1 to 50)
Sechi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Mori,G.B.,
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Sequence 566 from Patent BP1333094.
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BD011267
BD011267.1 GI:18639640
JP 2001081042-A/224.
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A61K38/00,A61K31/7088,A61K39/00,A61K48/00,A61P35/00,A61P43/00,
C07K5/10,
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                                                                                 OS Unidentified

PN JP 20010101042-A/224

PD 27-MAR-2001

PF 27-JUL-2000 JP 2000227474

PR 10-OCT-1996 US 08/746617,06-MAY-1997 US 08/851843 PR
25-APR-1997 US 08/846017,06-MAY-1997 US 08/91313 PR
09-MAX-1997 US 08/846017,06-MAY-1997 US 08/91313 PR
14-AUG-1997 US 08/912951,14-AUG-1997 US 08/913503 PI TI
R SECHI,JOACHIM LINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI GR.
MORIN,
PI CALVIN B HARLEY,WILLIAM H ANDREWS
PC AGINSS/00,A61831/7088,A61K39/00,A61848/00,A61895/00,A6184

PC COTKS/10,
COTKS/10,
COTKS/10,
COTKS/117,COTK7/06,COTK7/08,COTK16/40,CI2N9/12,
COTKS/10,COTKS/117,COTK7/06,COTK7/08,COTNI33/53,GOIN33/53,
CC COTS/103/66,GOIN33/53/CI2P21/08,A61K37/02,CI2N15/00 CC
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CC Topology: Linear;
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FT /organism="Unidentified"
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Human telomerase catalytic subunit
Patent: JP 2001081042-A 224 27-MAR-2001;
GERON CORP,UNIVERSITY TECHNOLOGY CORP
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Adv45884 Human CpG
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Ad56450 Immunosti
Ad489389 Allergic
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Ad128732 Guanosine
Ad287324 Non-antis
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               GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 300 summaries
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Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic; immunostimulatory; tumour; viral infection; bacterial infection; fungal infection; parasitic infection; cancer; asthma; infectious disease; allergy; immune deficiency; phosphorothioate; ss.

Immunostimulatory nucleic acid #64.

(first entry)

12-JUN-2001

ВР

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ADA13696
ADG29769
ADL80060
ADM65565
ADM65562
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AAX26508
ABX26136
ABH09453
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AAH39037
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Vaccinating against tumors, infectious diseases, allergies and asthmausing immunostimulatory Py-rich and TG nucleic acids.

Krieg AM, Schetter C, Vollmer J;

WPI; 2001-273485/28

25-SEP-1999; 99US-0156113P 27-SEP-1999; 99US-0156135P 23-AUG-2000; 2000US-0227436P

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25-SEP-2000; 2000WO-US026383

WO200122972-A2

Synthetic.

05-APR-2001

Disclosure; Page 39; 338pp; English.

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The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Th2 to a Th1 immune response and to activate immune cells. Note: the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present sequence may have a phosphorothioate backbone
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Les 20; Conservative
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Angiogenesis inhibitory oligonucleotide #73.

Angiogenesis inhibitor; 88; angiogenesis; solid tumour growth; tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;

ALIGNMENTS

AAF98948;

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The invention describes a method of treating non-allergic inflammatory disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases, such as psoriasis, eczema, allergic context dermatitis, latex dermatitis or inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease. This sequence represents an immunostimulatory nucleic acid
                                                                                                                                                                                                                                                                                        Treating non-allergic inflammatory diseases, such as psoriasis, ecze allergic contact dermatitis, latex dermatitis or inflammatory bowel disease by administering an immunostimulatory nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 BP; 0 A; 0 C; 8 G; 12 T; 0 U; 0 Other;
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  29-MAR-2002; 2002US-00112653.
                                                         29-MAR-2001; 2001US-0279642P
                                                                                                                                                                                                                                         WPI; 2003-521815/49
                                                                                                                                                                                        Krieg AM, Berg DJ;
                                                                                                       (KRIE/) KRIEG A M. (BERG/) BERG D J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       administering at least one antiangiogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.
rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound granulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
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                                                                                                                                                                                                                                                                                                                                                                                            (COLE-) COLEY PHARM GROUP INC
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les 20; Conserv
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Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament. Gaps ;; 0 ds, allergy, asthma, poly-G nucleic acid, aerosol formulation, hypo-responsive subject; immunostimulatory. 9; Length 20 0; Indels Score 20; DB Pred. No. 52; 0; Mismatches Fouron Y; Immunostimulatory nucleic acid #64. Disclosure; Page 6; 221pp; English 1 TTTTGGGGTTTTGGGGGTTTT 20 rrrregegrrrregegerrrr 20 100.0%; 02-FEB-2001; 2001US-00776479. 03-FEB-2000; 2000US-0179991P. ADB36450 standard; DNA; 20 Bratzler RL, Petersen DM, (first entry) Query Match
Best Local Similarity 100.
Matches 20; Conservative (BRAT/) BRATZLER R L. (PETE/) PETERSEN D M. WPI; 2003-657977/62. FOURON Y. US2003087848-A1. 04-DEC-2003 08-MAY-2003. Synthetic. ADB36450; FOUR/) X S X X I X X B X B X B Immunostimulatory; antiinflammatory; dermatological; antipsoriatic; antiulcer; gene therapy; vaccine; non-allergic inflammatory disease; psoriasis; eczema; allergic contact dermatitis; latex dermatitis; inflammatory bowel disease; ulcerative colitis; crohn's disease; ss.

Immunostimulatory nucleic acid #67.

US2003050268-A1

Synthetic.

13-MAR-2003.

(first entry)

25-SEP-2003

ACD99381;

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Gaps

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Score 20; DB 12; Length 20; Pred. No. 52; 0; Mismatches 0; Indels

1 TTTTGGGGTTTTGGGGTTTT 20

100.0%; ilarity 100.0%; Conservative 0

Query Match Best Local Similarity Matches 20; Conserv

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ADU89389 standard; DNA; 20 BP

4DU89389 RESULT

Sequence 20 BP; 0 A; 0 C; 8 G; 12 T; 0 U; 0 Other;

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                                                                                                                   especially in a hypo-responsive subject. The present sequence represents an immunostimulatory nucleic acid of the invention.
The invention relates to a method of treating or preventing allergy or asthma which comprises administering to a subject a poly-G mucleic acid in an aerosol formulation. The methods and compositions of the present invention are useful for diagnosing and/or treating asthma and allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ss; non-CpG; immunostimulatory; non-palindromic; immune response; proliferation; differentiation; cytokine; antibody production; B-cell; plasmacytoid dendritic cell; immunomodulator; gene therapy; chronic myelogenous leukaemia; melanoma; Kaposi's sarcoma; renal cell carcinoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADG76003 standard; DNA; 20
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ss, antiasthmatic; antiallergic; dermatological; antiinflammatory; antibacterial; virucide; immunoglobulin E antagonist; allergy; immunostimulator; asthma; rhinitis; urticaria; dermatitis; bacterial infection; viral infection.

Allergic response suppressor oligonucleotide #73.

10-FEB-2005 (first entry)

ADU89389;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Suppressing allergies, including asthma, rhinitis, urticaria and atopic dermatitis, in a subject, comprises administering a first and second dose of an immunostimulatory nucleic acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 73; 235pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               method of the invention.
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Best Local Simi
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This invention relates to novel immunostimulatory oligonucleotides that contain a non-palindromic sequence motif. Specifically, it refers to DNA coligonucleotides (without a CPG motif), which can stimulate an immune response in animals of the order of primate, including humans. The immune response is characterised by the proliferation, differentiation, cytokine cand antibody production in B-cells, as well as cell differentiation and cytokine production in plasmacytoid dendric cells. The present invention describes immunomodulator compositions that also comprise an antigen selected from, for example, viruses, bacteria, parasites, tumour cells and glycolipides. As such, these DNA oligos can be used in gene therapy for inducing B-cell activation, treating, preventing or ameliorating an immune system disorder or a tumoural disease including chronic myelogenous leukaemia, melanoma, Kaposi's sarcoma, and renal cell carcinoma. This oligonucleotide sequence is a non-CpG DNA oligo of the invention.

New immunostimulatory oligonuclectide comprising non-palindromic nucleic acid sequence motif, useful for inducing B-cell activation, treating, preventing or ameliorating immune system disorder or tumoral disease e.g.

WPI; 2004-053333/05.

Lopez RA;

Example 17; Page 80; 139pp; English.

melanoma

Fouron Y;

Bratzler RL, Petersen DM,

BRATZLER R PETERSEN D

FOURON Y

(PETE/) (FOUR/) (BRAT/)

WPI; 2004-833006/82.

23-APR-2004; 2004US-00831778. 03-FEB-2000; 2000US-0179991P. 02-FEB-2001; 2001US-00776479.

US2004235774-A1.

Synthetic.

25-NOV-2004

us-09-669-187a-73.szlm50.rng

RESULT 7 AAD64883

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The invention relates to a novel quantitative method for adding linear polynucleotide to solution containing a cation. The linear polynucleotide acceptor at lonear sequence with donor at one edge portion and acceptor at another edge portion. The optical detection is performed using this linear polynucleotide. The method of the invention is useful in medical fields such as clinical laboratory test and fields with cation fixed assay. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting apoptosis comprises preparing a sample from which cells have been removed and detecting at least one of nucleolin and PARP-I in the
                                                                                                                                                                                   Quantitative method of cation for clinical laboratory test, involves adding linear polynucleotide containing telomere repeat sequence with donor and acceptor at edge portions, to solution containing cation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Guanosine-rich oligonucleotide GRO J, used in apoptosis detection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 20; DB 10; Length 28; Best Local Similarity 100.0%; Pred. No. 53; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 28 BP; 0 A; 0 C; 16 G; 12 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                             Disclosure; Page 29; 8pp; Japanese
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             05-DEC-2001; 2001JP-00371975.
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                                                     05-DEC-2001; 2001JP-00371975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                      (TAKE/) TAKENAKA S.
(TUMK-) TUM KENKYUSHO KK.
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                                                                                                                                                 WPI; 2003-639772/61
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                                                                                                                                                                                                                                                                                                                                                                                                                                     invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to method for determining neoplastic state of a cell, involves detecting the presence of plasma membrane nucleotide in the cell or quantifying the amount of plasma membrane nucleolin in the cell. The invention is useful for diagnosing pre-malignant cells, malignant cells and lung small cell carcinoma. The present sequence is a non-antisense oligonucleotide
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                                                                                                                                                                                                        Neoplastic, malignancy; lung carcinoma; ss.
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                                                                                                                                                                     GRO J1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TTTTGGGGTTTTGGGGTTTT 20
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                                                     AAD64883 standard; DNA; 28 BP
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                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     MILLER D M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BATE/) BATES P J.
(TREN/) TRENT J O.
(XUXX/) XU X.
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                                                                                                                               11-MAR-2004
                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                                                                                    16-OCT-2003
                                                                                          AAD64883;
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(BATE/) N
(TREN/)
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Claim 9; SEQ ID NO 28; 66pp; English

sample.

JP2003169676-A.

17-JUN-2003

Unidentified.

Matches

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Gaps

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The present sequence is that of guanosine-rich oligonucleotide GRO J, which can be used in the method of the invention. The method is for the detection of apoptosis. It involves preparing a sample from which cells have been removed, and detecting nucleolin and/or poly(ADP-ribose) polymerase (PARP-1) in the sample, where the sample is blood, serum, plasma, tissue, tissue culture medium or sputum. Detection of nucleolin involves detection of a complex between nucleolin and a nucleolin binding molecule, preferably an anti-nucleolin antibody or a GRO, such as GRO J, which is characterised as a good plasma membrane nucleolin-binding GRO. The method allows detection of excessive apoptosis in a subject suspected of having AlDS, a neurodegenerative disease, an ischaemic injury, an
                                                                                                                                                                                                                                                                                                                                                     autoimmune disease, a tumour, a cancer (especially endocervical adenocercinoma, prostatic carcinoma, breast cancer, leukaemia and nonsmall cell lung carcinoma), a viral infection, an acute inflammatory condition or sepsis (all claimed).
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Sequence 28 BP; 0 A; 0 C; 16 G; 12 T; 0 U; 0 Other;

Gaps ô 100.0%; Score 20; DB 12; Length 28; 100.0%; Pred. No. 53; 0; Indels 0; Mismatches 20 TTTTGGGGTTTTGGGGTTTT 24 20; Conservative Local Similarity н Query Match Matches 8

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ADY53924 standard; DNA; 28 BP RESULT 10 ADY53924 

19-MAY-2005 (first entry) ADY53924;

Non-antisense GRO nucleolin-binding oligonucleotide GRO29A.

Diagnosis; therapy; tumor; cancer; neoplasm; cytostatic; nucleolin; ss; guanine-rich oligonucleotide; gene silencing; RNA interference; melanoma; lymphoma; sarcoma; glioma; leukemia; hepatocellular carcinoma.

Synthetic

US2005053607-A1.

10-MAR-2005.

09-OCT-2003; 2003US-00683480

08-APR-2002; 2002US-00118854

(BATE/) BATES P J. (MILL/) MILLER D M. (TREN/) TRENT J O. (xuxx/) xu x.

X nX Trent JO, Bates PJ, Miller DM,

WPI; 2005-213006/22.

Treating cancer in a subject comprises administering to the subject a therapeutically effective amount of an anti-nucleolin agent and a carrier.

Disclosure, SEQ ID NO 28; 32pp; English.

The invention relates to treating cancer in a subject comprises administering to the subject a therapeutically effective amount of an anti-nucleolin agent and a carrier. Also included is a pharmaceutical composition comprising a nucleolin antibody or an inhibitory RNA against nucleolin, and a carrier. The method and antibodies, RNA and composition are useful for treating cancer, such as melanoma, lymphoma, plasmocytoma, sarcoma, glioma, thymoma, leukemia, hepatoma, or breast, prostate, colon,

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This invention relates to a novel method for treating inflammation in a patient which comprises administering to the patient a composition comprising a GRO (guanosine-rich oligonucleotide). The invention may be useful for the development of compounds with an antinflammatory.

C analgesic, gynecological, hepatotropic, neuroprotective, nootropic, antisterinatic, antisterinatic, gastrointestinal-Gen. or antiuler activity whilst the disclosed sequence may prove useful for gene therapy. The methods are useful for treating inflammation associated with an acute inflammatory condition. The acute inflammatory condition is selected from primary dysmenorrhea, acute alcoholic liver disease and acute pancreatis. The inflammation may also be of Alzheimer's disease or associated with a chronic inflammatory disease. The chronic inflammatory disease is selected from rheumatoid arthritis, asthma, gastrointestinal tract disease, psoriasis, atherosclerosis, Crohns disease, ulcerative collisa alcohol, chronic alcoholic liver disease, non-alcoholic steatohopatitis and chronic pancreatitis. The present sequence is that of the oligonucleotide GRO J which was used during the development of the one-partition.
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liver, esophageal, brain, lung, ovary, or cervical cancer. The present sequence is a GRO (guanine-rich oligonucleotide) which binds to nucleolin (thereby inhibiting cancer cell growth).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treating inflammation, e.g. acute or chronic inflammation such as rheumatoid arthritis, asthma, psoriasis, and atherosclerosis, in a patient comprises administering to the patient a composition comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inflammation; antiinflammatory; analgesic; gynecological; hepatotropic; neuroprotective; nootropic; antiarthritic; antirheumatic; gastrointestinal-Gen.; antiulcer; gene therapy; dysmenorrhea; alcoholic hepatitis; pancreatitis; Alzheimers disease; rheumatoid arthritis; asthma; gastrointeetinal disease; psoriasis; atherosclerosis; Crohns disease; ulcerative colitis; GRO J; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inflammation treatment-related GRO J oligonucleotide SegID29.
                                                                                                                        Score 20; DB 14; Length 28;
                                                                                                                                                                Indels
                                                                                  Sequence 28 BP; 0 A; 0 C; 16 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                ;
                                                                                                                                           53;
                                                                                                                                                                0; Mismatches
                                                                                                                                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYLO-) UNIV LOUISVILLE RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; SEQ ID NO 29; 60pp; English
                                                                                                                                                                                                        1 TITIGGGTTITIGGGGTTIT 20
                                                                                                                                                                                                                                              24
                                                                                                                                                                                                                               S TTTTGGGGTTTTGGGGTTTT
                                                                                                                                                                                                                                                                                                                                                 ADZ58647 standard; DNA; 28 BP.
                                                                                                                      100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-OCT-2004; 2004WO-US033185
                                                                                                                                           100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-OCT-2003; 2003US-0510466P
                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                           Local Similarity 100.
les 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Girvan AC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2005-315628/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2005037323-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified,
                                                                                                                                                                                                                                                                                                                                                                                                                               14-JUL-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bates PJ,
                                                                                                                                                                                                                                                                                                                                                                                         ADZ58647;
                                                                                                                          Query Match
                                                                                                                                               Best Loca
Matches
                                                                                                                                                                                                                                                                                                           RESULT 11
                                                                                                                                                                                                                                                                                                                              ADZ58647
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                                                                                                                                                                                                                                                                                                                                                                            Telomere; stabilizer; telomerase inhibitor; cancer; neoplasm; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New carbazole compound stabilizing G-quadruplex of telomere, useful to treat telomerase-related disease e.g. cancer.
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to novel carbazole compounds which thermally
                                                                                                                                                                                                                                                                                                                                              G-quadruplex-forming carbazole-binding DNA Oxy28, SEQ ID NO:11.
                                                                         ö
                               100.0%; Score 20; DB 14; Length 28; 100.0%; Pred. No. 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 20; DB 14; Length 28; 100.0%; Pred. No. 53;
                                                                       Indels
Sequence 28 BP; 0 A; 0 C; 16 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 28 BP; 0 A; 0 C; 16 G; 12 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the structure is formed has not been provided
                                 Query Match 100.0%; Score 20; DE Best Local Similarity 100.0%; Pred. No. 53; Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 9; SEQ ID NO 11; 12pp; English
                                                                                                           1 TTTTGGGGTTTTGGGGTTTT 20
                                                                                                                               5 TTTTGGGGTTTTGGGGTTTT 24
                                                                                                                                                                                                                                     ADZ25617 standard; DNA; 28 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-OCT-2003; 2003US-00690984.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-OCT-2003; 2003US-00690984
                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wu J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2005-331984/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chang C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHAN/) CHANG T.
(CHAN/) CHANG C.
(WUJJ/) WU J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2005090671-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                          14-JUL-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-APR-2005.
                                                                                                                                                                                                                                                                       ADZ25617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chang T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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method has been developed for binding quadruplex nucleic acids. The method comprises contacting a quadruplex nucleic acid with a monoclonal antibody that selectively binds to quadruplex nucleic acid to form an antibody-quadruplex nucleic acid complex. The method can be used for detecting antibodies that bind to quadruplex nucleic acids and to collect antibodase that bind to quadruplex nucleic acids and to collect cartibodies that bind to quadruplex nucleic acids and to collect suitable for detecting, isolating and purifying quadruplex nucleic acids. The method is also suitable for detecting step can be carried out on a biological sample such as cerebrospinal fluid, tissues samples, blood samples or other sample cuspected of containing quadruplex nucleic acids from solutions and to purify aptamers from combinatorial libraries or heterospenous solutions, in particular to purify or detect DNN aptamers that specifically bind the thrombin molecule critical in the thrombin-catalysed, fibrin-clot cormation cascade of blood placelets. The antibodies can then be used to detect levels of a known therapeutic aptamer in a patient and monitor clearance and dosage levels in a treatment protocol involving the aptamer. The present sequence trepresents an oligonucleotide used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quadruplex nucleic acid and antibody binding assay useful for detecting and purifying antibodies and nucleic acids from a biological sample.
                                                                                                                                             Quadruplex DNA; antibody; binding; detection; isolation; purification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 20; DB 3; Length 32; 100.0%; Pred. No. 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 32 BP; 0 A; 0 C; 16 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                           Exemplary quadruplex nucleic acid SEQ ID NO:9.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Brown BA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            Hardin CC,
                                                                                                                                                                                                                                                                                                                                                                                       UYNC-) UNIV NORTH CAROLINA STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, Col 3; 11pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TTTTGGGGTTTTGGGGTTTT 20
AAZ57146 standard; DNA; 32 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP
                                                                                                                                                                                                                                                                                                                96US-00729598
                                                                                                                                                                                                                                                                                                                                                  95US-0005242P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ61979 standard; DNA; 39
                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            Pelsue SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003 (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-096139/08.
                                                                                                                                                                                                                                                                                                                                                                                                          JACK-) JACKSON LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                11-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                  12-OCT-1995;
                                                                        24-MAR-2000
                                                                                                                                                                                                                                         US6001657-A
                                                                                                                                                                                                                                                                             14-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                            Roberts JF,
                                                                                                                                                                                                       Synthetic.
                                      AAZ57146;
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AAQ61979
ID AAQ61
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AC AAQ61
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DT 25-MA
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Gaps

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100.0%; Prec. ...

20; Conservative

Matches

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Local Similarity

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The present sequence represents a primer from the present invention which describes human telomerase reverse transcriptase (hTRT). The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT cerombinant protein or polynucleoride, on administration of the compound; (B) preparation of recombinant telomerase by contacting a protein preparation of hTRT with a telomerase RNA component; (C) detection of hTRT with a sample by binding a relevant probe to the sample hTRT RNA or protein in a sample by binding a relevant probe to the sample of mplifying the product and correlating the presence of complex or amplifying the product with presence of hTRT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing hTRT expression; and (B) the use of an agent that causes an increase in cell correlation to create a medicament that inhibits ageing. A protein preparation of hTRT and the polynucleotide encoding hTRT can be used in the manufacture of medicaments for inhibiting the cancer of ageing or cancer. Inhibitors of telomerase activity can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of oppoliferation conditions especially cancer and ageing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein preparation of hTRT can also be used in the new methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 20; DB 2; Length 44;
Pred. No. 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 44 BP; 10 A; 10 C; 12 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chapman KB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Telomerase substrate utilisation primer 25-27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to treat conditions that are associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 200; 387pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lingner J, Nakamura T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
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                                                                                                                                                                                                                           970S-00844419.
970S-00846017.
970S-00851843.
970S-00854050.
970S-00911312.
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es 20; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNIV TECHNOLOGY CORP.
                                                                                                                                    97GB-00020890
                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-00915503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-171633/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GERON
                                                                                                                                01-OCT-1997;
GB2317891-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 14-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-AUG-1998
                                                                                                                                                                                                  01-OCT-1996
                                                                  08-APR-1998
                                                                                                                                                                                                                                  18-APR-1997
                                                                                                                                                                                                                                                                 25-APR-1997
                                                                                                                                                                                                                                                                                                       06-MAY-1997
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14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Andrews WH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV17008;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GERO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYTE-)
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV17008
   NAMES OF COLOR COL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents a guanine rich sequence derived from the Oxytricha telomeric region. This sequence forms an unusual structure termed a Gquartet. The formation of this structure is monovalent cation dependant and is disrupted by high temperature. Sequences which share the guanine rich nature of this telomeric sequence may be used to inhibit human type II phospholipase A2 activity. Oligomocleotides such as these may also be used for inhibiting activity of HSV, HIV, human cytomegalovirus or influenza virus, or for treating inflammatory and neurological disorders caused by phospholipase A2 activity in cases of hyperproliferation, malignancy, cardiovascular disease and snake bite. They may also be used for inhibiting division of malignant cells by modualting telomere length, which may also retard aging. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New modified oligo-nucleotide contg guanine quartet - inhibits activity of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length of chromosomes.
                                                                                                                             Inhibition; replication; herpes simplex virus; HSV; HIV; aging; human cytomegalovirus; influenza virus; influenze length; neurological disorders; phospholipes A2 activity; hyperproliferation; malignancy; cardiovascular disease; snake bite; malignancy; retard; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 39 BP; 0 A; 0 C; 20 G; 16 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Telomerase substrate utilisation primer 28-30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wyatt JR, Imbach JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 7; Page 36; 144pp; English.
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                                                                  Oxytricha telomeric sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93WO-US009297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92US-00954185.
04-NOV-1994 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anderson KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vickers TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1994-135613/16.
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                                                                                                                                                                                                                                                                                                                                                                  WO9408053-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-SEP-1992;
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Ecker DJ,

cell

Morin GB, Harley CB;

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Gaps

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0; Indels

high telomerase activity. A

Human, telomerase reverse transcriptase, hTRT; TRT; diagnosis, prognosis, cell proliferation, cancer; ageing; ribonucleoprotein; primer; ss.

Homo sapiens

Synthetic

AAV17009;

RESULT 15 AAV17009

Query Match Matches

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13-AUG-1998 (first entry)
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Matches 20; Conserv
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                                             Homo sapiens.
                                                                                                                       01-OCT-1997;
                                                                        GB2317891-A.
                                                                                                                                                                                                                           1997;
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                                                                                               08-APR-1998
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                                                                                                                                                             L8-APR-1997
                                                                                                                                                                         25-APR-1997
                                                                                                                                                                                                                                                                                                               Andrews WH;
                                   Synthetic
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                                                                                                                                                                                                                                                                                                   TR,
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                                                                                                                                                                                                                                                             (GERO-)
                                                                                                                                                                                      06-MAY-
                                                                                                                                                                                                                                                                           (UYTE-)
                                                                                                                                                                                                                         L4-AUG-
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HXXXH
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                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a primer from the present invention which describes human telomerase reverse transcriptase (hTRT). The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT cast compound is a modulator of hTRT, by detecting the change in hTRT cast combinant protein or polymuclecide, on administration of the compound; (B) preparation of hTRT with a telomerase by contacting a protein of the TRT with a telomerase BNA component; (C) detection of the TRT with a telomerase BNA component; (C) detection of the TRT with a telomerase BNA component; (C) detection of the TRT with a telomerase BNA component; (C) detection of the TRT with a telomerase of RNA detection, camplifying the product and correlating the presence of complex or amplification product with presence of hTRT in the sample, and (D) increasing the proliferation of a vertebrate cell by increasing hTRT castebrate cell proliferation to create a medicament that inhibits ageing. A protein preparation of hTRT and the polymuclectide encoding C hTRT can be used in the manufacture of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity and be used to the manufacture of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity and be used to the presence of the product of the new methods protein preparation of hTRT can also be used in the new methods
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                                                                                                                                                                                                                                                                                                                                        cell
                                                                                                                                                                                                                                                               Harley CB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 20; DB 2; Length 46; 100.0%; Pred. No. 54;
                                                                                                                                                                                                                                                               Chapman KB, Morin GB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 46 BP; 10 A; 12 C; 12 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Telomerase substrate utilisation primer 22-24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 200; 387pp; English
                                                                                                                                                                                                                                                              Lingner J, Nakamura T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TTTTGGGGTTTTGGGGTTTT 20
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                                                                                                                        97US-00844419.
97US-00846017.
97US-00851843.
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97US-00911312.
97US-00912951.
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UNIV TECHNOLOGY CORP.
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                                                                                     97GB-00020890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
              Homo sapiens
                                                                                     01-OCT-1997;
                                                                                                                                                            09-MAY-1997;
14-AUG-1997;
14-AUG-1997;
14-AUG-1997;
                                    GB2317891-A
                                                                                                              01-OCT-1996
                                                                                                                                    25-APR-1997
06-MAY-1997
                                                                                                                           18-APR-1997
                                                                                                                                                                                                                                                                             Andrews WH;
 Synthetic
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                                                                                                                                                                                                                         (GERO-)
                                                                                                                                                                                                                                        (UYTE-)
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The present sequence represents a primer from the present invention which describes human telomerase reverse transcriptase (hTRT). The present invention also describes the following methods: (A) determining whether a teecombinant protein or hTRT, by detecting the change in hTRT recombinant protein or polynucleotide, on administration of the compound; (C) preparation of recombinant telomerase by contacting a protein of the preparation of the compound; (C) detection of the hTRT with a telomerase RNA component; (C) detection of the hTRT RNA or protein in a sample by binding a relevant probe to the sample of hTRT RNA or protein in a sample by binding a relevant probe to the sample complex formed or in the case of RNA detection, and detecting the product and correlating the presence of hTRT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing hTRT camplification product with presence of hTRT in the sample; and (D) corrected and correlating the proliferation of a vertebrate cell by increasing hTRT caperate cell proliferation to create a medicament that inhibits ageing. A protein preparation of hTRT and the polynucleotide encoding the reflect of ageing or cancer. Inhibitors of felomerase activity and the new methods activity. A protein preparation of hTRT can also be used in the new methods
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Human, telomerase reverse transcriptase, hTRT; TRT; diagnosis; prognosis; cell proliferation; cancer; ageing; ribonucleoprotein; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harley CB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morin GB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 48 BP; 10 A; 14 C; 12 G; 12 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 200; 387pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lingner J, Nakamura T,
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97US-00846017.
97US-00851843.
97US-00854050.
97US-00911312.
97US-00912951.
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Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis;

Telomerase substrate utilisation primer 19-21.

13-AUG-1998 (first entry)

AAV17006;

cell proliferation; cancer; ageing; ribonucleoprotein; primer; ss.

Homo sapiens.

Synthetic

GB2317891-A 08-APR-1998

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The present sequence represents a primer from the present invention which describes human telomerase reverse transcriptase (hTRT). The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT recombinant protein or polynucleotide, on administration of the compound; (B) preparation of recombinant telomerase by contacting a protein or protein in a sample by binding a relevant probe to the sample hTRT RNA or protein in a sample by binding a relevant probe to the sample of hTRT RNA or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of RNA detection, and detecting the product and correlating the presence of complex or amplification product with presence of hTRT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing hTRT amplification product with presence of magine and increase in cell certebrate cell proliferation to create a medicament that inhibits ageing. A protein preparation of hTRT and the polynucleotide encoding hTRT can be used in the manufacture of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity can be used to treat conditions that are associated with high telomerase activity. A protein preparation of hTRT can also be used in the new methods
                                                     Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis; cell proliferation; cancer; ageing; ribonucleoprotein; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harley CB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 48 BP; 10 A; 14 C; 12 G; 12 T; 0 U; 0 Other;
                  Telomerase substrate utilisation primer 13-15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 200; 387pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cech TR, Lingner J, Nakamura T,
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97US-0084419.
97US-00846017.
97US-00851843.
97US-00954050.
97US-0091312.
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                                                                                                                                      Homo sapiens.
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06-MAY-1997
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14-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Andrews WH;
                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GERO-)
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The present sequence represents a primer from the present invention which describes human telomerase reverse transcriptase (hTRT). The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT recombinant protein or polymucleotide, on administration of the compound; (C) preparation of recombinant telomerase by contacting a protein preparation of hTRT with a telomerase RNA component; (C) detection of the hTRT with a telomerase RNA component; (C) detection of the hTRT with a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of RNA detection, and detecting the product and correlating the presence of hTRT in the sample; and (D) increasing the product with presence of hTRT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing hTRT camplification preparation of hTRT and the polynucleotide encoding hTRT can be used in the manufacture of medicament fat inhibiting the hTRT can be used in the manufacture of medicaments for inhibiting the ceffect of ageing or cancer. Inhibitors of telomerase activity can be used to treat conditions that are associated with high telomerase activity. A protein preparation of hTRT can also be used in the new methods
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Les 20; Conservative
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Matches
8
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variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing.

Example 1; Page 200; 387pp; English.

Pure and recombinant human Telomerase Reverse Transcriptase and its

Morin GB, Harley CB;

Chapman KB,

Nakamura T,

Lingner J,

Andrews WH;

Cech

WPI; 1998-171633/16.

UNIV TECHNOLOGY CORP.

GERON CORP

GERO-) UYTE-)

14-AUG-1997;

14-AUG-1997

96US-00044419-97US-008446119-97US-00846017-97US-00854050-97US-00911312-97US-00915503-

97GB-00020890

01-OCT-1997;

01-OCT-1996 35-APR-1997 09-MAY-1997 14-AUG-1997 06-MAY-1997

RESULT 20

Gaps

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0; Indels

100.0%; Score 20; DB 2; Length 48; 100.0%; Pred. No. 54;

0; Mismatches

Local Similarity 100 nes 20; Conservative

Matches

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Query Match

48

53

AAV17006 standard; DNA; 50 BP

RESULT 19
AAV17006
ID AAV17
XX

1 TTTTGGGGTTTTGGGGTTTT 20

ADF69702

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The present invention relates to a method for detecting differential methylation patterns in an helicase-like transcription factor (HLTF, also called HIPPIGA, Zbul, RUSHIA and Smarca) nucleotide sequence. The method involves obtaining samples from a patient and a healthy subject, assaying the samples for the presence of methylation within a nucleotide sequence and comparing the methylation patterns in the sample from the subject to those in the normal sample. HLTF modulator is useful for treating an HLTF-associated proliferative disease in a subject, where the disease is associated with methylation of an HLTF nucleic acid sequence, i.e. colon neoplasia and the compound induces HLTF expression. The method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention is useful in gene therapy. The present sequence is the human HLTF 5' unmethylated DNA fragment amplifying PCR primer.
                                                                                                                                                                                                                                                        Detecting differential methylation patterns in an HLTF nucleotide sequence, useful for diagnosing or treating colon neoplasia, comprises assay samples for the presence of methylation within a specific nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA methylation; HLTF; helicase-like transcription factor; HIP116a; RUSH1a; Smarca; proliferative disease; colon neoplasia; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human HLTF unmethylated DNA amplifying forward PCR primer, 1347UF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 29 BP; 1 A; 0 C; 9 G; 19 T; 0 U; 0 Other;
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Pred. No. 2.4e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                      Example; SEQ ID NO 50; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TTTTGGGGTTTTGGGGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 Trirgegerrireregrirr 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-OCT-2001; 2001US-0327537P.
                                         07-OCT-2002; 2002US-00266103.
                                                                                  05-OCT-2001; 2001US-0327537P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-OCT-2002; 2002US-00266103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 95.0%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADV09348 standard; DNA; 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-FEB-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer; gene therapy; ss
                                                                                                                             (MARK/) MARKOWITZ S D.
                                                                                                                                                                                                                    WPI; 2005-011663/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2005-011663/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MARK/) MARKOWITZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2004242510-A1
                                                                                                                                                                        Markowitz SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Markowitz SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-DEC-2004
02-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADV09348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes the human SLC5AB protein (I), which is a cell surface protein. (I) has cytostatic activity, and can be used in gene therapy. (I) can be used in detecting and treating SLC5AB-associated cancer. e.g. colon cancer, breast cancer, thyroid cancer or stomach cancer. (I) is also useful in screening assays, predictive medicine and in diagnostic and prognostic assays. The human SLC5AB gene is located on chromosome 12. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA methylation, HLTF; helicase-like transcription factor; HIP116a; Zbul; RUSH1a; Smarca; proliferative disease; colon neoplasia; cytostatic; PCR;
                                                                                                                                                                                           human; SLC5A8; cell surface protein; cytostatic; gene therapy; SLC5A8-associated cancer; colon cancer; breast cancer; thyroid cancer; stomach cancer; HLTF; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human HLTF 5' unmethylated DNA amplifying PCR primer, P-HLTF1347UF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New SLCSA8 polypeptide, useful for detecting and treating SLCSA8-associated cancer, e.g. colon, breast, thyroid or stomach cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 29 BP; 1 A; 0 C; 9 G; 19 T; 0 U; 0 Other;
                                                                                                                                                    Human HLTF methylation detection PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYCA-) UNIV CASE WESTERN RESERVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 77; Page 99; 207pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TTTTGGGGTTTTGGGGTTTT 20
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                      BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADV09385 standard; DNA; 29 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUN-2003; 2003WO-US018239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUN-2002; 2002US-0386653P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 95.0%;
Matches 19; Conservative
                      ADF69702 standard; DNA; 29
                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RUSHla; Smarca; prolifera
primer; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-062348/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention.
                                                                                                                                                                                                                                                                                                                                                    WO2003104427-A2
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                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Markowitz SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-FEB-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                         11-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                             18-DEC-2003
                                                                                                                                                                                                                                                                                      Synthetic
                                                               ADF69702;
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RESULT 21
ADV09385
ID ADV09385
XX
XX
DT 24-FE
XX
EN DB Human
XX
KW DNA m
KW RUSH1
KW Prime
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KW POOD
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KW POOD
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KW RUSH1
KW Prime
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KW Prime
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Gaps

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Length 29; Indels

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                                                                                                                                                                                                                                      The present invention relates to a method for detecting differential methylation patterns in an helicase-like transcription factor (HITF, also called HIP116a, ZDu1, RUSH1a and Smarca) nucleotide sequence. The method involves obtaining samples from a patient and a healthy subject, assaying the samples for the presence of methylation within a nucleotide sequence and comparing the methylation patterns in the sample from the subject to those in the normal sample. HITF modulator is useful for treating an HITF associated proliferative disease in a subject, where the disease is associated with methylation of an HITF mucleic acid sequence, i.e. colon neoplasia and the compound induces HITF expression. The method of the invention is useful in gene therapy. The present sequence is the human invention is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT28317-T28347 represent multi-G oligonucleotides. AAT28336-T28347 are multi-G oligonucleotides with multiple G strings, or G strings of 4 bases and over. These sequences are oligonucleotides of the invention. These sequences can be modified to become more nuclease resistant, using phosphorothioate, phosphorodithioate, or 3'-carbon modified links. To
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Multi-G oligonucleotide; antisense sequence; c-myb; nuclease resistant; phosphorothioate linkage; phosphorodithioate linkage; inhibitor; therapy; cell proliferation; smooth muscle cell; proliferation protein; vascular restenosis; arterial restenosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New modified oligo:nucleotide(s) contg. consecutive guanine residues -inhibit proliferation of smooth muscle cells, esp. to prevent arterial restenosis.
Detecting differential methylation patterns in an HLTF nucleotide sequence, useful for diagnosing or treating colon neoplasia, comprises assay samples for the presence of methylation within a specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 29 BP; 1 A; 0 C; 9 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unmethylated DNA amplifying PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Multi-G oligonucleotide T3-G4-T4-G4-T3.
                                                                                                                                                                            Claim 10; SEQ ID NO 13; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fisher EF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TTTTGGGGTTTTGGGGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT28342 standard; DNA; 18 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 95.0
les 19; Conservative
                                                                                                             nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-209848/21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-NOV-1996
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AAT28342
AAT28342
XX
AC AAT28
XX
DT 20-NO
XX
DX
DE Multi
XX
Multi
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cultured smooth muscle cells that are arrested in the GO phase, are induced to proliferate in the presence of the multi-G sequence. The cultured smooth muscle cells used in this method are attached to a solid support, and growth arrest is achieved on a starvation medium, followed by transfer to a normal growth medium to induce proliferation. The compounds that provide over 50% inhibition at a set dosage are selected as being useful for inhibiting vascular restenosis. The multi-G oligonucleotides are used to inhibit proliferation of smooth muscle cells, such as to prevent arterial restenosis. These sequences are not antisense sequences, but are thought to work in a similar way. The sequences are thought to act by binding to protein in similar way. The proliferation process. Compounds containing these multi-G oligonucleotides are not toxic, and their effect on cell proliferation is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, telomerase reverse transcriptase, hTRT; TRT; diagnosis; prognosis; cell proliferation; cancer; ageing; ribonucleoprotein; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a primer from the present invention which
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                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of oppoliferation conditions especially cancer and ageing.
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                                                                                                                                                                                                                                                                               Score 18; DB 2; Length 18;
Pred. No. 3.4e+02;
                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                     Sequence 18 BP; 0 A; 0 C; 8 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Telomerase substrate utilisation primer 19-21.
                                                                                                                                                                                                                                                                                          100.0%; Prec. ....
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                                                                                                                                                                                                                                                                                                                                               2 TITGGGGTTTTGGGGTTT 19
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970S-00846017.
970S-00851843.
970S-0091312.
970S-00912951.
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                                                                                                                                                                                                                                                                                    90.06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV17006 standard; DNA; 50
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
....heg 18, Conservative
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                                                                                                                                                                                                                        fully reversible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1997;
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Andrews WH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV17006;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYTE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 24
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the sequence AATT. (Updated on 25-MAR-2003 to correct PN field.)

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describes human telomerase reverse transcriptase (hTRT). The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT by detecting the change in hTRT recombinant protein or polynuclectide, on administration of the compound; (B) preparation of recombinant telomerase by contacting a protein properation of hTRT with a telomerase RNA component; (C) detection of the TRT RNA or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of RNA detection, amplifying the product and correlating the presence of complex or amplification product with presence of hTRT in the sample, and (D) increasing the proliferation of a vertebrate cell by increasing hTRT expression; and (E) the use of an agent that causes an increase in cell vertebrate cell proliferation to create a medicament that inhibits or ageing. A protein preparation of hTRT and the polynucleotide encoding hTRT can be used in the manufacture of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity can be used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                high telomerase activity. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New oligo:nucleotide(s) forming triple helix with target nucleic acid contain purine and pyrimidine tracts in specific orientations, useful therapeutically or diagnostically e.g. for inactivating HIV RNA, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein preparation of hTRT can also be used in the new methods
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.0%; Score 18; DB 2; Length 50; 100.0%; Pred. No. 3.5e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 50 BP; 12 A; 14 C; 12 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treat conditions that are associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example; Fig 14a; 101pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18
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92US-00826934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TITIGGGGTTITGGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ44008 standard; DNA; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Johnston BH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Marches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1993-214172/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Target sequence #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (STRI ) SRI INT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9312230-A1
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28-OCT-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ44008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic oligo-nucleotide(s) which bind target duplex DNA - forming colinear triplex to control transcription process in gene-specific fashion.
                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                  Sequence binding to and inhibiting the gene controlling Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                             C-myc; cancer; HIV-1; AIDS; collagenase; Alzheimers disease; EGF; epidermal growth factor; GSTpi; HMGCoA; thallasemia; Herpes simplex virus; nerve growth factor receptor; globin; ss.
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Pred. No. 1.1e+03;
0; Mismatches 2; Indels
                                                           26;
                                                                                       1; Indels
                                                      Score 17.4; DB 2; Length Pred. No. 6e+02; 0; Mismatches 1; Indels
                            Sequence 26 BP; 2 A; 1 C; 13 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 28 BP; 0 A; 0 C; 9 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 35; Page 30; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITITIGGITITIGGGGTTTT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TTTTGGGGTTTTGGGGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                      2 TTTGGGGTTTTGGGGTTTT 20
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                                                                                                                                                                                                                            BP.
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90.0%;
                                                         ch 87.0%;
1 Similarity 94.7%;
18; Conservative
                                                                                                                                                                                                                            AAQ04992 standard; DNA; 28
                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                     disease plague formation.
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                                                                                                                                                                                                                                                                                         (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kessler DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1990-195509/26.
                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HOGA/) HOGAN M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-DEC-1988;
                                                                                                                                                                                                                                                                                       25-MAR-2003
31-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-JUN-1990.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
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                                                                                                                                                                                                                                                          AAQ04992;
                                                                                       Matches
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8 X G
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The APP770 gene is the precursor protein responsible for production of plaque in Alzheimer's disease. Expression of this gene may be prevented by the formation of a triplex between the duplex target DNA sequence and an anti parallel or parallel synthetic oligonucleotide. A suitable target sequence is that from base -434 to -407 of the APP770 gene and a suitable antiparallel synthetic oligonucleotide sequence is shown. See also AAQ36219-362. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis;
                                                                                                                                                                 Synthetic oligo-nucleotide(s), prodn. useful e.g. for HIV-1 inhibition which bind to target sequence in duplex DNA forming colinear triplex by binding to major groove.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Morin GB, Harley CB;
                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell proliferation; cancer; ageing; ribonucleoprotein; primer;
                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                        84.0%; Score 16.8; DB 2; Length 90.0%; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                 Sequence 28 BP; 0 A; 0 C; 9 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chapman KB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Telomerase substrate utilisation primer 28-30
                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lingner J, Nakamura T,
                                                                                                                                                                                                                    Example 6; Col 22; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                             1 TTTTGGGGTTTTGGGGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                            (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96US-00724643.
97US-00846119.
97US-00846117.
97US-00854050.
97US-0091312.
97US-00912551.
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                                     89US-00453532
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                                                             88US-00287359
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ID AAV17009 standard; DNA; 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                               Kessler DJ;
                                                                                                                                         WPI; 1993-035718/04
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                                     22-DEC-1989;
                                                               20-DEC-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-AUG-1997;
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            05-JAN-1993
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25-APR-1997
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                                                                                                               Hogan ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV17009;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GERO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYTE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The APP770 gene is the precursor protein responsible for production of plaque in Alzheimer's disease. Expression of this gene may be prevented by the formation of a triplex between the duplex target DNA sequence and an anti parallel or parallel synthetic oligonucleotide. A suitable target sequence is that from base -434 to -407 of the APP770 gene and a suitable parallel synthetic oligonucleotide sequence is shown. See also AAQ36219-362. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alzheimer's disease; amyloid precursor protein; plaque; triplex; target;
                                                                                                                                                     Alzheimer's disease; amyloid precursor protein; plaque; triplex; target;
                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic oligo-nucleotide(s), prodn. useful e.g. for HIV-1 inhibition which bind to target sequence in duplex DNA forming colinear triplex by binding to major groove.
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Pred. No. 1.1e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 28 BP; 0 A; 0 C; 9 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APP4anti, targetted to a region of APP770 gene.
                                                                                                                              APP4par, targetted to a region of APP770 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 6; Col 22; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTTGGGGTTTTTGGGGTTTT 20
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                                     AAQ36268 standard; DNA; 28 BP.
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90.0%;
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                                                                                                    (first entry)
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Best Local Similarity 90..
Local 18; Conservative
                                                                                        (revised)
                                                                                                                                                                                                                                                                                                                                                   Kessler DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
                                                                                                                                                                                                                                                                                                                                                                          WPI; 1993-035718/04.
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                                                                                                                                                                                                                                                                       22-DEC-1989;
                                                                                                                                                                                                                                                                                                20-DEC-1988;
                                                                                       25-MAR-2003
07-JUN-1993
                                                                                                                                                                                                                    US5176996-A
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07-JUN-1993
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                                                                                                                                                                                                                                             05-JAN-1993
                                                                                                                                                                   duplex; ss
                                                                                                                                                                                                                                                                                                                                                  Hogan ME,
                                                                                                                                                                                            Synthetic.
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                                                               AAQ36268
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(UYTE-) UNIV TECHNOLOGY CORP.
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AAV17007/c
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                                                                                                                                                                                                                                                                                                                      The present sequence represents a primer from the present invention which describes human telomerase reverse transcriptase (hTRT). The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT recombinant protein or polymucleotide, on administration of the compound; (B) preparation of recombinant telomerase by contacting a protein or protein in a sample by binding a relevant probe to the sample hTRT RNA or protein in a sample by binding a relevant probe to the sample of hTRT RNA or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of RNA detection, amplification product with presence of hTRT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing hTRT captebrate cell proliferation to create a medicament that inhibits ageing. A protein preparation of hTRT and the polymucleotide encoding hTRT can be used in the manufacture of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity can be used to the asset of the lower of the lower activity. A protein preparation of hTRT can also be used in the new methods
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                                                                                                                               Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 44 BP; 10 A; 10 C; 12 G; 12 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                      Example 1; Page 200; 387pp; English
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970S-00846017.
970S-00851843.
970S-00911312.
970S-00912951.
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                                                                    WPI; 1998-171633/16.
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06-MAY-1997;
09-MAY-1997;
14-AUG-1997;
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AAV17008/C
ID AAV17
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AC AAV17
XX
DT 13-At
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DT 13-At
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DT 13-At
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DT 13-At
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DS Huma
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The present sequence represents a primer from the present invention which describes human telomerase transcriptase (hTRT). The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT test compound is a modulator of hTRT, by detecting the change in hTRT crecombinant protein or polynucleotide, on administration of the compound; (C) preparation of hTRT with a telomerase by contacting a protein of the hTRT with a telomerase By contacting a protein of the hTRT with a telomerase By contacting a protein of the hTRT with a telomerase RNA component; (C) detection of the hTRT RNA or protein in a sample by binding a relevant probe to the sample complex formed or in the case of RNA detection, and detecting the product and correlating the presence of complex or amplification product with presence of hTRT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing hTRT can agent that causes an increase in cell capters ageing. A protein preparation of hTRT and the polynucleotide encoding the treat conditions that are associated with high telomerase activity. A protein preparation of hTRT can also be used in the new methods
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cell proliferation; cancer; ageing; ribonucleoprotein; primer; ss.
                                                                                                                                                                                           variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing.
Harley CB;
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   Chapman KB, Morin GB,
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   Lingner J, Nakamura T,
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97US-0084419.
97US-0081617.
97US-00851843.
97US-0091312.
97US-00911312.
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Matches 18; Conservative
                                                                                                   WPI; 1998-171633/16.
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14-AUG-1997;
14-AUG-1997;
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06-MAY-1997
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                                  Andrews WH;
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   Cech TR,
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ABZ05743;
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                                                                                                                                                                                   Cech TR,
                                                                                                               GERO-)
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                                                                                                               Harley CB;
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                                                                                                                  Chapman KB, Morin GB,
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                                                                                                               Lingner J, Nakamura T,
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  97US-00915503
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AAV17004 standard; DNA; 48
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                                                GERON CORP.
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  14-AUG-1997;
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25-APR-1997;
06-MAY-1997;
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                                                                                                                  Cech TR, L
Andrews WH;
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Best Local S
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                                                                    (UYTE-)
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AAV17004/C
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The present sequence representations by present the present into present and secribes human telomerase reverse transcriptase (hTRT). The present invention also describes the following methods: (A) determining whether a cast compound is a modulator of hTRT, by detecting the change in hTRT recombinant protein or polymucleotide, on administration of the compound; (B) preparation of recombinant telomerase by contacting a protein or preparation of hTRT with a telomerase by contacting a protein of the hTRT RNA or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of RNA detection, amplification product with presence of hTRT in the sample; and (D) increasing the presence of hTRT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing hTRT certebrate cell proliferation to create a medicament that inhibits againg. A protein preparation of hTRT and the polymucleotide encoding C hTRT can be used in the manufacture of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity can be used to treat conditions that are associated with high telomerase activity. A protein preparation of hTRT can also be used in the new methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present sequence represents a primer from the present invention which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; leukocyte; gene expression profiling; allograft rejection; atherosclerosis; congestive heart failure; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing.
                                                                                                                                                                                                                                                                                                                         Chapman KB, Morin GB, Harley CB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 200; 387pp; English.
                                                                                                                                                                                                                                                                                                                     Lingner J, Nakamura T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TTTTGGGGTTTTGGGGTTTT 20
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97US-00854050.
97US-00911312.
97US-00912951.
97US-00915503.
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                                                                                                                                                                                                                                          UNIV TECHNOLOGY CORP.
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Matches 18; Conservative
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                                                                                                                                                                                                    GERON CORP
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                                                                                                                         14-AUG-1997;
                                                                               4-AUG-1997;
                                              14-AUG-1997;
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WO200023604-A1.
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                                                                                                                                                                                                                                                                                                                                           invention
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                                                                                                                                                                                                                                                                                                                                       The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ00812) each having 50 base pairs (bp). The system is useful for leukocyte expression profiling. It is particularly useful for flagmosting a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient, predicting disease complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
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                                                                                                                                                                                                              New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.
                                                                                                       Prentice J, Phillips J;
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    lemnae alphal-tubulin telomerase primer DNA.

                                                                                                       Altman P, P; Johnson F;
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                                                                                                       muth J, Fry K, Matcuk G, A
Woodward R, Quertermous T,
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                                                                                                                                                                                                                                                                                                   Claim 1; Page 513; Opp; English.
20-OCT-2000; 2000US-0241994P 08-JUN-2001; 2001US-0296764P
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98DE-01048486
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nes 18; Conservative
                                                              (BIOC-) BIOCARDIA INC.
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                                                                                                                                                                   WPI; 2002-636525/68
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                                                                                                         Wohlgemuth J,
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protists comprises a sequence (I) encoding a protein and having, at its 3, and 5, ends, native flanking regulatory sequences (RS) selected from stylonychia lemmes and with terminal telomeric sequences. (A) are used for production of proteins in protists, particularly functional heterologous proteins. (A) provide overexpression of foreign proteins in protists, e.g. at 7-15% of total proteins. Bukaryotic protists can be grown simply and on a large scale to high cell density with short generation times and have metabolic and other properties similar to those of multicellular organisms (contrast prokaryotes). In the macronucleus genome of protists, most genes are amplified, resulting in high expression rates even under normal conditions. This sequence represents a primer used in the construction of the expression vector described in the
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                                                                           for eukaryotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 16; DB 3; Length 20;
Pred. No. 2.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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    lemnae expression vector construct primer XbaApatel.

                                                                           This invention describes a novel expression vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 8 A; 12 C; 0 G; 0 T; 0 U; 0 Other;
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Claim 4; Page 45; 51pp; German.
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Les 16; Conservative
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Sequence 19 BP; 11 A; 8 C; 0 G; 0 T; 0 U; 0 Other;

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of multicellular organisms (contrast prokaryotes). In the macronucleus genome of protists, most genes are amplified, resulting in high expression rates even under normal conditions. This sequence represents a primer used in the construction of the expression vector described in the
                                                                                                            invention
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Sequence 30 BP; 10 A; 13 C; 5 G; 2 T; 0 U; 0 Other;

ö Score 16; DB 3; Length 30; Pred. No. 2.3e+03; 0; Indels 80.0%; Scor. 100.0%; Pred. No. ... 0; Mismatches 16 rrrrececriricese 13 TTTTGGGGTTTTGGGG Conservative Local Similarity les 16; Conserv ~ 28 Query Match Matches 셤 ઠે

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Gaps

ADV45884 standard; DNA; 19

ВЪ ADV45884; Human CpG site probe SEQ ID NO 1411.

(first entry)

10-MAR-2005

DNA methylation; 88; probe; cancer; neoplasm; squamous cell carcinoma.

Homo sapiens

WO2004110246-A2.

23-DEC-2004.

14-MAY-2004; 2004WO-US015382.

15-MAY-2003; 2003US-0471488P.

(ILLU-) ILLUMINA INC.

Bibikova M; Fan J,

WPI; 2005-057693/06

Identifying differentially methylated genomic CpG dinucleotide sequences associated with cancer, comprises measuring level of methylated genomic CpG dinucleotide sequences for genomic targets in sample and comparing to reference level.

Example 4; Page 17; Opp; English.

Claim 28; SEQ ID NO 1411; 89pp; English.

The invention relates to a mehtod of identifying differentially methylated genomic CpG dinucleotide sequences associated with cancer, comprising measuring the level of methylated genomic CpG dinucleotide equences for two or more of the genomic targets in sample, and comparing the level of methylation at genomic CpG dinucleotide sequences in the sample to a reference level of methylated genomic CpG dinucleotide sequences in the sample to a reference level of methylated genomic CpG dinucleotide sequences associated with cancer in an individual. The level of methylation of the differentially methylated genomic CpG dinucleotide sequences is used to diagnose cancer in the individual, predict the course of cancer, predict the susceptibility of cancer, stage the progression of cancer, predict the likelihood of overall survival, and predict the likelihood of recurrence of cancer for individual. The level of methylation of the differentially methylated genomic CpG dinucleotide sequences in the sample is also used to determine the effectiveness of a treatment course undergone by the individual. The cancer is preferably adenocarcinoma or squamous cell carcinoma. The probes are useful for detecting methylation of genomic CpG dinuclectide sequences of two or more genomic targets. The present sequence represents a CpG site probe. 

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Detecting an indicium of a disease in a heterogeneous biological sample comprises contacting the nucleic acid sample with an agent that modifies unmethylated cytosine, and detecting hypermethylated or hypomethylated
                                                                                                                                                                        Disease diagnostic, CpG; nucleic acid amplification; cancer detection; p14; HLTF; MINT31; MINT2; methylation; PCR; primer; 88.
                  Gaps
                  ö
Length 19;
                  Indels
77.0%; Score 15.4; DB 14; 94.1%; Pred. No. 3.9e+03; iive 0; Mismatches 1;
                                                                                                                                                       HLTF non-methylation-specific PCR forward primer.
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                                                                                                                                                                                                                                                           11-APR-2003; 2003WO-US011023.
                                                                                                                                                                                                                                                                            11-APR-2002; 2002US-00123071.
                                                      recentritecertrr 3
                                    4 TGGGGTTTTGGGGTTTT
                                                                                                   ACF58129 standard; DNA; 43
                                                                                                                                     15-JAN-2004 (first entry)
                    Conservative
                                                                                                                                                                                                                                                                                             (EXAC-) EXACT SCI CORP
                                                                                                                                                                                                                                                                                                                                WPI; 2003-845337/78.
Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                      WO2003087390-A2
                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                             nucleic acid.
                                                                                                                                                                                                                                        23-OCT-2003
                                                                                                                                                                                                                                                                                                                Shuber AP;
                                                                                                                    ACF58129;
                                                                                RESULT 37
                                                                                          ACF58129
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The invention relates to detecting an indicium of a disease in a heterogeneous biological sample. The method involves (a) isolating a heterogeneous nucleic_acid sample comprising a CpG-containing target template from a heterogeneous biological sample; (b) contacting the nucleic acid sample with an agent that modifies unmethylated cytosine; (c) performing an amplification reaction on the target template using at least one chimeric primer that comprises a first portion that is not specific for the target template and a second portion, where the second portion is specific for the first or option, where the second portion is specific for the CpG-containing target template if the template comprises an unmodified cytosine at predetermined position; and (d) detecting the presence of an amplification product as an indicium of a disease. The method is useful for detecting indicia of cancer in a biological sample, for detecting cancer detection, for infectious disease diagnostics. The new method makes it possible to detect a disease disease diagnostics. The new method makes it possible to detect a disease according of hypermethylation at multiple loci, which milling and makes it possible to detect a disease assaying of hypermethylation at multiple loci, which indicate a higher risk of colorectal cancer

Sequence 43 BP; 4 A; 5 C; 16 G; 18 T; 0 U; 0 Other;

Query Match

77.0%; Score 15.4; DB 10; Length 43;

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                                                                                                                                                     mixed lineage kinase; MLK; asthma; at-risk haplotype; MAP3K9; antiasthmatic; respiratory-gen.; antinflammatory; antirheumatic; antipsoriatic; neuroprotective; gastrointestinal-gen.; respiratory disease; chronic obstructive pulmonary disease; chronic botructive pulmonary disease; chronic bronchitis; inflammation; ss; primer; PCR.
         Gaps
         ;
0
         Indels
         1;
                                                                                                                                      MAP3K9 marker amplification reverse primer #1146.
Pred. No. 4e+03;
         0; Mismatches
                                                                                                                                                                                                                                                                                                                      Hakonarson H, Gurney ME, Halapi E;
                         20
                                                                                     BP
                                                                                                                                                                                                                                                                           14-JUL-2003; 2003US-0487072P. 05-APR-2004; 2004US-0559611P.
                                                                                                                                                                                                                                                           14-JUL-2004; 2004WO-US022446.
94.1%;
                                                                                                                                                                                                                                                                                                     (DECO-) DECODE GENETICS EHF.
                          4 TGGGGTTTTGGGGTTTT
                                           TGGGGTTTTGTGGTTTT
                                                                                     ADW84828 standard; DNA; 20
                                                                                                                       (first entry)
         16; Conservative
                                                                                                                                                                                                                                                                                                                                      WPI; 2005-122681/13.
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                         WO2005007144-A2.
                                                                                                                                                                                                        Unidentified.
                                                                                                                      07-APR-2005
                                                                                                                                                                                                                                          27-JAN-2005.
                                                                                                      ADW84828;
                                                                    RESULT 38
ADW84828/c
                                                                                     셤
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The invention relates to the movel use of a mixed inhase (mix.)

associated with a risk factor selected from an at-risk haplotype for associated with a risk factor selected from an at-risk haplotype for associated with a risk factor selected from an at-risk haplotype for asthma, at-risk haplotype in MAR3K9 gene, polymorphism in MAR3K9 mucleic acid, dysregulation of MAR3K9 much expression, dysregulation of MAR3K9 much expression. The invention of much of complex comprises: a method for the diagnosis or identification of usceptibility to asthma a method for the diagnosis or identification of many of complex comprises; a method for assessing the response to treatment with an Much family kinase mucleic acid inhibitor in a target population or in an ample; a method for assessing the response to treatment with an Much an at-risk haplotype for asthma, at-risk haplotype in the MAR3K9 mucleic acid, dysregulation of MAR3K9 gene, polymorphism in the MAR3K9 mucleic acid, dysregulation of MAR3K9 gene, polymorphism in the MAR3K9 mucleic acid, dysregulation of MAR3K9 gene, polymorphism in the MAR3K9 mucleic acid, dysregulation of MAR3K9 gene, polymorphism in the MAR3K9 mucleic acid, dysregulation of MAR3K9 gene, polymorphism in the MAR3K9 mucleic acid, dysregulation of treatment with an Much inhibitor in a target population including an individual with an at-risk haplotype for asthma, as above; a kit for assaying a sample for the presence or assessing the response to individual with an Much inhibitor in a target population including an individual with an at-risk haplotype for asthma, as above; a kit for assaying a sample for the presence or absence of at least one haplotype comprising 2 or more alleles associated with asthma comprising: at least one specific allele; a reagent kit for assaying the presence of at least one haplotype comprising 2 or more alleles associated were alleles associated with a second mucleic acid capable of detecting at least one specific allele; a reagent selecting at least one appecific alleles assoc Use of mixed lineage kinase family kinase inhibitor in the manufacture of a medicament for treatment of asthma associated at-risk haplotype for asthma, at-risk haplotype in MAP3K9 gene or increased MLK1 protein expression or activity. The invention relates to the novel use of a mixed lineage kinase (MLK) Disclosure; Fig 12; 640pp; English.

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cherecting 2 or more beging activities: antiaethmatic, respiratory chinase inhibitor has the following activities: antiaethmatic, respiratory gen., antinflammatory, antirheumatic, antiarthmitic, antipsoriatic, gen., antinflammatory antirheumatic, antiarthmitic, antipsoriatic, inhibitor is useful for the treatment of asthma associated with a risk inhibitor is useful for the treatment of asthma associated with a risk factor selected from at-risk haplotype for asthma, at-risk haplotype in MAPRY 9 mcMa. Activity and/or increased management of cusceptibility to asthma. The inhibitor is also useful for the treatment of other respiratory diseases associated with MAPRY or other members of the JMK pathway such as chronic obstructive pulmonary disease. chronic bronchitis and other inflammatory diseases such as rheumatoid arthritis, polymuclocide sequence represents a reverse primer which is used in amplifying a marker of the MAPRY sinase, where MAPRY is used in the management of management o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting and/or differentiating prostate cell proliferative disorders in a subject by contacting genomic with reagent(s) that distinguishes between methylated and non-methylated CpG dinucleotides in target nucleic
the haplotype, and reagents for detection of the label, and a reagent kit for assaying a sample for the presence of at least one haplotype comprising 2 or more alleles comprising: at least one nucleotide sequence that is at least partially
                                                                                                                                                               complementary to a part of nucleotide sequence of MAP3K9, capable of acting as a primer for a primer extension reaction and capable of detecting 2 or more specific alleles of the haplotype. The MLK family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell proliferation; hyperproliferation; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŝ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 BP; 11 A; 8 C; 0 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.0%; Score 15.2; DB 14;
85.0%; Pred. No. 4.7e+03;
ive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prostate cancer gene PCR primer SEQ ID NO 376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TTTTGGGGTTTTGGGGTTTT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
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10-MAY-2004; 2004EP-00090187.
21-JUL-2004; 2004EP-00090292.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2004; 2004WO-US040289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2003; 2003EP-00090414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEA51773 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-AUG-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neoplasm; PCR; primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2005-425434/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EPIG-) EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Devos T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cottrell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2005054517-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-JUN-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 39
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The invention relates to a novel quantitative method for adding linear polynucleotide to solution containing a cation. The linear polynucleotide contains telomere repeat sequence with donor at one edge portion and acceptor at another edge portion. The optical detection is performed using this linear polynucleotide. The method of the invention is useful in medical fields such as clinical laboratory test and fields with cation fixed assay. The present sequence is used in the exemplification of the
adding linear polynucleotide containing telomere repeat sequence wi
donor and acceptor at edge portions, to solution containing cation.
                                                                                                                                                                                                                                                                                                       Sequence 31 BP; 3 A; 0 C; 16 G; 12 T; 0 U; 0 Other;
                                                                 Disclosure; Page 16; 8pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TTTTGGGGTTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 rrragggrirraggggrir 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADJ94145 standard; DNA; 36 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                             17; Conservative
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                  invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADJ94145;
                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 41
    FFX8X500000000X8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                             The invention describes a method of detecting and/or differentiating between prostate cell proliferative disorders in a subject comprising contexting genomic DNA isolated from a biological sample with at least contexting genomic DNA isolated from a biological sample with at least cone reagent, or series of reagents that distinguishes between methylated cone reagent, or series of reagents that distinguishes between methylated cone reagent mucleic acids e.g. HISTONE H4. Also described are: a treated mucleic acids e.g. HISTONE H4. Also described are: a treated concerts at least on urmethylated cytosine base of the casponent DNA sequence to uracil or another base that is detectable comprising at lest 16 contiguous numberlocides of a treated genomic DNA sequences complementary to them; an oligomer comprising a sequence of sequence selected from SEQ ID NO: 60-295, 1029-1076, 1117-1120, 1172-1175 and sequences complementary to them; an oligomer comprising a sequence of at least 9 contiguous nucleotides that is complementary to, or hybridizes under moderately stringent or stringent conditions to a treated genomic DNA sequence above; as et of oligomers comprising at least two oligomer comprising at least two congrishing between or among prostate cell proliferative disorder of a distinguishing between or among prostate cell proliferative disorder of sensitive restriction enzyme, and at least one mucleic acid molecule or peptide nucleic acid molecule comprising a contiguous sequence at least of conflementary to, or hybridiazes under moderately criningent or stringent conditions to a sequence selected from SEQ ID NO: 60-295, 1029-1076, 1117-1120, 1172-1175 and their complements. The cuerbod, and discreting and/or differentiating between or among cell conditions to a sequence selected from SEQ ID NO: conflictative disorders. Hills sequence represents a primer used in the continue of gene encoding a prostate cell proliferation associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.0%; Score 15.2; DB 14; Length 22; 85.0%; Pred. No. 4.7e+03; ive 0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 22 BP; 3 A; 0 C; 7 G; 12 T; 0 U; 0 Other;
                                             Example 3; SEQ ID NO 376; 164pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TTTTGGAGTTATAGGGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTTGGGGTTTTGGGGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADJ94146 standard; DNA; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 85.0
es 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ94146;
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Matches
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ADJ94146
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Gaps

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Length 31; Indels

Score 15.2; DB 10; Pred. No. 4.8e+03; 0; Mismatches 3; 0; Mismatches

76.0%; 85.0%;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel quantitative method for adding linear polynucleotide to solution containing a cation. The linear polynucleotide contains telomere repeat sequence with donor at one edge portion and acceptor at another edge portion. The optical detection is performed using this linear polynucleotide. The method of the invention is useful in medical fields such as clinical laboratory test and fields with cation fixed assay. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                 Quantitative method of cation for clinical laboratory test, involves adding linear polynucleotide containing telomere repeat sequence with donor and acceptor at edge portions, to solution containing cation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 76.0%; Score 15.2; DB 10; Length 36; 1 Similarity 85.0%; Pred. No. 4.8e+03; 17; Conservative 0; Mismatches 3; Indels
                                                                                                                              ds; linear polynucleotide; cation; telomere repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 36 BP; 4 A; 0 C; 16 G; 16 T; 0 U; 0 Other;
                                                                                             Oligonucleotide of the invention #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 15; 8pp; Japanese.
                                                                                                                                                                                                                                                               05-DEC-2001; 2001JP-00371975
                                                                                                                                                                                                                                                                                                05-DEC-2001; 2001JP-00371975
                                                                                                                                                                                                                                                                                                                               TAKENAKA S.
TUM KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-639772/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                               JP2003169676-A.
                                                                                                                                                                                                                              17-JUN-2003
                                                                                                                                                                                                                                                                                                                               (TAKE/)
(TUMK-)
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ds; linear polynucleotide; cation; telomere repeat.

JP2003169676-A. Unidentified

17-JUN-2003.

Oligonucleotide of the invention #13

(first entry)

06-MAY-2004

Quantitative method of cation for clinical laboratory test, involves

05-DEC-2001; 2001JP-00371975. 05-DEC-2001; 2001JP-00371975

(TAKE/) TAKENAKA S. (TUMK-) TUM KENKYUSHO KK.

PI; 2003-639772/61

(first entry)

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Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic; munuostimulatory; tumour; viral infection; bacterial infection; tungal infection; cancer; asthma; infection; pacterial infection; munuostimulatory; immune deficiency; phosphorothicate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                             Vaccinating against tumors, infectious diseases, allergies and asthmausing immunostimulatory Py-rich and TG nucleic acids.
                                           Immunostimulatory nucleic acid #616.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 101; Page 52; 338pp; English
                                                                                                                                                                                                                                                                 25-SEP-1999; 99US-0156113P.
27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
                                                                                                                                                                                                                                     25-SEP-2000; 2000WO-US026383
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(COLE-) COLEY PHARM GMBH
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                                                                                                                                                                            WO200122972-A2.
             12-JUN-2001
                                                                                                                                                                                                        05-APR-2001.
                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                         Krieg AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ008152) each having 50 base pairs (bp). The system is useful for leukocyte expression profiling. It is particularly useful for predicting a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient, predicting disease complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus, rheeumatoid arthritis, osteoarthritis or cytomegalovirus infection
                                                                                                                                                                                                                    17, leukocyte; gene expression profiling; allograft rejection; atherosclerosis; congestive heart failure; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prentice J, Phillips
                                                                                                                                                                                          Human leukocyte gene expression profiling probe SEQ ID NO 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.0%; Score 15.2; DB 6; Length 50; 85.0%; Pred. No. 4.9e+03;
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, Johnson F;
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Woodward R, Quertermous T,
 TTTTGGGGTTTTGGGGTTTT 20
                 ||| ||||||||| ||| ||| TTTAGGGGTTT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 357; Opp; English.
                                                                                                    ABZ01038 standard; DNA; 50 BP
                                                                                                                                                                                                                                                                                                                                                                                                                   20-OCT-2000; 2000US-0241994P.
                                                                                                                                                                                                                                                                                                                                                                                      22-OCT-2001; 2001WO-US047856
                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BIOC-) BIOCARDIA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-636525/68.
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                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                              09-JAN-2003
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                                                                                                                                ABZ01038;
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Vollmer

Schetter C,

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The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acides can be pyrimidine rich (py-rich) or thymidine (T) rich The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae) had not compositive, bacterial antigens (e.g. toxoplasma, and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is stable useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Thi immune response and to activate immune cells. Note: the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24 BP; 0 A; 0 C; 7 G; 17 T; 0 U; 0 Other;
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Matches 16; Conserv
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1 TITIGGGGTITIGGGGTTTI

9 TTTTGTTATTTTGGGGTTTT 28

AAF99500 standard; DNA; 24 BP

RESULT 43
AAF99500
ID AAF99
XX
AC AAF99

AAF99500

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The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Thi immune response and to activate immune cells. Note: the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strand displacement amplification; primer; detection; probe; reporter; fluorescent donor; quencher dye; ss.
                                                                                                                                                                                                                                                                                                   Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 74.0%; Score 14.8; DB 4; Length 24; 1 Similarity 88.9%; Pred. No. 6.9e+03; 16; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                             Vollmer
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25-SEP-2000; 2000WO-US026383.
                                            99US-0156113P.
99US-0156135P.
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                                                                                        23-AUG-2000; 2000US-0227436P
                                                                                                                                      (IOWA ) UNIV IOWA RES FOUND
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                                                                                                                                                               COLE-) COLEY PHARM GMBH
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                                                                  27-SEP-1999;
                                            25-SEP-1999;
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                                                                                                                                                                                                             Krieg AM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acids can be primidiatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae haemophilus, campylobacteridium, Becherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or firmune deficiency. The present sequence can also be used to redirect a Thi to a Thi immune response and to activate immune cells. Note: the present sequence may have a phosphorothioate backbone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.
infectious disease; allergy; immune deficiency; phosphorothioate; ss
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Claim 101; Page 55; 338pp; English.

Vollmer J;

Schetter C,

Krieg AM,

WPI; 2001-273485/28

25-SEP-1999; 99US-0156113P. 27-SEP-1999; 99US-0156135P. 23-AUG-2000; 2000US-0227436P.

25-SEP-1999;

(IOWA ) UNIV IOWA RES FOUND.

(COLE-) COLEY PHARM GMBH

25-SEP-2000; 2000WO-US026383

WO200122972-A2

Synthetic

05-APR-2001

Immunostimulatory nucleic acid #614.

WO200122972-A2

Synthetic

05-APR-2001,

(first entry)

12-JUN-2001

AAF99498;

AAF99498 standard; DNA; 24 BP.

1 TTTTGGGGTTTTGGGGTT 18

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Query Match

Best Loca Matches

24

7 TTTTGTGGTTTTGTGGTT

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Gaps ö

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This invention describes a novel signal primer (I) comprising a reporter probe (II) and an adapter oligonucleotide (III) hybridized to (II), such that (I) comprises intermolectularly base-paired portion and a single-stranded target binding sequence. (I) comprises (II), which in the conformational structure which brings a fluorescent donor/quencher dye conformational structure which brings a fluorescent donor/quencher dye conformational structure which brings a fluorescent donor/quencher donor fluorescence, and an adapter oligonucleotide (III) hybridized to conformation and adapter oligonucleotide (III) hybridized to conformation and adapter oligonucleotide (III) hybridized to conformation of a secondary structure is substantially prevented; (b) separating (I) from (III) in a target-dependent manner; and (c) detecting the formation of secondary structure as an indication of the target sequence; where (I) comprises an adapter oligonucleotide to the target sequence; where (I) comprises an adapter oligonucleotide to secondary structure when not hybridized to a complementary sequence; (b) separating the second oligonucleotide complementary to (I) which forms a secondary structure when not hybridized to a complementary sequence; (c) as an indication of the presence of target sequence. Detection of a variety of different target is simplified as the adapter oligonucleotide to to which the second oligonucleotide hybridizes comprises a sequence which the second oligonucleotide hybridizes comprises a sequence which the second oligonucleotide hybridizes comprises a sequence which coligonucleotide hybridizes comprises a sequence which coligonucleotide hybridizes comprises a sequence which the second oligonucleotide hybridizes comprises a sequence which the second oligonucleotide hybridizes comprises a sequence of the formation of a variety of definement target sequence. The adapter probe may be used for detection of a variety of different target sequences. The adapter oligonucleotide such that repert probe may be used for d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anglogenesis inhibitor; ss; anglogenesis; solid tumour growth; tumour metastasis; precancercus lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial anglogenesis; blade neovascularisation; telangiectasia; heemophiliac joint; anglofibroma; wound gramulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         less costly, to synthesize than reporter probes as they do not require labeling for use
fluorescence quenching mechanisms, comprising a reporter probe and an adaptor oligonucleotide hybridized to the probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                        Example 2; Page 11; 16pp; English
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Included is a kit comprising a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject nucleic acids, and instructions for administering them to a subject leaving a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metasteasis, precancerous lesion, theumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma hypertrophic scars. The present sequence is an antiangiogenic nucleic
                                                                                                                                                                             Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth; tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection, neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
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                                                                                                                                                                                                                                                                         The invention relates to inhibiting angiogenesis in a subject,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 14.8; DB 6; Length 24;
Pred. No. 6.9e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24 BP; 0 A; 1 C; 7 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Angiogenesis inhibitory oligonucleotide #883.
                                                                                                                                                                                                                                      Claim 2; Page 31; 276pp; English.
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14-DEC-2001; 2001WO-US048458.
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                                                                                                          Bratzler RL;
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                                                                                                                         The invention relates to inhibiting angiogenesis in a subject, comprising administering at least one antiangiogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, conneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, hypertrophic scars. The present sequence is an antiangiogenic nucleic acid of the invention
                                               Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.
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                                                                                               Claim 2; Page 35; 276pp; English
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The invention relates to inhibiting angiogenesis in a subject, comprising administering at least one antiangiogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous leason, rheumatchid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to methods for treating or preventing cancer, involving administering to a subject having or at risk of developing cancer immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies. The methods are useful for
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                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 6.9e+03;
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/note= "phosphorothioate backbone"
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treating or preventing cancer such as basal cell carcinoma, bladder cancer, bone cancer, brain and central nervous system (CNS) cancer, breast cancer, cornective tissue cancer, cosphageal cancer, colon and rectum cancer, connective tissue cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, nelanoma, myeloma, oral cavity cancer, ovarian cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin cancer, stomach cancer, testicular cancer, and uterine cancer. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of the invention
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74.0%; Score 14.8; DB 6; Length 24;
Best Local Similarity 88.9%; Pred. No. 6.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels
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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.	n on: February 15, 2006, 18	Title: US-09-669-187A-73  Perfect score: 20 Sequence: 1 ttttggggttttggggtttt 20 Scoring table: IDENTITY NUC Gapop 10-0 , Gapext 1.0	41078325 seqs, 233935. hits satisfying chose: length: 0 length: 50	Post-processing: Minimum Match 0%	1: gt s the er tha ved by ved by	1 16.8 84.0 37 6 CP301952 CF301955 AA916364 AA916364 AB916364 AB7968934 AZ794869 AZ794869 AZ794869 AZ794869 AZ8007733 AZ807733 AZ807733 AZ807733 AZ807733 AZ807733 AZ807733 AZ507969	C 9 14.4 72.0 46 1 A1671079 A1671079 A1671079 E27703.x C 11 14.4 72.0 46 1 A156499 A1564869 Qx66h112.x C 11 14.4 72.0 48 10 C2918128 A156499 C5218128 Qx66h112.x C 13 14.4 72.0 49 1 A1475390 A1475390 L182901.x A1475390 L100447-5 C 15 14.4 72.0 50 10 CZ559680 BX35366 Arabidops C 17 14.2 71.0 33 10 BK355866 BX35866 Arabidops C 17 14.2 71.0 43 10 CG72753 CG72753 111907300 CZ470781 C6535-5p CG722753 111907300 CG72753 111907300 CG72753 113907300 CG729919 CG729919 L119116E0 C 21 13.8 69.0 46 8 H71330 H71330 YUS5d08.s1

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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryz
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1 (Dases 1 to 37)

1 (Dases 1 to 37)

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Inpublished (1997)

Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Trace considered overall poor quality
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84.0%; Score 16.8; DB 6; Length 37;
Best Local Similarity 90.0%; Pred. No. 1.4e+04;
Matches 18; Conservative 0; Mismatches 2; Indels
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                                                      ORGANISM
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JOURNAL
COMMENT
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AUTHORS
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Homo sapiens (human)
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Best Local Similarity 85.0
Matches 17; Conservative
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                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                              wk79f07.x1 NCI CGAP Panl Homo sapiens cDNA clone IMAGE:2421637 3' similar to TR:000599 CO01. ;contains element MSR1 repetitive element;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
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/clone_lib="NCI_CGAP_Pan1"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Sal1;
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Sal1;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"
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/clone_lib="NCI_CGAP_Br7"
/note="Organ: bFeast; Vector: pCMV-SPORT4; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.2 kb. Life Technologies catalog
#:10985-018"
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                       Length 37;
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                                                                                                                                                     80.0%; Score 16; DB 1; Le
100.0%; Pred. No. 2.8e+04;
ive 0; Mismatches 0;
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/db_xref="taxon:9606"
/clone="IMAGB:2421637"
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100.0%; Pre
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Unpublished (1997)
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Best Local Similarity
Matches 16; Conserv
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AI813791/c
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A1468834 1NCI CGAP Lyml2 Homo sapiens CDNA clone INAGE:1999 ti42008.x1 NCI CGAP Lyml2 Homo sapiens CDNA clone INAGE:2133135 3' similar to SW:FRP2 RAT P10164 ACIDIC PROLINE-RICH PROTEIN PRECURSOR ;contains element MSR1 repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
Unpublished (1997)
Unpublished (1997)
Email: Robert Strausberg, Ph.D.
Email: Capabbs-romail.nih.gov
Life Technologies catalog #: 11547-015
DNA Sequencing Dy: Washington University Genome Sequencing Center
DNA Sequencins. NGI-GAP clone distribution information can be
found through the I.M.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Arabidopsis thaliana T-DNA flanking sequence GK-111H11-012331,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="DH10B"
/clone_lib="NCI_CGAP_Lym12"
/note="Vorgan: lymph node; Vector: pCMV-SPORT6; Site_1:
Anto="Vorgan: lymph node; Vector: pCMV-SPORT6; Site_2: NotI; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.25 kb. Life Technologies catalog #: 11547-015"
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Arabidopsis thaliana
Bukaryota, Viridiplantaes, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                      Hominidae, Homo.

1 (bases 1 to 31)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP ttp://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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85.0%; Pred. No. 5.8e+04;
iive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trace considered overall poor quality Insert Length: 1016 Std Error: 0.00 Seq primer: -40VP from Gibco High quality sequence stop: 1. Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:2133135"
/tissue_type="lymphoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TITIGGGTTTTGGGGTTTT 20
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Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                            Rm. 308, Bio 84112, USA
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AZ807733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (31-MR-2004) Weisshaar B., Max-Planck-Institut fuer Submitted (31-MR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence has been recovered from the right border of the T-DNA. It indicates an insertion close to or within gene A1917190. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated http://www.mpiz-koeln.mpg.de/GABI-Kat/.
                                                                                                                   An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics Plant Mol. Biol. 53 (1-2), 247-259 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="PCR was performed on DNA from Arabidopsis thaliana plants (TI) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment (s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed.
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2M0048017R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0048017 R, genomic survey sequence.
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1 Chases 1 to 32)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Rally, M., Rose, M., Rose, R., Stokes, R., Stokes, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="GK-111H11-012331"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                            High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines BioTechniques 35 (6), 1164-1168 (2003)
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                                                                           Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
Weisshaar,B.
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                                                                                                                                                                                                                                                                                                                                                                                        4 (bases 1 to 31)
Rosso,M.G., Li,Y., Strizhov,N. and Weisshaar,B.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
     Bioinformatics 19 (11), 1441-1442 (2003)
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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF12972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xi10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidaa; Muridae; Murinae; Mus.

1 (bases 1 to 27)
Dunn,D., Aoyagi,W., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedérsen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ807733 20-FEB-200
2M0070H16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Male"
/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse lobb plasmid UUGCIM library"
/note="Vector: PWD42IV; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030
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                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: row: O column: 17
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 32.
Location/Qualifiers
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Submitted (13-0CT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
FOR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versaillee). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at thtp://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.info.gen.fr).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tilinear EST 16-DEC-1999 tilinear EST 16-DEC-1999 tilinear EST 16-DEC-1999 similar to TR:00599 000599 CONI.; contains element MER22 repetitive element; mRNA sequence.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing Dy: Washington University Genome Sequencing Center

Clone distribution: NGI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
                                             I-DNA integration into the Arabidopsis genome depends on sequences
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic_DNA"
/db_xref="taxon:3702"
/clone="577E03"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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1 (Dases 1 to 40)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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    .39
    organism="Arabidopsis thaliana"

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1. .39
/note="T-DNA flanking sequence
           Lepiniec, L., Caboche, M. and Lecharny, A.
                                                                                of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
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                                                                                                                                                                                       2 (bases 1 to 39)
Balzergue, S.
Direct Submission
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Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114 gib|A123072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
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577E03, genomic survey sequence.
577E03, genomic survey sequence.
577E03, genomic survey sequence.
Au590961.
575E00961.
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                                                                                                                                  Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0070 row: H column: 16
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0070H16"
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Location/Qualifiers
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Conservative
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                                                                                                                  Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
borderline ovarian carcinoma, cDNA made by oligo-dT
priming. Directionally cloned. Size-selected on agarose
gel, average insert size 500 bp. Primary library,
non-amplified.
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/lab host="DH108"
/clone_lib="NCI CGAP_Ut3"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.45 kb. Life Technologies catalog #:
11541-018"
                                                                                                                                                                                                                                                                                                                                                                                                                      AIS64592

tp98d09.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2207345 3'
similar to SW:PRP3_MOUSE P05143 PROLINE-RICH PROTEIN MP-3 ;, mRNA
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 2)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP ttp://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/organism="Homo sapiens"
/mol_type="mRNA"
/morganism="Tref="taxon:9606"
/clone="IMAGE:2207345"
/tissue_type="poorly-differentiated endometrial
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                                                                                                                                                   72.0%; Score 14.4; DB 1; Length 46; 93.8%; Pred. No. 1.2e+05;
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Best Local Similarity 93.8
Matches 15; Conservative
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                                                                                                                                                          /mol_type="mrkma"
/mol_type="mrkma"
/db xref="texon:8606"
/clone="IMAGE:22888885"
/tissue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
/lab host="hH108"
/clone_lib="NCI_CGAP_Ut2"
/note="organ: uterus; Vector: pCMV-SPORT6; Site_1: Sal1;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"
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qx66h12.x1 NCI CGAP Ov36 Homo sapiens cDNA clone IMAGE:2006375 3'
similar to SW:NHPX_HUWAN P55769 NHP2/RS6 FAMILY PROTEIN YEL026W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
cDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: I.M.A.G.B. Consortium, LiNL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LiNL at:
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 404)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP ttp://www.ncbi.nlm.com.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/lab_host="DH10B"
/clone lib="NCI_CGAP_Ov36"
/note="Organ: ovary; Vector: pAMP1; mRNA made from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     www-bio.llnl.gov/bbrp/image/image.html
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     Trace considered overall poor quality Insert Length: 1514 Std Brror: 0.00 Seq primer: -40UP from Gibco High quality sequence scop: 1. Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref=taxon:9606"
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// Lissue_type="leaf"
/db xref="taxxon:4577"
/ Lissue_type="leaf"
/db host="dault"
/lab_host="DH108"
/clone lib="4011"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamH1; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'http://www.mutransposon.org/project/RescueMu', Grid
V was grown at University of Arizona in 2003. DNA was
extracted from leaf strips, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH108
cells were transformed and then screened on LB plates with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A1475390 49 bp mRNA linear EST 14-APR-1999 t18291.x1 NCI CGAP CO14 Homo sapiens CDNA clone INAGE:2153616 3' similar to SW:PRPM HUMAN P10161 SALIVARY PROLINE-RICH PROTEIN PO ;contains element MSR1 repetitive element ;, mRNA sequence.
                                                                         CZ918128 48 bp DNA linear GSS 08-AUG-2005 4021008810.1EL_Y1 4021 - RescueMu Grid V Zea mays genomic, genomic
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0
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                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Peprantophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
1 (bases 1 to 48)
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855 California Ave, Palo Alto, CA 94304, USA
721 S27
722 S227
Fax: 650 725 8221
Email: walbot@stanford.edu
Reverse complemented post-ligation sequence from source sequence.
Place: 4021008 row: 1
Class: transposon-tagged.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
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                                                                                                                                                                                                                                                                                                                                                                                           Department of Biological Sciences
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CZ918128.1 GI:71937386
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AI475390.1 GI:4328435
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93.8%;
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Homo sapiens (human)
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                                    RESULT 12
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Parayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
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Arabidopsis thaliana T-DNA flanking sequence GK-275E01-015095,
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An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="moderately-differentiated adenocarcinoma" /lab host="DHIOB" /clone_lib="NCI_CGAP_CO14" /note="Organ: colon; Vector: pCWV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.7 kb. Life Technologies catalog #: 11531-019"
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Arabidopsis thaliana
Bukaryota, Viridiplantaes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                                                          Hominidae; Homo.

1 (bases 1 to 49)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trace considered overall poor quality Insert Length: 1596 Std Brror: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 1. Location/Qualifiers
                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2153616"
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AL943577
AL943577.1 GI:24400175
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                                                                                                                                                                                       Tumor Gene Index
Unpublished (1997)
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Best Local Similarity
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/close_lib="Drosophila melanogaster PL strains, transposon insertion flanking sequences"
/note="Drosophila melanogaster was mutagenized by remobilization of the piggyBac vector pBac(GAL4D,EXFP) remobilization of the piggyBac vector pBac(GAL4D,EXFP) (Horn et al. 2003 Genetics 163: 647-661) (FlyBase ID Fbtp0017476) as described by Hacker et al. 2003 (Proc Natl Acad Sci USA 100: 7726). Each strain in the collection has an independent insertion of the mutator transposon and the name of each strain begins with the letters PL. Genomic DNA was prepared from samples from each PL strain, DNA segments flanking the transposon insertion sites were amplified by inverse PCR, and the inverse PCR products were sequenced as described by Bellen et al. 2004 (Genetics 167: 761-781)."
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An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics Plant Mol. Biol. 53 (1-2), 247-259 (2003)
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Arabidopsis thaliana T-DNA flanking sequence GK-521H07-020048,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosida, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                  piggyBAC.
The piggyBAC insertion position is 47 in the 50 bases. This
insertion position refers to the first base of the 4 base target
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                                                      Sequence recovery method was inverse PCR. Sequence orientation is forward strand relative to 5' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and
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                                                                                                                                                                                                                                                                                                               /organism="Drosophila melanogaster"
/mol type="genomic DNA"
/db_xref="taxon:7227"
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                                                                                                                                                                                                   recognition sequence.
Class: transposon-tagged.
Location/Qualifiers
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                              Email: RHoskins@lbl.gov
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                                                                                                                                                                                                                                                                                                            Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zucchtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At5g11660. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequence to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
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/db_xref="teaxon:3702"
/clone="GK-275001-015095"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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Karpen,G., Bellen,H., Rubin,G. and Spradling,A.
The Berkeley Drosophila Genome Project Gene Disruption Project
Unpublished (2001)
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Drosophila melanogaster
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta, Pterygota,
Neoptera, Eddopterygota, Diptera; Brachycera; Muscomorpha;
Ephydroidea, Drosophilidae, Drosophila.
                                                                                    Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and
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Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
                                                                                                                                       High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines BioTechniques 35 (6), 1164-1168 (2003)
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                                                                                                                                                                                                                                                                                    Li,Y., Rosso,M.G., Strizhov,N. and Weisshaar,B. Direct Submission
   Plant Mol. Biol. 53 (1-2), 247-259 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Arabidopsis thaliana"
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Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                     Weisshaar,B.
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Gaps

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Length 50; Indels for

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/db xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/dev_stage="bhl08"
/clone_lib="ll19 - RescueMu Grid AA"
/clone lib="ll19 - RescueMu Grid AA"
/clone lib="ll19"
/clone l
                                                                                                                                                                                                                                                            1119073D02.2EL xl 1119 - RescueMu Grid AA Zea mays genomic, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001) Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

    (bases 1 to 43)

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Tel: 650 723 2227
Fax: 650 725 8221
Faxi: 650 125 8221
Faxi: 650 125 8221
Faxi: 650 125 8221
Forbible ligation sequence from source sequence.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1119073 row: 35
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c06535-5prime Exelixis piggyBac PB insertions Drosophila
melanogaster genomic Sequence recovered from 5' end of piggyBac,
Gaps
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/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
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Pred. No. 1.4e+05;
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   0; Mismatches
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                                                                1 TTTTGGGGTTTTTGGGGTTT 19
                                                                                                                          37 TTTTGGGGTTTAGAGGTGT 19
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84.2%;
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Best Local Similarity 84.2
Matches 16, Conservative
      16; Conservative
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CG722753
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                                                                                    Submitted (131-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Submitted (131-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone te59. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpi.z.koeln.mpg.de/GABI-Kat/.
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Direct Submission
Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
humquery@sanger.ac.uk Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes, Cyprinidae, Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="GK-521H07-020048"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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Further details: http://www.sanger.ac.uk/Projects/D_rerio/
Location/Qualifiers
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         4 (bases 1 to 33)
Li,Y., Rosso,M.G., Strizhov,N. and Weisshaar,B.
Direct Submission
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Pred. No. 1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Arabidopsis thaliana"
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0; Mismatches 3
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/db_xref="taxon:7955"
/clone="DREY-63F21"
/tissue_type="Testis"
/note="vector pindigoBAC-536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic_DNA"
/db_xref="taxon:3702"
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84.2%;
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DR63F21T/c
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL PUBMED

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Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
Contact: Walbot V.
Department of Biological Sciences
Stanford University
                                                                                                                                          Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantaes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                               855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Tel: 650 725 8227
Emai: 60 725 8227
Emai: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 119116 row: 36
Class: transposon-tagged.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL940076 31 bp DNA linear GSS 01-APR.
Arabidopsis thaliana T-DNA flanking sequence GK-244B11-014397,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Zea mays"
/moi type="genomic DWA"
/cultivar="mixed background W23/A188/B73/K55"
/tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.0%; Score 14.2; DB 10;
84.2%; Pred. No. 1.5e+05;
ive 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic survey sequence.
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                      CG729919 GI:37772091
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Matches 16; Conservative
survey sequence.
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                                                                                                      Zea mays
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AL940076/c
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/db xref="texton:722"
/clone_lib="Exelixis piggBac PB insertions"
/note="vector: piggBac PB (denbank accession number
/note="vector: piggBac PB (denbank accession number
AY515146); An isogenic w- Drosophila melanogaster strain
was mutagenized by remobilization of transposable
elements. We remobilized the PB element using
Hsp70:piggyBac transposase from a single ammunition
element on either the X or third chromosome. We induced
transposase expression by immersing bottles in a
circulating 37cC water bath for a daily (days 3-10 after
egg-laying) 1-h heat shock. We outcroseed the resulting
dysgenic males to an isogenic w- strain. New insertions
were identified on the basis of a change in eye color
(third chromosome ammunition) or the appearance of w+ male
progeny (X chromosome ammunition). All lines were mapped
to a chromosome by standard genetic methods, examined for
homozygous viabality, and used for recovery of flanking
genomic sequence by inverse PCR."
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                                                                                                                                                                                                                                                    Thibbault, S. T., Singer, M. A., Miyazaki, W. Y., Milash, B., Dompe, N. A., Singh, C. M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H. L., Singh, C. M., Cheung, A., Erickson, C., Fisher, W. W., Greer, K., Hartouni, S. R., Howie, E., Jakkula, L., Joo, D., Killpack, K., Laufer, A., Mazzotta, J., Smith, R. D., Stevens, L. M., Stuber, C., Tan, L. R., Ventura, R., Woo, A., Zakrasjek, I., Zhao, L., Chen, F., Swimmer, C., Kopczynski, C., Duyk, G., Winberg, M. L. and Margolis, J. A complementary transposon tool kit for Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                piggyBac element.
The piggyBac insertion position is 47 in the 50 bases. This insertion position refers to the first base of the 4 base TTAA target recognition sequence.
Class: transposon insertion site.
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                                                                                                                       Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Eukaryota, Metazoa, Arthropoda, Brachycera; Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.

1 (bases 1 to 50)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berkeley Drösophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
Email: Rhoskins@lbl.gov
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="isogenic w- strain"
                                                                                                      Drosophila melanogaster (fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  using P and piggyBac
Nat. Genet. 36 (3), 283-287 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Roger A Hoskins
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  genomic survey sequence.
                                                    CZ470781.1 GI:62964794
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source

PEATURES

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Gaps

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GSS 01-APR-2004

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RESULT 20 CG729919 LOCUS DEFINITION

Query Match

Matches

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Tel: 314 286 1800
Fax: 314 286 1800
Figure 1: 14 286 1800
Figure 2: 156
Figure 2: 156
Figure 3: 15
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Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Auktinan, M., Kucaba, T., Lacy, M., Le, N., Le, N., Mardis, E., Moore, B., Morris, W., Yarsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Treyaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
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2M0004A05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0004A05 F, genomic survey sequence.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                               Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
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Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
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0
                                                                                                                                                                                                                                                                                       Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .46
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3781127"
/db_xref="taxon:966"
/clone="IMAGE:230031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
Mus musculus
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AZ774479.1 GI:12899972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone f26h11. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated (GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (TI) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA trangment (s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
                                                                                                                                                                                                                          An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics Plant Mol. Biol. 53 (1-2), 247-259 (2003)
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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/db_xref="teaxon:302"
/clone="GK-24811-314397"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
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Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
   identification of T-DNA insertion mutants in Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                 High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
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                                                                                                                                                                 Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K.
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                                                                      Bioinformatics 19 (11), 1441-1442 (2003)
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Best Local Similarity 88.2
Matches 15; Conservative
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PEATURES

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/mol_type="mrNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="INAGE:162721"
/lab_host="DH108"
/clone lib="Soares NFL T GBC_S1"
/clone lib="Soares"
/
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Unpublished (1997)
Contact: Robert (1997)
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing Dy: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 7)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP ttp://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Email: cgapbs-r@mail.nih.gov

Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Insert Length: 1352 Std Brror: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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                                                                                                Unpublished (1997)
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                                                                      Tumor Gene Index
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114 [gp]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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IMAGE:1627271 3' Fimilar to TR:Q33563 Q33563 EATRO 164 KINETOPLAST
;contains L1.t1 L1 repetitive element ;, mRNA sequence.
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                   plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-" /clone_lb="Mouse_lokb plasmid UUGCIM library" /note="Vector: PWD42nv, Purified genomic DNA from musculus C57BL/6J (male) was obtained from the Jackson
                                    Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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   Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
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                                                                                                                                                                                                                                                                                                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0004 row: A column: 05
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Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 33.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0004A05"
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1 (bases 1 to 37)
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                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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Rm. 308, Bio
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Matches 16; Conserv
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AI018534/C
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Gaps

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4; Indels

EST 13-APR-1999

linear

mRNA

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REFERENCE

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CF295607 39 bp mRNA linear EST 14-AUG-2003 30DGS--05-K02.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa (japonica cultivar-group) cDNA clone 30DGS--05-K02, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZ579518 Ause 10kb plasmid UUGCIM linear GSS 13-DEC-2000 1M0367G03F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0367G03 F, genomic survey sequence.
AZ579518 GI:11693947 GSS.
          by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Enhartorideae; Oryzaa.

1 (Dases 1 to 39)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Large-scale Sequencing Analysis of Rice ESTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University YoongJi, KyeongJi, KyeongJi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355
                                                                                                                                                                                                     Gaps
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    .39
/organism="Oryza sativa (japonica cultivar-group)"

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                                                                                                                                                                                                   4; Indels
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                                                                                                                                            Score 13.6; DB 2;
Pred. No. 2.5e+05;
0; Mismatches 4;
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                                                                                                                                              68.0%;
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Best Local Si
Matches 16;
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CF295607/c
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AZ579518/c
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                                                                                                                                                                                                                                                                  /tissue_type="poorly differentiated adenocarcinoma with signet ring cell features"
/lab_host="DH100"
/lab_host="DH100"
/clone_lib="NH10"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"
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Hominidae; Homo-
Hominidae; Homo-
Hominidae; Homo-
Hominidae; Homo-
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE974781 38 bp mRNA linear EST 04-OCT-20
001680831R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951175 3',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 13.6; DB 1;
Pred. No. 2.5e+05;
0; Mismatches 4;
Insert Length: 1210 Std Error: 0.00 Seg primer: -40UP from Gibco High quality sequence stop: 1. Location/Qualifiers
                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2140844"
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80.0%;
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BE974781
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Best Local Similarity
Matches 16; Conserv
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BE974781
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ORGANISM

SOURCE

REFERENCE AUTHORS JOURNAL

TITLE

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Zuechtungsforsching, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At3g10360. Details on the protocols used for generation of the sequence are described in References 1.3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mgo.de/GABI-Kat/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion.
                                                                                                                                                                                                                                                                                                                                                                                                                                  An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics Plant Mol. Biol. 53 (1-2), 247-259 (2003)
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/note="PCR was performed on DNA from Arabidopsis thaliana plants (TI) which were transformed with the T-DNA from vector pAC16 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA
                                             Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicctyledons; core eudicctyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic_DNA"
/db_xref="taxon:3702"
/clone="GR-7470:370438"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li,Y., Rosso,M.G., Strizhov,N. and Weisshaar,B.
Direct Submission
Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
                                                                                                                                                                                       Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database the identification of T-DNA insertion mutants in Arabidopsis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines BioTechniques 35 (6), 1164-1168 (2003)
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                                                                                                                                                                                                                                                                                                   Bioinformatics 19 (11), 1441-1442 (2003)
12874060
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                        Arabidopsis thaliana (thale cress)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwalp4 (gql 4712114|gbl AR129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
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                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab host="E. Coli strain XLIO-Gold, T1-resistant, F-" /clone_lib="Mouse_lokb plasmid UUGCIM library" /note="Tvector: PUP42nv; Purified genomic DNA from M. musculus G57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                    Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunm@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0367 row: G column: 03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/mol_type="genomic DNA"
farrain="C57BL/6J"
/db xref="taxon:10090"
/clone="UUGCIM0367G03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plate: 0367 row: G column: 03
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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   musculus (house mouse)
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/lab host="stands the proof of the pr
                                                                                                                                                                                                                                                                                                                                       Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Rhanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
Public, Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. Trace considered overall poor quality Possible reversed clone: similarity on wrong strand This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
                                                                                                                                                 Eukaryona; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1004-468"
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High quality sequence stop: 1
POLYA=No.
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/cultivar="Williams"
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AI442438.1 GI:4296179
                                                                              Glycine max (soybean)
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COMMENT

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/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42Iv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent B. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts.
                                                                                                                                                                                                                                                                                                                                                                            AZ634906 13-DEC-200 A3 bp DNA linear GSS 13-DEC-200 DN490P20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0490P20 R, genomic survey sequence.
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0
                 Length 43;
                                                                                Indels
          68.0%; Score 13.6; DB 1;
80.0%; Pred. No. 2.5e+05;
ive 0; Mismatches 4;
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Insert Lengch: 10000 Std Error: 0.00
Plate: 0490 row: P column: 20
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 43.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/clone="UUGC1M0490P20"
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Query Match
Best Local Similarity 80.09
Matches 16; Conservative
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Fax: 801 585 7177
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Gaps

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Matches

ORIGIN

KEYWORDS SOURCE ORGANISM ACCESSION VERSION

REFERENCE

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Oryza sativa (japonica cultivar-group)

SM Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

Enthartoideae; Oryzeae; Oryza.

SKim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K.W., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Lupublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193
                                                                                                                                                                                                                                        CF300934 11-AUG-2003 1AEAF-05-J13.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--05-J13, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSS 04-OCT-2000
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//note="Vector: pCR4-TOPO; Site 1: EcoR1; mRNA was capped
with oligoribonucleotides and Then used as templates for
RT-PCR."
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1M0295E09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0295E09 F, genomic survey sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Glires; Rodentia;

Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 44)
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryza sativa (japonica cultivar-group)"
|mol_type="mRNA"
|cultivar="Nackdong"
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/clone="7LEAF--05-J13"
/tissue_type="leaf"
/dev_stage="7 days_after_germination"
/lab_host="E.coli DH10B"
  4
0; Mismatches
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neopters, Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilade; Drosophila.
Ephydroidea; Drosophilade; Drosophila.
E 1 (bases 1 to 43)
Singh,C.M., Buchholz,R., Demsky,M., Fawcett,R., Francis-Lang,H.L.,
Ryner,L., Cheung,L.M., Chong,A., Erickson,C., Fisher,W.M.,
Greer,K., Hartouni,S.R., Howie,E., Jakkula,L., Joo,D., Killpack,K.,
Laufer,A., Mazzottea,J., Smith,R.D., Stewens,L.M., Stuber,C.,
Tan,L.R., Ventura,R., Woo,A., Zakrajsek,I., Zhao,L., Chen,F.,
Swimmer,C., Kopczynski,C., Duyk,G., Winberg,M.L. and Margolis,J.
A complementary transposon tool kit for Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="isogenic w- strain"
/db xref="taxon:7227"
/clone_lib="Exelixis P element XP insertions"
/note="Vector: P element XP (GenBank accession number
/note="Vector: P element XP (GenBank accession number
/note="Vector: P element XP (GenBank accession number
AY515149); An isogenic w- Drosophila melanogaster strain
was mutagenized by remobilization of transposable
elements. For the P element XP, we selected an easily
mobilized ammunition element among inserts hopped onto the
Binsinscy balancer. New insertions were collected in vials
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                                                                                                                                                                                                                                                                                                                                                             GSS 29-APR-2005
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                                                                                                                                                                                                                                                                                                                                                                                                              melanogaster genomic Sequence recovered from 3' end of P element,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The P element insertion position is 1 in the 43 bases. This insertion position refers to the first base of the 8 base target recognition sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence recovery method was inverse PCR. Sequence orientation is forward strand relative to 5' end of {\bf P}
                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Roger A Hoskins
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                    d01604-3prime Exelixis P element XP insertions Drosophila
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                                                         Length 43;
                                                                                                                                                                                                                                                                                                                                                             linear
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                                                         Score 13.6; DB 9;
Pred. No. 2.5e+05;
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Nat. Genet. 36 (3), 283-287 (2004)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                             43 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CZ472331
CZ472331.1 GI:62966344
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80.0%;
                                                                                                               16; Conservative
                                                         Query Match
Best Local Similarity
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PUBMED COMMENT

JOURNAL

TITLE

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Gaps

Query Match

source

FEATURES

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Acyrthosiphon pisum (pea aphid)
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Contact: D. Tagu
INRA Rennes
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Best Local Similarity 80.0
Matches 16; Conservative
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CN751963
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of puble [A132114]gb] AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantas Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnolitophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                       Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus G57BL/60 (male) was obtained from the Jackson
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
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                                                                                                                                                                                                                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0295 row: E column: 09
Seg primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C578L/6J"
                                                                                                                                                                                                                                                                                                                                                                                               Class: plasmid ends
High quality sequence stop: 44.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="UUGC1M0295E09"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Male"
                                                                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
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CF298361/c
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="textaxon:39947"
/clone="7LEAF--01-110"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/dev_stage="7 days after germination"
/dev_stage="0 days after germination"
/dev_stage="0 days after germination"
/done="Nector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
1 (Bases I to 45)
Hunter, W., Martinez-Torres, D., Rabbe, Y., Sabater-Munoz, B.,
Stern, D., Tagu, D. and Wincker, P.
An expressed sequence tags database for the pea aphid Acyrthosiphon
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APHL3ED ACYTCHOSiphon pisum CDNA Clone ApHL3SDXXIA6
                                                                                                                                                                                    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, KyeongJi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355
1 (bases 1 to 45)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Unpublished (2003)
Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Risk of contamination by bacterial sequences from obligatory (Buchnera) or facultative endosymbionts.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 45;
                                                                                                                                                                                                                                                                                                                                                    Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
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Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
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80.0%; Pred. No. 2.5e+05;
ive 0; Mismatches 4;
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/mol_type="mRNA"
/cultivar="yr2"
/db_xref="teaxon:7029"
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46 bp DNA linear GSS 16-FEB-2001
2M0045M14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0045M14 R, genomic survey sequence.
AZ793049
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                                                                                                            /lab_lobe_forture.
//clone_lib=forture.
//clone_lib
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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/clone lib="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/60 (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 46)
Dunn, D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.0%; Score 13.6; DB 7; Length 45; 80.0%; Pred. No. 2.5e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                           /dev_stage="third instar nymph (L3)"
/lab_host="TOP10"
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Insert Length: 10000 Std Error: (
Plate: 0045 row: M column: 14
Seq primer: CACACAGAAACAGCTATGACC
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/mol type="genomic DNA"
/strain="C57BL/6J"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/clone="UUGC2M0045M14"
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Location/Qualifiers
tissue type="head"
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Mus musculus
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Fax: 801 585 7177
Email: ddunn@genet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16; Conservative
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VERSION
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was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xiii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (Basea 1 to 47)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Diamid innerts
Unpublished (2000)
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2M0030G22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0030G22 R, genomic survey sequence.
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/clone lib="Mouse lokb plasmid UUGCNN library."
/note="Vector: PWD42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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                                                                                                                                                                                                                                                                                                                                                                                                                Match 68.0%; Score 13.6; DB 9; Length 46; Local Similarity 80.0%; Pred. No. 2.5e+05; es 16; Conservative 0; Mismatches 4; Indels
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Insert Length: 10000 Std Error: 0.00
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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University of Utah Genome Center
University of Utah
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
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RESULT 41
TA131B05Q/c
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BX171071/c
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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Marram., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Marram., Hillier,L., Allen,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wyle,T., Lennon,G., Soares,B., Wilson,R. and
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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This clone is available royalty-free through LLNL , contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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/db_xref="texon:10090"
/clone="IMAGE:1381585"
/tissue_type="mammary gland"
/tissue_type="mammary gland"
/lone_lib="Soares mammary gland NMLWG"
/clone_lib="Soares mammary gland NMLWG"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from mammary
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Contact: Marra Winouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                  68.0%; Score 13.6; DB 9; Length 47; larity 80.0%; Pred. No. 2.5e+05; Conservative 0; Mismatches 4; Indels
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Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
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The WashU-HHMI Mouse EST Project
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Mus musculus
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Matches 1
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LOCUS
DEFINITION
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 39
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KEYWORDS
SOURCE
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gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 50)

Humphray, S. J., Huckle, E. and Durham, J. L.

Direct Submission
Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSS 28-JAN-2003
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R. Plasterk and N.V.
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Danio rerio genomic clone DKEY-174112, genomic survey sequence.
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T. brucei sheared genomic DNA clone 131b05, reverse sequence,
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 50;
                                                                                                                                                                                                                Length 49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was generated from the T7 end of is part of the Daniokey BAC Library created by Keygene. Further details:
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80.0%; Pred. No. 2.5e+05;
ive 0; Mismatches 4;
                                                                                                                                                                                                          68.0%; Score 13.6; DB 1;
80.0%; Pred. No. 2.5e+05;
ive 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.sanger.ac.uk/Projects/D_rerio/.
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-174112"
/tissue_type="Testis"
/note="vector pindigoBAC-536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              humquery@sanger.ac.uk Unpublished
                                                                                                                                                                                                                                                                                                               1 TTTTGGGGTTTTTGGGGTTTT 20
                                                                                                                                                                                                                                                                                                                                              28 TTCAGGGGTTTTTGGTTTTT 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TITIGGGGTTTTGGGGTTTT 20
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BX171071.1 GI:28002776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Danio rerio (zebrafish)
Danio rerio
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Best Local Similarity 80.0°
Matches 16; Conservative
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1 (bases 1 to 24)
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Best Local Similarity
Matches 16; Conserv
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Gaps

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/clone lib="4021 - RescueMu Grid V"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHi, Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription units: For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/' Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHi and BgIII, and ligated to form circular plasmids. DH10B calls were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Enail: cgapbs-remail.nih.gov
Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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/note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1:
Sall; Site_2: Notl; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A1439312 30-MAR-1999
1596212.X1 NCI CGAP_LYM12 Homo sapiens CDNA clone IMAGE:2134798 3'
similar to SW.FRP2 HUMAN PO2812 SALIVARY PROLINE-RICH PROTEIN
PRECURSOR ; contains MER22.b2 TAR1 repetitive element ;, mRNA
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/mol_type="mRNA"
/db_refe"taxon:900
/clone="INAGE:2134798"
/tissue_type="lymphoma, follicular mixed small and large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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0
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Score 13.4; DB 10;
Pred. No. 2.9e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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93.3%;
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1 (bases 1 to 34)
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Best Local Similarity 93.3
Matches 14; Conservative
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KEYWORDS
SOURCE
ORGANISM
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TITLE
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                               Direct Submission

Direct Submission

Direct Submission

Direct Submission

Direct Submission

Direct Sanger Centre, The Wellcome Trust Genome Sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CB10 1SA, E-mail: barrell@eanger.ac.uk and

nhl@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared

to give a tight size distribution (

4 kb). The v + i method used for the library construction is

described in detail in Smith, H. and Venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects. In

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).

Email: nelsayedetigr.org

Details of T. brucei sequencing at the Sanger Centre are available

at http://www.sanger.ac.uk/Projects/T_brucei/.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C2916406 30 bp DNA linear GSS 08-AUG-2009
4021001C10.2EL_y1 4021 - RescueMu Grid V Zea mays genomic, genomic
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1 (bases 1 to 30)
Walbot, V.
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Possible ligation site of ends cut by 2 different endonucleases.
Possible ligation site of ends cut by 2 different endonucleases.
Plate: 4021001 row: C column: 10
Class: transposon-tagged.
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/mol_type="qenomic DNA"
/mol_type="qenomic DNA"
/db_xref="taxon:4577"
/tisuue_type="leaf"
/lab_nost="adult"
/lab_nost="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 24;
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              Melville, S.E., Rajandream, M.A. and Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stanford University
855 California Ave, Palo Alto, CA 94304, USA
7E1: 650 723 2221
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 67.0%; Score 13.4; DB 11;
Best Local Similarity 93.3%; Pred. No. 2.9e+05;
Matches 14; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Trypanosoma brucei"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/strain="TREU927"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db xref="taxon:5691"
/clone="131b05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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Homo sapiens
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Matches 14; Conserv
      AI865173
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                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index.

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 37)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                    Gaps
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Pred. No. 3e+05;
 Pred. No. 3e+05;
0; Mismatches
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/organism="Homo sapiens"
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93.3%;
                                                                  34 GGGGTTTTTGGGTTT 20
                                                5 GGGTTTTGGGGTTT 19
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Best Local Similarity 93.3
Matches 14; Conservative
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AI280814
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AI280814/c
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/note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1: '
/note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1: '
/note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1: '
/note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1: Organ: lymph node; Vector: lymph node; Capacity node; I lost no
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Mus musculus
Eukaryotza, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Eukaryotza, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Menen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Nidedrhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
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22 bp DNA linear GSS 16-FEB-200
1M0555122F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0555122 F, genomic survey sequence.
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/db_xref="taxon:9606"
/clone="IMAGE:2411785"
/tissue_type="lymphoma, follicular mixed small and large
                                                                                                                                                                                                                                                                                                                                     Hominidae; Homo.

1 (bases 1 to 49)

NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tunor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rømail.nih.gov
Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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University of Utah Genome Center
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AZ761211.1 GI:12869877
AI865173.1 GI:5529280
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                                                                                                                  Homo sapiens (human)
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMA2 (gil 4732114 [94] AF123072.1]. a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AJ590891 24 bp DNA linear GSS 15-JAN-2004
Arabidopsis thaliana T-DNA flanking sequence, left border, clone
                           B
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GSS; left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.

T-DNA integration into the Arabidopsis genome depends on sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-" /clone lib="Mouse 10kb plasmid UTGCIM library" | hote="Vector: PWD42nv; Purified genomic DNA from M.musculus CF18L/6J (male) was obtained from the Jackson
                    Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory Mouse DNA Resource
                                                                                                                                                  0.00
                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.
Plate: 0555 row: I column: 22
Seq primer: GGTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
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EMBO Rep. 3 (12), 1152-1157 (2002)
12446565
                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="UUGC1M0555122"
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15; Conservative
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     University of Utah
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                                                                         Tel: 801 585 5606
Fax: 801 585 7177
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Best Local Similarity
Matches 15; Conserv
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Direct Submission

Direct Submission

Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue

Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue

Gaston Cremieux, 91057 Evry cedex, FRANCE

PCR was performed on DNA from transformants of Arabidopsis thaliana

plants from INRA (Versailles). The DNA fragment (8) resulting from

the PCR were directly sequenced from the left or the right border

to determine the genomic sequence flanking the insertion. T-DNA

derived sequences were removed. Information to order the

corresponding mutant line and a link to a database providing a

graphical display of the insertion site are available at

http://dbsgap.versailles.inra.fr/publiclines/. This sequence has

been generated in the framework of the French plant genomics

program 'Genoplante' (http://www.genoplante.com and

http://genoplante-info.infobiogen.fr).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (nouse mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Buarchontoglires; Rodentia;

Sciurognathi; Muroidea; Murinae; Mus.

1 (bases 1 to 37)

1 (bases 1 to 37)

1 (bases 1 to 37)

1 slam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah
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1M0352C18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0352C18 R, genomic survey sequence.
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ilarity 83.3%; Pred. No. 3.5e+05;
Conservative 0; Mismatches 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Arabidopsis thaliana"
/mol_type="qenomic DNA"
/db_xref="taxon:3702"
/clone="576D12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="T-DNA flanking sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 601 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0352 row: C column: 18
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /ecotype="Wassilewskija"
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Location/Qualifiers
1. .37
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Li Y., Rosso, M.G., Strizhov, N. and Weisshaar, B.

Li Y., Rosso, M.G., Strizhov, N. and Weisshaar, B.

Li Y., Rosso, M.G., Strizhov, N. and Weisshaar, B.

Li Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer

Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer

Zuechtungsforschung, Carl-von-Linne-Weg 10, Kooln, 50829, Germany

This sequence has been recovered from the left border of the T-DNA.

It indicates an insertion within the locus defined by BAC clone

R3F19. Details on the protocols used for generation of the sequence

are described in References 1-3. The sequences are generated at the

MPI for Plant Breeding Research in the context of the GABI-Kat

project. GABI-Kat is part of the German Plant Genomics program

designated 'GABI'. Information on line availability can be found

at: http://www.mpiz-veoln.mgo.de/GABI-Kat/.
                                                                                                                                                                                                                                                  AL944738 1-100-4 AL bp DNA linear GSS 01-APR-2004
Arabidopsis thaliana T-DNA flanking sequence GK-284D09-015289,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Weisshaar,B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
Plank Mol. Biol. 53 (1-2), 247-259 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note_FPCR was performed on DNA from Arabidopsis thaliana plants (TI) which were transformed with the T-DNA from vector pAC16 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed.
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/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyl rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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/mol_type="genomic DNA"
/db_xref="taxon:3702"
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BioTechniques 35 (6), 1164-1168 (2003)
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                                                                                    g
                                                                                                                                                                                                                                                                                                                          (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pwalva! (glafa712114|gp|AR129072.1), a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Unpublished
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 40)
                                                                                                                                                                        /lab host="B. Coli strain Xil0-Gold, Tl-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
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3 US-10-131-827-1029 Sequence 10; 3 US-09-406-074-4 Sequence 4, 3 US-09-406-074-3 Sequence 3, 3 US-09-438-486A-60 Sequence 60	3 US-10-131-827-5465 Sequence 54	3 US-08-851-843A-60 Sequence 50	3 US-08-974-549A-557 Sequence 55 3 US-08-854-050-30 Sequence 30	3 US-08-854-050-60 Sequence 60	3 US-UY-43U-3Z3-3U Sequence 3U,	3 US-09-402-181B-557 Sequence 557	3 US-09-721-456-557 Sequence 557	3 IIS-09-766-253-60 Sequence 30,	3 US-10-054-295-30 Sequence 30,	3 US-10-054-295-60 Sequence 60,	3 US-09-438-486A-30 Sequence 30, 3 US-10-131-827-4217 Semience 427	3 US-10-131-827-7605 Sequence 760	3 US-08-879-457-2 Sequence 2,	3 US-08-851-843A-43 Sequence 2,	3 US-08-851-843A-45 Sequence 45,	3 US-08-974-549A-113 Sequence 113	3 US-08-854-050-45 Sequence 45,	3 US-09-430-323-43 Sequence 43,	3 US-09-430-323-45 Sequence 45,	3 US-09-402-181B-113 Sequence 113	3 US-09-721-456-113 Sequence 113 3 US-09-766-253-43 Semience 43.	3 US-09-766-253-45 Sequence 45,	3 US-10-054-295-43 Sequence 43,	3 US-09-438-486A-43 Sequence 43,	3 US-09-438-486A-45 Sequence 45,	3 US-09-495-714C-101 Sequence 352	3 US-08-956-171E-2244 Sequence 22	3 US-08-781-986A-2244 Sequence 22	2 US-08-403-888A-142 Sequence 143	2 US-08-149-096A-7 Sequence 7,	3 US-09-422-978-842 Sequence 84;	3 US-09-422-978-2476 Sequence 24	2 US-08-227-180B-26 Sequence 26,	2 US-08-186-229-6 Sequence 49,	2 US-08-470-124-6 Sequence 6,	2 US-08-207-901-29 Sequence 29,	3 US-09-780-049-86 Sequence 86,	6 PCT-US92-10792-46 Sequence 46,	6 PCT-US92-10792-47 Sequence 47, 6 PCT-US92-10792-48 Sequence 48,	6 PCT-US92-10792-51 Sequence 51,	6 PCT-US92-10792-52 Sequence 52,	3 US-09-422-978-8417 Sequence 841 3 HS-09-672-1268-4 Semience 4	5 03-03-8/2-128B-4 6 PCT-US92-10792-34 Sequence 34,	6 PCT-US92-10792-35 Sequence 35,	6 PCT-US92-10792-38 Sequence 38,	3 US-09-206-898-8 Sequence 8,	5 US-US-3-8 Sequence 9, 6 PCT-US93-08329-3 Sequence 3,	3 US-10-131-827-5127 Sequence 512	3 US-09-422-978-8042 Sequence 804
US-10-131-827-1029 Sequence 10; US-09-406-074-4 Sequence 4, US-09-406-074-3 Sequence 3, US-09-438-486A-60 Sequence 60	3 US-10-131-827-5465 Sequence 54	3 US-08-851-843A-60 Sequence 50	3 US-08-974-549A-557 Sequence 55 3 US-08-854-050-30 Sequence 30	3 US-08-854-050-60 Sequence 60	3 US-UY-43U-3Z3-3U Sequence 3U,	3 US-09-402-181B-557 Sequence 557	3 US-09-721-456-557 Sequence 557	3 IIS-09-766-253-60 Sequence 30,	3 US-10-054-295-30 Sequence 30,	3 US-10-054-295-60 Sequence 60,	3 US-09-438-486A-30 Sequence 30, 3 US-10-131-827-4217 Semience 427	3 US-10-131-827-7605 Sequence 760	3 US-08-879-457-2 Sequence 2,	3 US-08-851-843A-43 Sequence 2,	3 US-08-851-843A-45 Sequence 45,	3 US-08-974-549A-113 Sequence 113	3 US-08-854-050-45 Sequence 45,	3 US-09-430-323-43 Sequence 43,	3 US-09-430-323-45 Sequence 45,	3 US-09-402-181B-113 Sequence 113	3 US-09-721-456-113 Sequence 113 3 US-09-766-253-43 Semience 43.	3 US-09-766-253-45 Sequence 45,	3 US-10-054-295-43 Sequence 43,	3 US-09-438-486A-43 Sequence 43,	3 US-09-438-486A-45 Sequence 45,	3 US-09-495-714C-101 Sequence 352	3 US-08-956-171E-2244 Sequence 22	3 US-08-781-986A-2244 Sequence 22	2 US-08-403-888A-142 Sequence 143	2 US-08-149-096A-7 Sequence 7,	3 US-09-422-978-842 Sequence 84;	3 US-09-422-978-2476 Sequence 24	2 US-08-227-180B-26 Sequence 26,	2 US-08-186-229-6 Sequence 49,	2 US-08-470-124-6 Sequence 6,	2 US-08-207-901-29 Sequence 29,	3 US-09-780-049-86 Sequence 86,	6 PCT-US92-10792-46 Sequence 46,	6 PCT-US92-10792-47 Sequence 47, 6 PCT-US92-10792-48 Sequence 48,	6 PCT-US92-10792-51 Sequence 51,	6 PCT-US92-10792-52 Sequence 52,	3 US-09-422-978-8417 Sequence 841 3 HS-09-672-1268-4 Semience 4	5 03-03-8/2-128B-4 6 PCT-US92-10792-34 Sequence 34,	6 PCT-US92-10792-35 Sequence 35,	6 PCT-US92-10792-38 Sequence 38,	3 US-09-206-898-8 Sequence 8,	5 US-US-3-8 Sequence 9, 6 PCT-US93-08329-3 Sequence 3,	3 US-10-131-827-5127 Sequence 512	3 US-09-422-978-8042 Sequence 804
0 50 3 US-10-131-827-1029 Sequence 10; 0 24 3 US-09-406-074-4 Sequence 4, 0 46 3 US-09-406-074-3 Sequence 3, 0 22 3 US-09-438-486A-60 Sequence 60	0 50 3 US-10-131-827-5465 Sequence 54	26 3 US-08-851-843A-60 Sequence 50	0 26 3 US-08-974-549A-557 Sequence 55 0 26 3 US-08-854-050-30 Sequence 30	0 26 3 US-08-854-050-60 Sequence 60	0 26 3 US-09-430-323-30 Sequence 30	0 26 3 US-09-402-181B-557 Sequence 55	0 26 3 US-09-721-456-557 Sequence 557	0 26 3 US-09-766-253-30 Sequence 30,	0 26 3 US-10-054-295-30 Sequence 30,	0 26 3 US-10-054-295-60 Sequence 60,	0 26 3 US-09-438-486A-30 Sequence 30, 0 50 3 US-10-131-827-4217 Semience 427	0 50 3 US-10-131-827-7605 Sequence 760	0 15 3 US-08-879-457-2 Sequence 2,	0 15 3 US-08-8/5-119-2 Sequence 2, 0 15 3 US-08-851-843A-43 Sequence 43.	0 15 3 US-08-851-843A-45 Sequence 45,	0 15 3 US-08-974-549A-113 Sequence 113	0 15 3 US-08-854-050-45 Sequence 45,	0 15 3 US-09-430-323-43 Sequence 43,	0 I5 3 US-09-430-323-45 Sequence 45, 0 15 3 US-09-467-932-2 Sequence 2.	0 15 3 US-09-402-181B-113 Sequence 113	0 15 3 US-09-721-456-113 Sequence 113 0 15 3 US-09-766-253-43 Semience 43.	0 15 3 US-09-766-253-45 Sequence 45,	0 15 3 US-10-054-295-43 Sequence 43,	0 15 3 US-09-438-486A-43 Sequence 43,	0 15 3 US-09-438-486A-45 Sequence 45,	0 19 3 US-09-495-714C-101 Sequence 101	0 50 3 US-08-956-171E-2244 Sequence 22	0 50 3 US-08-781-986A-2244 Sequence 220	0 21 2 US-08-403-888A-142 Sequence 142	0 26 2 US-08-149-096A-7 Sequence 7,	0 47 3 US-09-422-978-842 Sequence 84;	0 47 3 US-09-422-978-2476 Sequence 24	0 20 2 US-08-227-180B-26 Sequence 26,	0 30 2 US-08-186-229-6 Sequence 49,	0 30 2 US-08-470-124-6 Sequence 6,	0 50 2 US-08-207-901-29 Sequence 29,	0 20 3 US-09-780-049-86 Sequence 86,	0 20 6 PCT-US92-10792-46 Sequence 46,	0 20 6 PCT-US92-10792-47 Sequence 47, 0 20 6 PCT-US92-10792-48 Sequence 48,	0 20 6 PCT-US92-10792-51 Sequence 51,	0 20 6 PCT-US92-10792-52 Sequence 52,	0 21 3 US-09-422-978-8417 Sequence 841 0 24 3 HS-09-672-1268-4 Sequence 4	0 26 6 PCT-US92-10792-34 Sequence 34,	0 26 6 PCT-US92-10792-35 Sequence 35,	0 26 6 PCT-US92-10792-38 Sequence 38,	0 31 3 US-09-206-898-8 Seguence 8,	0 31 6 PCT-US93-08329-3 Sequence 3,	0 50 3 US-10-131-827-5127 Sequence 512	0 21 3 US-09-422-978-8042 Sequence 804
3 US-10-131-827-1029 Sequence 10; 3 US-09-406-074-4 Sequence 4, 3 US-09-406-074-3 Sequence 3, 3 US-09-438-486A-60 Sequence 50	4.4 72.0 50 3 US-10-131-827-5465 Sequence 54	4.2 71.0 26 3 US-08-851-843A-50 Sequence 50	4.2 /1.0 26 3 US-08-9/4-549A-55/ Sequence 55 4.2 71.0 26 3 US-08-854-050-30 Sequence 30	4.2 71.0 26 3 US-08-854-050-60 Sequence 60	4.2 /1.0 26 3 US-U9-43U-3Z3-30 Sequence 3U,	4.2 71.0 26 3 US-09-402-181B-557 Sequence 55	4.2 71.0 26 3 US-09-721-456-557 Sequence 55.	4.2 /1.0 26 3 US=09=/86-253-30 Sequence 30,	4.2 71.0 26 3 US-10-054-295-30 Sequence 30,	4.2 71.0 26 3 US-10-054-295-60 Sequence 60,	4.2 /l.0 26 3 US-09-438-486A-30 Sequence 30, 4.2 71.0 50 3 US-10-131-827-4217 Sequence 427	4.2 71.0 50 3 US-10-131-827-7605 Sequence 760	4 70.0 15 3 US-08-879-457-2 Sequence 2,	4 /0.0 15 3 US-08-8/3-43 Sequence 2, 4 70.0 15 3 US-08-851-843A-43 Semience 43.	4 70.0 15 3 US-08-851-843A-45 Sequence 45,	4 70.0 15 3 US-08-974-549A-113 Sequence 113	4 70.0 15 3 US-08-854-050-45 Sequence 45,	4 70.0 15 3 US-09-430-323-43 Sequence 43,	4 70.0 IS 3 US-09-430-323-45 Sequence 45,	4 70.0 15 3 US-09-402-181B-113 Sequence 113	4 70.0 15 3 US-09-721-456-113 Sequence 113 4 70.0 15 3 US-09-766-253-43 Sequence 43.	4 70.0 15 3 US-09-766-253-45 Sequence 45,	4 70.0 15 3 US-10-054-295-43 Seguence 43,	4 70.0 15 3 US-09-438-486A-43 Sequence 43,	4 70.0 15 3 US-09-438-486A-45 Sequence 45,	14 /0:0 30 3 03-10-131-82/-3323 sequence 33/ 3.8 69.0 19 3 US-09-495-714C-101 Sequence 101	3.8 69.0 50 3 US-08-956-171E-2244 Sequence 22	3.8 69.0 50 3 US-08-781-986A-2244 Sequence 220	3.6 68.0 21 2 US-08-403-888A-142 Sequence 142	3.6 68.0 26 2 US-08-149-096A-7 Sequence 7,	3.6 68.0 47 3 US-09-422-978-842 Sequence 84.	3.6 68.0 47 3 US-09-422-978-2476 Sequence 24	3.4 67.0 20 2 US-08-227-180B-26 Sequence 26,	3.2 66.0 30 2 US-08-186-229-6 Sequence 49,	3.2 66.0 30 2 US-08-470-124-6 Sequence 6,	3.2 66.0 50 2 US-08-207-901-29 Sequence 29,	2.8 64.0 20 3 US-09-780-049-86 Sequence 86,	2.8 64.0 20 6 PCT-US92-10792-46 Sequence 46,	64.0 20 6 PCT-US92-10792-47 Sequence 47, 64.0 20 6 PCT-US92-10792-48 Sequence 48.	2.8 64.0 20 6 PCT-US92-10792-51 Sequence 51,	2.8 64.0 20 6 PCT-US92-10792-52 Sequence 52,	2.8 64.0 21 3 US-09-422-978-8417 Sequence 841	2.8 64.0 26 6 PCT-US92-10792-34 Sequence 34,	2.8 64.0 26 6 PCT-US92-10792-35 Sequence 35,	2.8 64.0 26 6 PCT-US92-10792-38 Sequence 38,	2.8 64.0 31 3 US-09-206-898-8 Sequence 8,	2.8 64.0 31 6 PCT-US93-08329-3 Sequence 3,	2.8 64.0 50 3 US-10-131-827-5127 Sequence 512	2.6 63.0 21 3 US-09-422-978-8042 Sequence 804

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STREET: One Liberty Place - 46th Floor CITY: Philadelphia
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Best Local Similarity
Matches 20; Conservat
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Patent No. 5952490
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Oligonucleotides Having A Conserved G4 Core
TITLE OF INVENTION: Sequence
NUMBER OF SEQUENCES: 146
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP
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Seguence 25,
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-09-396-196G-27658
            US-08-987-574-12
US-08-535-168-12
US-09-017-974-12
US-08-682-255A-12
US-09-429-130-12
US-08-779-599-53
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PCT-US93-07743-9
PCT-US93-08329-9
PCT-US93-08329-10
US-08-171-389-27
US-08-123-936-27
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US-08-482-080A-27
US-09-354-947-27
US-09-993-346-27
PCT-US93-12388-27
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US-10-131-827-5760
US-08-117-952-297
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PCT-US95-06639-61
PCT-US96-11786-12
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US-10-053-883-89
US-07-753-738B-3
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-09-661-858-46
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APPLICANT: Cech, Thomas R.
APPLICANT: Lingura. Toachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: APATLO, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew Lib
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STRIE: California
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CUNTRY: U.S.A.
ZIP: 19103
ZIP: 19103
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,888A
FILING DATE: 12-UN-1995
CLASSIFICATION: 435
FRICK APPLICATION NATA:
APPLICATION NUMBER: 09/954,185
FILING DATE: 29-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legaard
REGISTRATION NUMBER: 1SIS-1229
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 39
TYPE: NUCleic acid
STRANDEDNESS: SINGle
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Length 44;
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
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LOCATION: 1..44

LOCATION: 1..44

GCHER INFORMATION: /note= "hairpin primer"
US-08-974-549A-568
                                                                                                                                                                015389-002610US
                                 APPLICATION NUMBER: US/08/974,549A FILING DATE: 19-NOV-1997 CLASSIFICATION: 536 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/724,643 FILING DATE: 01-OCT-1996 PRIOR APPLICATION DATA: US 08/844,419
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 568
SEQUENCE CHARACTERISTICS:
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APPLICANT: Lingmer, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Harley, Calvin B.
APPLICANT: Harley, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             015389-002930US
                                                                                                                                                                          PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 25-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: APPLICATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 576-0300
TELEFAX: (415) 576-0300
TELEFAX: (415) 576-0300
TELEFAX: (415) 576-0300
TELEFAX: AA base Dairs
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US-08-974-549A-568
; Sequence 568, Application US/08974549A
; Patent No. 6166178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TTTTGGGGTTTTGGGGTTTT 20
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TYPE: nucleic acid
STRANDEDNESS: single
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ADDRESSEE: Townsend
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Sequence 568 Application US/09402181B
Patent No. 6610839
GENERAL INFORMATION:
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: PLOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
PRIOR APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: OL-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: APPLICATION NUMBER: 36,429
REFERENCE/ADOCKET NUMBER: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 20; DB 3; Length 44; Best Local Similarity 100.0%; Pred. No. 7; Matches 20; Conservative 0; Mismatches 0; Indels
                          Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerage
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew
STREET: Two Embarcadero Center, 9th Floor
                                                                                                                                                                                                               CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECTULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TITIGGGGTTTTGGGGTTTT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 57¢
TELEPAX: (415) 576-C
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 25-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: US 08/724,643
FILING DATE: 10-OCT-1996
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 10-CT-1996
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: UNMBER: US 08/724,643
FILING DATE: UNMER: US 08/724,643
FILING DATE: UNMBER: US 08/724,643
FILING DATE
                   APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                              STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 42, Application US/09430323
Sequence 42, Application US/09430323
Select No. 6309867
GENERAL INFORMATION:
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Greeg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TTTTGGGGTTTTGGGGTTTT 20
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Matches 20; Conservative
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US-09-430-323-42
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-No. 6617110-2000
CCASSIFICATION: CUNKNOWN->
PRIOR APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 10-NOV-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
APPLICATION NUMBER: US 08/851,050
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 10-OCT-1997
             Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 20; DB 3; Length 44; larity 100.0%; Pred. No. 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                      ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco CATTE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 1..44
OTHER INFORMATION: /note= "hairpin primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 568:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 01-0CT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-0CT-1997
ATTORNEY/AGENT INPORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (415) 576-0200
                                                                                                                                                                                                                                                                                      ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
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LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TTTTGGGGTTTTGGGGTTTT
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Best Local Similarity
Matches 20; Conserv
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                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <unversion.
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1..44
OTHER INFORMATION: /note= "hairpin primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 568:
                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-ARR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 10-0CT-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 10-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 568:
                                                                                                      COUNTRY: USA
ZIP: 9411-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 568, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamira, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TTTTGGGGTTTTGGGGTTTT 20
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                   STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-402-181B-568
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US-09-721-456-568
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GENERAL INFORMATION:
APPLICANT: CECH, THOMAS R.
APPLICANT: LINGRER, JOACHIM
APPLICANT: LINGRER, JOACHIM
APPLICANT: CHAPMAN, KAREN B.
APPLICANT: MORIN, GENEG B.
APPLICANT: MORIN, GENEG B.
APPLICANT: MORIN, GENEG B.
APPLICANT: MORIN, GENEG B.
APPLICANT: MILLIAM H.
TITLE OF INVENTION: TELOMERASE VARIANTS
FILE REFERENCE: 018/062
CURRENT APPLICATION NUMBER: US/09/438,486A
CURRENT FILING DATE: 1999-11-12
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                                                                                                                                                                                                                                                                                                                                                   Version #1.30
                                                                                                ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFREATER, (415) 576-0300
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
Andrews, William H.
TITLE OF INVENTION: No. 6921664el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PATENTIN Release #1.0, Veri
CURRENY OF APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION NUMBER: US/84,050
FILING DATE: CDKNOWN-
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 10-CT-1996
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 10-CT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 42, Application US/09438486A Patent No. 6927285
                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TTTTGGGGTTTTGGGGTTTT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 44 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JS-09-438-486A-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: United States of America
ZIP: 94111
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: 08 08/724,643
FILING DATE: 01-0CT-1996
ATTORNEY/AGENT INFORMATION:
NAME: APPLE
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELECOMMUNICATION:
                                                                                                                                                                                                                            Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6808880el Telomerase
NUMBER OF SEQUENCES: 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-3an-2001
CLASSIPICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ): DESCRIPTION: /desc = "DNA"
); SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-766-253-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 576-0200
                                                     ; Sequence 42, Application US/09766253; Patent No. 6808880; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 42, Application US/10054295
Patent No. 6921664
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rrrregegrrrregegrrrr 44
                                                                                                                         APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 44 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Morin, Gregg B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 42: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
          RESULT 8
US-09-766-253-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gragg B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SUCURNES: 727
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION NUMBER: US 08/851,312
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,312
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
PRIOR APPLICATION NUMBER: US 08/911,951
PRIOR APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                       .
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                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 567, Application US/08974549A Patent No. 6166178
                                                                                                                                                                                                                               MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TITIGGGTTTTGGGGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 rrrregegrrrregegrrrr 46
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.00
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Two Embarcade
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-974-549A-567
                                                                                                                                                                                                                                                                                 US-08-851-843A-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                       FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-09-438-486A-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94111
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: BA PC COMPATIBLE
COMPUTER: PATEMIN PC-DOS/MS-DOS
SOFTWARE: PATEMIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILLING DATE: 06-MAY-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cech, Thomas R.
APPLICANT: Lingmer, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Raren B.
APPLICANT: Morin, Greegs B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
ADDRESSEE: TOWNEATS
STREEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randclph T.
REGISTRATION NUMBER: 36,429
REFRENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/851,843
PRIOR FILING DATE: 1997-05-06
PRIOR PELING DATE: 1997-06-25
PRIOR PELING DATE: 1997-04-25
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1997-04-18
PRIOR PILING DATE: 1997-04-18
PRIOR PILING DATE: 1996-10-01
NUMBER OF SEQ ID NOS: 223
SEQ ID NO 42
LENGTH: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
US-08-851-843A-41
; Sequence 41, Application US/08851843A
; Patent No. 6093809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TTTTGGGGTTTTGGGGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 rrrrdgágárrrragagárrrr 44
                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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STATE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRNI APPLICATION DATA:
APPLICATION DATE: 29-Oct-1999
CLASSIFICATION: <a href="https://documents.com/">CURRNI APPLICATION</a>; CLASSIFICATION: <a href="https://documents.com/">CURRNICATION</a>; CURKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 20; DB 3; Length 46; 100.0%; Pred. No. 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                    FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
RELEPHONE: (415) 576-0200
INFORMATION FOR SEQ 1D NO: 41: SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
ITYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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STATE: California
COUNTRY: United States of America
JABER: US 08/846,017
25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 41, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TTTTGGGGTTTTGGGGTTTT 20
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Matches 20; Conservative
                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-430-323-41
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COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cech, Thomas R.
APPLICANT: Cech, Thomas R.
APPLICANT: Linguer, Joachim
APPLICANT: Linguer, Joachim
APPLICANT: Indamma, Toru
APPLICANT: Morin, Greeg B.
APPLICANT: Morin, Greeg B.
APPLICANT: Marley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6251836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                               PRINK APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
TELEPAK: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAMEKKY: -
LOCATION: 1..46
OTHER INFORMATION: /note= "hairpin primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 41, Application US/08854050; Patent No. 6261936; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TTTTGGGGTTTTGGGGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 TTTTGGGGTTTTGGGGTTTT 46
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Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-974-549A-567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-08-854-050-41
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APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRIT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-No. 6617110-2000
CLASSIFICATION: CURKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3; Length 46;
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                                                                                         FILING DATE: 14-AUG-1997

APPLICATION NUMBER: U8 08/915,503

FILING DATE: 14-AUG-1997

ATORICA AGENT INFORMATION:
NAME: Ausenbus, Scott L.
REGISTRATION NUMBER: 42,271

REFERENCE/DOCKET NUMBER: 015389-002620US

TELEPHONE: (415) 576-0200

INFORMATION FOR SEQ ID NO: 567:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs

TYPE: nucleic acid
STREE CHARACTERISTICS:
LENGTH: 46 base pairs

TYPE: nucleic acid
STREE CHARACTERISTICS:
LENGTH: 46 base pairs

TYPE: nucleic acid
STREE CHARACTERISTICS:
LENGTH: 46 base pairs

TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1..46
OTHER INFORMATION: /note= "hairpin primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 567:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .,
                                   FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 567, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-402-181B-567
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US-09-721-456-567
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; Sequence 567, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
STRIES: California
CCUNTRY: USA
ZIP: 94111-3834
COMPUTER: ISM PC Compatible
COMPUTER: Ploppy disk
COMPUTER: Selection
COMPUTER: Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                       NAME: Apple, Randoh T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 41:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          )

DESCRIPTION: //desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-09-430-323-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 ririrgegeririrgegeriri 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
US-09-402-181B-567
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SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION: UNMBER: US/09/766,253
FILING DATE: 19-Jan-2001
APPLICATION NUMBER: US/08/46,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US/08/24,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: APPLE 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 15:389-002920US
TELEPONE: (415) 576-020
INFORMATION FOR SEQ ID NO: 41:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6921664el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 20; DB 3; 100.0%; Pred. No. 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: «Unknown»
PPLICATION NUMBER: US 08/846,017
PILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 41, Application US/10054295
Patent No. 6921664
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 46 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 20; Conservative
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US-10-054-295-41
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Chapman, Karen B.
Morin, Greeg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6808880el Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                              PILLING DATE: 25-APR 1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997

APPLICATION NUMBER: 36,429

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002610US

TELEPPONE: (415) 576-0300

TELEPPONE: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1..46

COTHER INFORMATION: /note= "hairpin primer"

SEQUENCE DESCRIPTION: SEQ ID NO: 567:
US-09-721-456-567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. ...
      US 08/844,419
                         FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: California COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 41, Application US/09766253 Patent No. 6808880 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TTTTGGGGTTTTGGGGTTTT 20
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Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 46 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20; Conservative
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Best Local Similarity
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US-09-766-253-41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GOFTWARE: Patentin Release #1.0, Version #1.30
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/86,017
RILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
FILING DATE: 18-APR-1997
FILING DATE: 10-APR-1997
FILING DATE: 10-APR-1997
FILING DATE: 10-APR-1997
CLASSIFICATION:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                     ALUNESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California
                                                                                                                                                                     APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Greeg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       015389-002930US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                     Sequence 37, Application US/08851843A Patent No. 6093809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 40, Application US/08851843A
Patent No. 6093809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TTTTGGGGTTTTGGGGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE DOCKET NUMBER: 0153
TELECOMPUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTER.FSTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Apple, Randolph T. REGISTRATION NUMBER: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Apple, Randolph T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 20, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inear
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US-08-851-843A-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-851-843A-37
                                                                US-08-851-843A-37
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APPLICANT: CECH, THOMAS R.
APPLICANT: LINGORNATION:
APPLICANT: CECH, THOMAS R.
APPLICANT: CHAPMAN, KAREN B.
APPLICANT: CHAPMAN, KAREN B.
APPLICANT: CHAPMAN, KAREN B.
APPLICANT: HARLEY, CALVIN
TITLE OF INVENTION: GENE FOR HUMAN TELOMERASE REVERSE TRANSCRIPTASE AND
TITLE OF INVENTION: TELOMERASE VARIANTS
FILE REFERENCE: 018/062
CURRENT APPLICATION NUMBER: 08/81,843
PRIOR APPLICATION NUMBER: 08/846,017
PRIOR APPLICATION NUMBER: 08/846,017
PRIOR PLILING DATE: 1997-04-25
PRIOR APPLICATION NUMBER: 08/844,419
PRIOR PLILING DATE: 1997-04-25
PRIOR APPLICATION NUMBER: 08/844,419
PRIOR PLILING DATE: 1997-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 20; DB 3; Length 46; Best Local Similarity 100.0%; Pred. No. 7; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 20; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels
FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996

ATTORNEY AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 41, Application US/09438486A; Patent No. 6927285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 TTTTGGGGTTTTGGGGTTTT 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 TTTTGGGGTTTTGGGGTTTT 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 19
US-09-438-486A-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-054-295-41
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LENGTH: 46
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Length 48;
                                                        APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCES: 727
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDIE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENIT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 10-NOV-1997
CLASSIFICATION NUMBER: US/08/974,549A
FILING DATE: 10-NOV-1997
PRIOR APPLICATION NUMBER: US/08/44,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION NUMBER: US/08/846,017
PRIOR APPLICATION NUMBER: US/08/846,017
PRIOR APPLICATION NUMBER: US/08/846,017
PRIOR APPLICATION NUMBER: US/08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION NUMBER: US/08/851,843
FILING DATE: 09-MAY-1997
PRIOR APPLICATION NUMBER: US/08/91,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US/08/912,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: US-OCT-1997
ATPONEY/AGENT INFORMATION:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: US-OCT-1997
ATPONEY/AGENT PROPARATION:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: US-OCT-1997
ATPONEY/AGENT PROPARATION:
AMANE: AND PURCHANATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 564:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: 1..48
; OTHER INFORMATION: /note= "hairpin primer"
US-08-974-549A-564
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Flam PC-COMPATIBLE
COMPUTER: Flam PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURSTITION SYSTEM: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION NUMBER: US 08/724,643
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Makamura, Toru
APPLICANT: Marley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and STREET: Two Pro.
CITV
                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pirs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 22
US-08-974-549A-564
i Sequence 564, Application US/08974549A
j Patent No. 6166178
i GENERAL INFORMATION:
j APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: United States of America ZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rrrrccccrrrrccccrrrr 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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RESULT 24
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   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Two Embarcaders denter, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
COUNTRY: United States of America
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 10-OCT-1996
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: ASSETTION: 536
PRIOR APPLICATION: 536
PRIOR APPLI
0;
                                                                                                                                                                                                                                                                                                                   Sequence 37, Application US/08854050

Patent No. 6261836

GENERAL INFORMATION:
APPLICANT: Ccch, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Makamura, Toru
APPLICANT: Makamura, Toru
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 37:
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                          1 TTTTGGGGTTTTTGGGGTTTT 20
                                                                                                                                                 rrrregegrirregegrirr 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                RESULT 23
US-08-854-050-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-854-050-37
Matches
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Ouery Match 100.0%; Score 20; DB 3; Length 48; Best Local Similarity 100.0%; Pred. No. 7; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILING DATE: US/08/854,050
FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California COUNTRY: United States of America
                                                                                                                                                                                                                                                                          APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Greeg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TILLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION S36
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/44,419
FILING DATE: 18-APR-1997
CLASSIFICATION S36
PRIOR APPLICATION S36
PRIOR APPLICATION S36
ATTORNEY/AGENT INFORMATION:
NAME: APPLE 01-0CT-1996
CLASSIFICATION UNDERR: 36,429
RECTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
RECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                  Sequence 40, Application US/08854050 Patent No. 6261836
1 TITIGGGGTTTTGGGGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48 base pairs
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STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                            US-08-854-050-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-854-050-40
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Gaps . 0

Conservative

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ZIF: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <a href="https://documer.com/">Unknown></a>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                          STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                       Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: NO. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 20; DB 3;
Pred. No. 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                        STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 564, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
                                   Application US/09430323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION TELEPHONE: (415) 576-020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                  APPLICANT: Gech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TTTTGGGGTTTTGGGGTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 576-C
INFORMATION FOR SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.08;
                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: other I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 20; Conservative
                                        Sequence 40, Applicati
Patent No. 6309867
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 27
US-09-402-181B-564
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                US-09-430-323-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                    Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 0-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/44,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: California COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Apple, Randolph T. REGISTRATION NUMBER: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                      Sequence 37, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TTTTGGGGTTTTGGGGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TririceGerririceGerrir 48
TTTTGGGGTTTTGGGGTTTT 20
                                                                                                                                                                                                                            APPLICANT: Cech, Thomas R.
Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Similarity
Matches 20; Conserv
                                                                                                              RESULT 25
US-09-430-323-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-430-323-37
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MEDIUM TITEM: FLODRY GIBNE

COMPUTER: IMPERIONALIBLE

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARRE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/721,456

FILING DATE: 12-No. 6617110-2000

CLASSIFCATION NUMBER: US/08/974,549A

FILING DATE: 19-NOV-1997

APPLICATION NUMBER: US 08/44,419

FILING DATE: 10-NOV-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997
                                                                                                                                                                                                                                                                                                                                      Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: /note= "hairpin primer" SEQUENCE DESCRIPTION: SEQ ID NO: 564:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
                                                                                         Sequence 564, Application US/09721456 Patent No. 6617110 GENERAL INFORMATION:
                                                                                                                                                                       APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Nahamura, Karen B.
Morin, Gregg B.
Harley, Calvin B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 564: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: -
LOCATION: 1..48
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                 JS-09-721-456-564
                                      RESULT 28
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CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: BLODRY disk
CONFUNTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-SE9-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/854,650
FILING DATE: 05-APR-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 08-APR-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 08-APR-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-APR-1997
APPLICATION NUMBER: US 08/854,050
                                                                                   Chapman, Karen B.

Morin, Gregg B.

Harly, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 20; DB 3; Length 48; Best Local Similarity 100.0%; Pred. No. 7; Matches 20; Conservative 0; Mismatches 0; Indels
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LOCATION: 1..48
CTHER INFORMATION: /note= "hairpin primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 564:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
APPLICATION NUMBER: WO PCT/US97
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
                                                                                                                                                                                                                                                                                                                          STREET: Two Embarcadero
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Ausenhus, Scott L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 TTTTGGGGTTTTGGGGTTTT 48
APPLICANT: Cech, Thomas R. Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 576-03(
INFORMATION FOR SEQ ID NO: 564:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-402-181B-564
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ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                               APPLICANT: Ccch, Thomas R.
Lingner, Joachim
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 680880el Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 19-Jan-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                    US-09-766-253-40; Sequence 40, Application US/09766253; Sequence 40, Application US/09766253; Patent No. 6808880; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 37, Application US/10054295; Patent No. 6921664; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                           CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-054-295-37
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                                            100.0%; Score 20; DB 3; Length 48; 100.0%; Pred. No. 7;
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                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: RC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: NO. 6808880el Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INPORMATION FOR SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United States of America ZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                     Sequence 37, Application US/09766253
Patent No. 6808880
GENERAL INFORMATION:
                                                                                                                                  1 TTTTGGGGTTTTGGGGTTTT 20
                                                                                                                                                                            29 rrrrccccrrrrccccrrrr 48
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: California
                                         Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
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Best Local Similarity
Matches 20; Conserv
US-09-721-456-564
                                                                                                                                                                                                                                               RESULT 29
US-09-766-253-37
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COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
                                                                                                                                                                                                                                                                                                                                                                                             NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 40:
                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       )

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-766-253-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
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GENERAL INFORMATION:

APPLICANT: CECH, THOMAS R.

APPLICANT: LINGHER, JOACHIM

APPLICANT: LINGHER, JOACHIM

APPLICANT: CHAPMAN, KAREN B.

APPLICANT: CHAPMAN, KAREN B.

APPLICANT: HARLEY, CALVIN

APPLICANT: ANDREWS, WILLIAM H.

TITLE OF INVENTION: GENE FOR HUMAN TELOMERASE REVERSE TRANSCRIPTASE AND TITLE OF INVENTION: TELOMERASE VARIANTS

PILE REFERENCE: 018/062
                                                                                                                                   CORPUTER: FLOPPY disk
COMPUTER: FLOPPY disk
COMPUTER: 1BM PC Compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION BARE: 18/40.202
FILING DATE: 08/854,050
FILING DATE: CURROWN-
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 10-OCT-1996
ATTORNEY AGENT INFORMATION:
NAME: AND STACK AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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Pred. No. 7;
Mismatches 0;
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CURRENT FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 08/651,843
PRIOR PILING DATE: 1997-05-06
PRIOR PILING DATE: 1997-04-25
PRIOR PILING DATE: 1997-04-25
PRIOR FILING DATE: 1997-04-18
PRIOR PILING DATE: 1997-04-18
PRIOR APPLICATION NUMBER: 08/844,419
PRIOR APPLICATION NUMBER: 08/724,643
PRIOR APPLICATION NUMBER: 08/724,643
PRIOR PILING DATE: 1996-10-01
                                           COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 20; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 37, Application US/09438486A Patent No. 6927285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; P:
Matches 20; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                             COMPUTER READABLE FORM:
              STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 33
US-09-438-486A-37
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Nakamura, Toru
Chapman, Karen B.
Morin, Greeg B.
Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: No. 6921664el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 556
                                                                                                                                          ADDRESSEE: Townsend and Townsend and Crew
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
Andrews, William H.
TITLE OF INVENTION: No. 6921664el Telomerase
UNMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/854,050
FILING DATE: «Unknown»

APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APF-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APF-1997
APPLICATION NUMBER: US 08/724,643
APTICATION DATE: 01-0CT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                       STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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Patent No. 6921664
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 rrrrccccrrrrccccrrrr 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 576-(
INFORMATION FOR SEQ ID NO: 37
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                     ZIP: 94111
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US-10-054-295-40
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1 TTTTGGGGTTTTGGGGTTTT 20
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                   94111
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Matches
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US-09-438-486A-40
                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-09-438-486A-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   us-us-usb-usba-qu

sequence 40, Application US/09438486A

sequence 40, Application US/09438486A

sequence 40, Application US/09438486A

setent No. 692728B

setent INFORMATION:

APPLICANT: LINGMER, JOACHIM

APPLICANT: CECH, THOMAS R.

APPLICANT: CHAPMAN, KAREB

APPLICANT: HARLEY, CALVIN

APPLICANT: HARLEY, CALVIN

APPLICANT: ANDREWS, WILLIAM H.

TITLE OF INVENTION: GENE FOR HUMAN TELOMERASE REVERSE TRANSCRIPTASE AND

TITLE OF INVENTION: TELOMERASE VARIANTS

FILE REFERENCE: 0184062

CURRENT APPLICATION NUMBER: US/09/438,486A

CURRENT FILING DATE: 1997-01-12

PRIOR FILING DATE: 1997-05-06

PRIOR FILING DATE: 1997-04-18

PRIOR FILING DATE: 1997-04-18

PRIOR FILING DATE: 1997-04-18

PRIOR FILING DATE: 1996-10-01

NUMBER OF SEQ ID NOS: 223

SOFTWARE: Patentin Ver. 3.2

SOFTWARE: Patentin Ver. 3.2
                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                     DB 3; Length 48;
                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                     Query Match 100.0%; Score 20; DE Best Local Similarity 100.0%; Pred. No. 7; Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 39, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                      1 TITIGGGTTTTGGGGTTTT 20
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                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
NUMBER OF SEQ ID NOS: 223
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 37
LENGTH: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 34
US-09-438-486A-40
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US-08-851-843A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 40
LENGTH: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29
                                                                                                                                          FEATURE:
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Sequence 566, Application US/08974549A

Sequence 566, Application US/08974549A

Patent No. 6166178

APPLICANT: Linguer, Joachim
APPLICANT: Linguer, Toru
APPLICANT: Morth, Greeg B.
APPLICANT: Morth, Greeg B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
TITLE OF INVENTES: 727

CORRESPONDENCE ADDRESS: 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 100.0%; Score 20; DB 3; Length 50; Local Similarity 100.0%; Pred. No. 7.1; nes 20; Conservative 0; Mismatches 0; IndelB
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FLING DATE: US-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION NUMBER: US/08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NUMBER: APPLICATION:
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPRAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 39: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OLESCHIE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA"
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Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingmer, Joachim
APPLICANT: Chapmer, Toru
APPLICANT: Moralin, Gregg B.
APPLICANT: Moralin, Gregg B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: NO. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor STREET: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: United States of America ZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA"
                                                                          Sequence 39, Application US/08854050 Patent No. 6261836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TITIGGGGTTTTGGGGTTTT 20
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 20, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                            RESULT 37
US-08-854-050-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-854-050-39
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                                           CITY: San Francisco
CITY: San Francisco
COUNTER: USA
ZIP: 94111-3834
COMMUTER: ISABABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC COMPATIBLE
OPERATING SYSTEM: PC COMPATIBLE
OPERATING SYSTEM: PC COMPATIBLE
OPERATING DATE: 19-NOV-1997
CLASSIFICATION NUMBER: US/08/974,549A
PILING DATE: 19-NOV-1997
CLASSIFICATION NUMBER: US 08/44,419
FILING DATE: 10-NOV-1996
PRIOR APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION NUMBER: US 08/844,419
FILING DATE: 09-NAX-1997
PRIOR APPLICATION NUMBER: US 08/851,843
FILING DATE: 09-NAX-1997
PRIOR APPLICATION NUMBER: US 08/851,843
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17889
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: -.

LOCATION: 1..50

LOCATION: 1..50

GTHER INFORMATION: /note= "hairpin primer"
US-08-974-549A-566
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 566
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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                       Gaps
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100.0%; Score 20; DB 3; Length 50; 100.0%; Pred. No. 7.1;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
FILING DATE: 29-Sep-1997
CLASSIFICATION: <a href="https://documents.com/">CURRENTON DATE: 29-Sep-1997</a>
                                                                                       Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 20; DB 3; Length 50; Pred. No. 7.1;
                                                                                                                                                                                                                       ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco CTATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: /note= "hairpin primer" SEQUENCE DESCRIPTION: SEQ ID NO: 566:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR AMPLICATION DATA:

APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-ARR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 09-MAX-1997
APPLICATION NUMBER: US 08/851,030
FILING DATE: 09-MAX-1997
APPLICATION NUMBER: US 08/911,312
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 11-AUG-1997
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 015389-002620US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ausenhus, Scott L. REGISTRATION NUMBER: 42,271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION
Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 rrrrecectriricectrir 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 576-0.
INFORMATION FOR SEQ ID NO: 566
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 20; Conserv
  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-402-181B-566
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 10-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3; Length 50; 7.1;
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                                                                                                                                                                                                                                                                                                                 STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                     APPLICANT: Cech, Thomas R.

Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Greeg B.
Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 20;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLGGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 39
US-09-402-181B-566
; Sequence 566, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
                                        Sequence 39, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TITIGGGTTTIGGGGTTT 20
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

100.0%;

Best Local Similarity 100.0%;

Matches 20; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 576-(
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (415)
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                       US-09-430-323-39
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Gaps

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Indels

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Gaps

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100.0%; Score 20; DB 3; Length 50; 100.0%; Pred. No. 7.1; 0; Indels ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: California
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE POCKET NUMBER: 015389-002920US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6808880el Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                              Sequence 39, Application US/09766253;
Patent No. 6808880;
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                              1 TTTTGGGGTTTTGGGGTTTT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 576-C
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
                                                Query Match
Best Local Similarity
Matches 20; Conserv
US-09-721-456-566
                                                                                                                                                                                                                                                                                            US-09-766-253-39
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                                                                                                                                                                                                                                                                                       Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-No. 6617110-2000
CLASSIFCATION: CUNKNOWN:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                 STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California COUNTRY: USA ZIP: 9411-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION: 1..50
COTHER INFORMATION: /note= "hairpin primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 566:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 14-AUG-1997
APPLICATION WUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAPELICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 05-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
                                                                  Sequence 566, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
                                                                                                                                      APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA
                      RESULT 40
US-09-721-456-566
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Gaps

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100.0%; Score 20; DB 3; Length 50; ilarity 100.0%; Pred. No. 7.1; Conservative 0; Mismatches 0; Indels
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APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TTTTGGGGTTTTGGGGTTTT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
NAKAMURA, TORU
CHAPMAN, KAREN B.
MORIN, GREGG B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Two bulkers
CITY: San Francisco
cmatE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JS-08-851-843A-39/c
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COMPUTER: IBM PC Compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: CURROWN:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 10-OCT-1996
ATTORNEY/AGENT INFORMATION:
WANTE: AND ARTHORNEY ARTHORNEY APPLICATION NUMBER: US 08/724,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 20; DB 3; Length 50; 100.0%; Pred. No. 7.1; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                         Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6921664el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLGGY: linear
MOLECTULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ 1D NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                               Sequence 39, Application US/10054295
Patent No. 6921664
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TTTTGGGGTTTTGGGGTTTT 20
                                                                                                                  APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 20; Conservative
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                               US-10-054-295-39
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Sequence 39, Application US/09438486A Patent No. 6927285 GRNERAL INFORMATION: APPLICANT: CECH, THOMAS R. APPLICANT: LINGNER, JOACHIM

RESULT 43 US-09-438-486A-39

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, OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide US-09-438-486A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
APPLICANT: MORIN, CARLOS B.
APPLICANT: HARLEY, CALVIN
APPLICANT: HARLEY, CALVIN
TITLE OF INVENTION: GENE FOR HUMAN TELOMERASE REVERSE TRANSCRIPTASE AND
TITLE OF INVENTION: TELOMERASE VARIANTS
FILE REFERENCE: 018/062
CURRENT FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 08/846,017
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1996-10-01
NUMBER OF SED ID NOS: 223
SOFTWARE: PATENTIN VOR: 2.23
SOFTWARE: PATENTIN VOR: 3.25
LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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COMPUTER: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,842*
CLASSIE****
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
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Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Namura, Toru
APPLICANT: Namura, Toru
APPLICANT: Morin, Gregg B.
APPLICANT: Morin, Gregg B.
APPLICANT: Andrews, William H.
ITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, 8th Floor
                                       APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION NUMBER: US 08/911,312
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION UNMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 105389-002610US
TELEGOMUNICATION INFORMATION:
TELEGOMUNICATION INFORMATION:
TELEGOMUNICATION INFORMATION:
TELEGOMUNICATION INFORMATION:
TELEGOMUNICATION INFORMATION:
TELEGOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1..50
OTHER INFORMATION: /note= "hairpin primer'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TREET: Two bulders
CITY: San Francisco
STATE: California
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 39, Application US/08854050 Patent No. 6261836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 566:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TTTTGGGGTTTTGGGGTT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 18; Conservative
                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
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US-08-854-050-39/c
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US-08-974-549A-566/C
; Sequence 566, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Linger, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gaedim
APPLICANT: Morin, Gaegg B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
INUMBER OF SEQUENCES: 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.0%; Score 18; DB 3; Length 50; ilarity 100.0%; Pred. No. 50; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILLING DATE: 19-NOV-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILLING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEE: Townsend and Townsend and Crew LLP: Two Embarcadero Center, Eighth Floor
San Francisco
FILING DATE: 18-APR-1997
CLASSIFICATION
PRIOR APPLICATION
PRIOR APPLICATION
ADDITOR APPLICATION
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
RELEPANGINICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/851,843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TTTTGGGGTTTTGGGGTT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 rrrresecrirresecrr 1
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-851-843A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
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Gaps
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Patent No. 6610839

GENERAL INFORMATION:

Ingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVERTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 633

CORRESPONDENCE ADDRESS:

STREET: Two Enbarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
         PRIOR PRESENTATION NUMBER: US/99/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-ARR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 10-CCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: APPLE, RANGOLDP T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION UNDERRE: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3;
50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.0%; Score 18; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                        (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 39: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 90.0%; Sc
Best Local Similarity 100.0%; P.
Matches 18; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 50 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TITTGGGGTTTTGGGGTT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-402-181B-566/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 48
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Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
                                                                                                                                                                                                                                 90.0%; Scot.
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                    CLASSIPICATION: 536
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDABR:
FILING DATE: 06-WAY-1997
CLASSIPICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIPICATION: 536
                          UMBER: US/08/854,050
09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 39, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TTTTGGGGTTTTGGGGTT 18
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Best Local Similarity 100.
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US-09-430-323-39/c
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Length 50;
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PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INPORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
APPLICATION NUMBER: US 08/911,312
APPLICATION NUMBER: US 08/912,951
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 10-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Andrews, William H.
TITLE OF INVENTION: No. 6808880el Telomerase
UNMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
            CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-No. 6617110-2000
CLASSIFICATION: UNKNOWN:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.0%; Score 18; DB 3; 100.0%; Pred. No. 50;
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Patent No. 6808880
GENERAL INFORMATION:
Lingner, Joachim
Lingner, Joachim
Nakamura, Toru
Chapmen, Karen B.
Maran, Gregg B.
Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TTTTGGGGTTTTGGGGTT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 566:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1..50
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 TTTTGGGGTTTTTGGGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-766-253-39/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
Andrews, William H.
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
RADRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 18; DB 3; Length 50;
Pred. No. 50;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: /note= "hairpin primer"; SEQUENCE DESCRIPTION: SEQ ID NO: 566: US-09-402-181B-566
                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
                                                                                               FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997

FILING DATE: 09-MAY-1997

FILING DATE: 09-MAY-1997

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: WO 08/915,503

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: WO PCT/US97/17885

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997
            FILING DATE: 01-OCT-1996
PPDLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 566:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 566, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 90.0%; Scc
Best Local Similarity 100.0%; P.
Matches 18; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGGTT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 49
US-09-721-456-566/c
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Gaps . 0

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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Ploor
CITY: San Francisco
STATE: California
COMPTRY: United States of America
ZIP: 94111
COMPTRE RADABLE FORM:
MEDIUW TYPE: Floppy disk
COMPTRE: REDABLE FORM:
MEDIUW TYPE: Floppy disk
COMPTRE: REDABLE FORM:
MEDIUW TYPE: PLOOPY disk
COMPTRE: Lab PC comparatible
COMPTRE: Lab PC comparatible
COMPTRE: RADABLE FORM:
MEDIUW TYPE: PLOOF MAS-DOS
CURRENT APPLICATION NUMBER: 18/60/766,253
FILING DATE: 197-04-25
APPLICATION NUMBER: 18/70/76,253
FILING DATE: 197-04-25
APPLICATION NUMBER: 18/70/76,253
FILING DATE: 197-04-25
ATTORNEY/AGRY TWFORMYTON:
MENE: APPLICATION NUMBER: 015399-002920US
FILING DATE: 197-04-25
ATTORNEY/AGRY TWFORMYTON:
MENE: APPLICATION NUMBER: 015399-002920US
FILERDHOME: (415) 576-0200
FILERDHOME: (415) 576-0200
FILERDHOME: (415) 576-0200
FILERDHOME: (415) 576-0200
FILERDHOME: CHARACTERESTICS:
LENGTH: 50 base pairs
FURCHIST SO base pairs
FURCHIST SO base pairs
FURCHIST TOPOLOGY: Innear
MOLECULE TYPE: other mulcled caid
STRANDEDNESS: single
MOLECULE TYP
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Search completed: February 15, 2006, 21:14:09 Job time : 48.9587 secs

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8         84.0         48         5         US-10-053-758-37         Sequence 3.7           8         84.0         48         5         US-10-053-758-40         Sequence 40           8         84.0         48         5         US-10-054-295-37         Sequence 3.7           8         84.0         48         5         US-10-054-611-37         Sequence 3.7           8         84.0         48         5         US-10-054-611-40         Sequence 4.7           8         84.0         48         5         US-10-054-611-40         Sequence 4.7           8         84.0         48         8         US-10-054-611-40         Sequence 5.6           8         84.0         48         8         US-10-07-564         Sequence 5.6           8         84.0         48         8         US-10-877-022-564         Sequence 5.6           8         40         6         6	16 80.0 16 3 US-09-76-253-61 Sequence 51 80.0 16 3 US-09-76-253-61 Sequence 61 80.0 16 3 US-09-76-253-61 Sequence 61 80.0 16 3 US-09-76-253-61 Sequence 61 80.0 16 5 US-10-054-295-61 Sequence 61 80.0 16 5 US-10-054-295-61 Sequence 61 80.0 16 5 US-10-054-295-61 Sequence 61 80.0 16 8 US-10-87-11-61 Sequence 61 80.0 16 8 US-10-877-124-114 Sequence 11 80.0 16 8 US-10-877-124-114 Sequence 11 80.0 16 8 US-10-877-124-114 Sequence 11 80.0 16 8 US-10-877-124-114	4 77.0 10 10 10.51.1166-990-39 Sequence 11   4 77.0 19 8 US-11166-990-39 Sequence 12   4 77.0 19 9 US-10-973-783-1416 Sequence 12   4 77.0 25 9 US-10-956-157-129722 Sequence 12   4 77.0 26 10 US-11049-446-60 Sequence 12   76.0 26 5 US-10-085-906-51 Sequence 51   8 74.0 22 9 US-10-708-204-1790 Sequence 16   8 74.0 22 9 US-10-708-204-1790 Sequence 17   8 74.0 22 9 US-10-708-204-1790 Sequence 17   8 74.0 22 9 US-10-708-204-1790 Sequence 17   8 74.0 24 3 US-98-326-735 Sequence 73   8 74.0 27 9 US-10-708-204-1790 Sequence 17   8 74.0 27 9 US-10-708-204-1790 Sequence 17   8 74.0 27 9 US-10-708-204-1790 Sequence 17   8 74.0 28 9 US-10-708-204-179	4.8 74.0 24 3 US-09-776-479-694 Sequence 69 4.8 74.0 24 3 US-09-776-479-694 Sequence 69 4.8 74.0 24 3 US-09-776-479-692 Sequence 69 4.8 74.0 24 3 US-09-776-479-692 Sequence 69 4.8 74.0 24 3 US-09-776-479-694 Sequence 69 4.8 74.0 24 3 US-09-776-479-694 Sequence 69 4.8 74.0 24 5 US-10-112-653-665 Sequence 69 4.8 74.0 24 5 US-10-017-955-694 Sequence 69 4.8 74.0 24 6 US-10-140-013-32 Sequence 69 4.8 74.0 24 6 US-10-140-013-32 Sequence 69 4.8 74.0 24 6 US-10-314-578-692 Sequence 69 4.8 74.0 24 6 US-10-314-578-693 Sequence 69 4.8 74.0 24 6 US-10-314-578-893 Sequence 69 4.8 12.0 24 6 US-10-314-578-894 Sequence 69 4.8 12.0 24 6 US-10-314-578-894 Sequence 69 4.9 12.0 24 6 US-10-314-	4.0 24 6 US-10-309-775A-6 4.0 24 8 US-10-309-775A-6 4.0 24 8 US-10-811-778-694 Sequence 69 4.0 24 8 US-10-811-778-694 Sequence 69 4.0 24 8 US-10-811-778-883 Sequence 89 4.0 17 8 US-10-845-667-285 Sequence 28 2.0 23 8 US-10-945-667-1250 Sequence 12 2.0 23 8 US-10-845-667-1480 Sequence 12 2.0 50 6 US-10-131-827-5465 Sequence 51 2.0 25 7 US-10-719-956-215749 Sequence 51 2.0 25 7 US-10-719-956-215749 Sequence 51 2.0 25 7 US-10-719-956-215749 Sequence 51 2.0 25 7 US-10-719-960-519045 Sequence 51 2.0 25 3 US-09-843-660 Sequence 51 2.0 26 3 US-09-843-660 Sequence 50 2.0 26 3 US-09-448-60 Sequence 60 2.0 26 5 US-10-053-758-60 Sequence 60

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RESULT 2
US-09-776-479-73
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sequence 73, Application US/09776479
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spublication No. US2004067902A9
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spublication No. US2004067902A9
spublication No. US204040
spublication No. Transminostimulatory Nucleic Acids for the TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Treatment of Asthma and Allergy
spublication NUMBER: US/09/776,479
cURRENT APPLICATION NUMBER: US 60/179,991
spior Filing DATE: 2000-02-03
spiorware Fago for Windows Version 3.0
seQ ID NO 73
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 20; DB 3; Length 20; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 20; Conservative 0; Mismatches 0; Indels
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FILE REFERENCE: C1037/7013 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/776,479
CURRENT FILING DATE: 2001-02-02
FRIOR APPLICATION NUMBER: US 60/179,991
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 73
LENGTH: 20
                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-776-479-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Synthetic Sequence US-09-776-479-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TTTTGGGGTTTTGGGGTTTT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-112-653-67
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                                                                                                                                                                                                                                                                                                                                            Sequence 130181,
Sequence 164159,
Sequence 235930,
Sequence 84, Appl
                                                                                                  Sequence 141, App
Sequence 93343, A
Sequence 95877, A
Sequence 103736,
Sequence 142300,
Sequence 142301,
Sequence 142301,
Sequence 142301,
Sequence 142301,
Sequence 142301,
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Sequence 80391, A
Sequence 80391, A
Sequence 90443, A
Sequence 188477,
Sequence 188477,
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          Sequence 1070, Ap
                                653453,
161728,
912559,
                                Sequence Sequence 3
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  US-10-719-956-1070
US-10-719-956-1070
US-10-719-906-653453
US-10-719-900-91259
US-10-719-900-91259
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US-10-843-527-134311
US-10-843-527-134311
US-10-843-527-134311
US-11-060-756-164159
US-11-060-756-164159
US-11-060-756-164159
US-10-257-017B-90443
US-10-257-017B-90443
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US-10-257-017B-90443
US-10-257-017B-90443
US-10-257-017B-188477
US-10-257-017B-188477
US-10-257-017B-188477
US-10-257-017B-188477
US-10-257-017B-188477
US-10-473-126-1035
US-10-473-126-1035
US-10-473-126-1035
US-10-473-126-1036
US-10-881-118-128-107
US-10-973-783-898-107
US-10-973-783-898-107
US-09-776-479-358

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Sequence 67, Application US/10112653
Sequence 67, Application US/10112653
Publication No. US2003005026841
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Krieg, Daniel J.
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
TITLE REFERENCE: CO1039/70060(AMS)
CURRENT APPLICATION NUMBER: US/10/112,653
CURRENT FILING DATE: 2002-03-29
PRIOR PILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 1040
TTTTGGGGTTTTGGGGTTTT 20
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APPLICANT: Bratzler, Robert L.
APPLICANT: Petersen, Deanna M.
APPLICANT: Fouron, Yves
TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
TITLE OF INVENTION: Treatment of Asthma and Allergy

Sequence 73, Application US/09776479 Publication No. US20030087848A1 GENERAL INFORMATION:

RESULT 1 US-09-776-479-73

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Gaps

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Length 20; Indels

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; OTHER INFORMATION: Synthetic Sequence US-10-314-578-73
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Best Local Similarity 100.
Matches 20; Conservative
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1 Sequence 73, Application US/10017995

2 Sequence 73, Application US/10017995

3 Publication No. US20030055014A1

3 GENERAL INFORMATION:

3 APPLICANT: Bratzler, Robert L.

4 TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids

5 FILE REFERENCE: C1037/7025 (HCL/MAT)

6 CURRENT FILING DATE: 2001-12-18

7 FILE REPERENT FILING DATE: 2000-12-14

7 NUMBER OF SEQ ID NOS: 1093

7 SOFTWARE: FastSEQ for Windows Version 3.0

7 SEQ ID NO 73

7 LENGTH: 20
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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
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US-10-314-578-73
US-10-314-578-73
Sequence 73, Application US/10314578
Publication No. US20030212026A1
SEQUENCE INFORMATION:
APPLICANT: Kineg, Arthur M.
APPLICANT: Vollmer, Gorg
TITLE OF INVENTION: Immunostimulatory Nucleic Acids
FILE REPERENCE: C1039/7035 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/10/314,578
CURRENT APPLICATION NUMBER: US 60/156,113
PRIOR APPLICATION NUMBER: US 60/156,113
PRIOR APPLICATION NUMBER: US 60/156,113
PRIOR APPLICATION NUMBER: US 60/156,135
PRIOR PLING DATE: 1999-09-27
PRIOR FILING DATE: 1999-09-27
PRIOR FILING DATE: 1909-09-27
PRIOR PLING DATE: 1000-08-23
NUMBER OF SEQ ID NOS: 1145
SEQ ID NOS: 1145
LENGTH. 20
                                                                                                                                ; OTHER INFORMATION: Synthetic Oligonucleotide US-10-112-653-67
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                            TYPE: DNA ORGANISM: Artificial Seguence
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 20; Conserva
                       SEQ ID NO 67
LENGTH: 20
                                                                                                                             FEATURE:
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APPLICANT: Bates, Paula J
APPLICANT: Trent, John O
APPLICANT: Trent, John O
APPLICANT: Trent, John O
APPLICANT: Xi, Xiaohua
TITLE OF INVENTION: A NEW METHOD FOR THE DIAGNOSIS AND PROGNOSIS OF MALIGNANT
TITLE OF INVENTION: DISEASES
FILE REPERENCE: 9799910-
CURRENT APPLICATION NUMBER: US/10/118,854
CURRENT FILING DATE: 2003-04-08
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.2
SEQ ID NO 28
LENGTH: 28
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### Septicant: Bratzler, Robert L.

### APPLICANT: Bratzler, Robert L.

### APPLICANT: Fouron, Yves

### TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the ITILE OF INVENTION: Treatment of Asthma and Allergy

### FILE REFERENCE: C1037/7013 (HCL/MAT)

### CURRENT FILING DATE: 2004-04-23

### PRIOR APPLICATION NUMBER: US/10/831,778

### PRIOR APPLICATION NUMBER: US/10/831,778

### PRIOR PILING DATE: 2000-02-03

### WUMBER OF SEQ ID NOS: 1093

### SOFTWARE: FastSEQ for Windows Version 3.0

### ENGTH: 20
  Length 20;
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                                               Indels
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Query Match
100.0%; Score 20; DB 6; 1
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0;
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Pred. No. 1.2e+02;
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Pred. No. 1.2e+02;
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; OTHER INFORMATION: synthetic oligonucleotide
US-10-118-854-28
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100.0%; Pre
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ORGANISM: Artificial Sequence
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Best Local Similarity
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Sequence 29, Application US/10961479

Sequence 29, Application US/10961479

Publication No. US20050187176A1

GENERAL INFORMATION:

APPLICANT: BATES, PAULA J.

APPLICANT: BARVE, SHIRISH S.

TITLE OF INVENTION: METHOD FOR INHIBITING NF-KAPPA B SIGNALING AND USE TO TITLE OF INVENTION: METHOD FOR INHIBITING NF-KAPPA B SIGNALING AND USE TO TITLE OF INVENTION: METHOD FOR INHIBITING NF-KAPPA B SIGNALING AND USE TO TITLE OF INVENTION: METHOD FOR INHIBITING NF-KAPPA B SIGNALING AND USE TO CURRENT FILING DATE: 2004-10-08

CURRENT FILING DATE: 2003-10-10

NUMBER OF SEQ ID NOS: 43

SEQ ID NO 29

LENGTH 28

LENGTH 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 28;
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US-10-690-984-11
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100.0%; Score 20; DB 9; L
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0;
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100.0%; Score 20; DB 9; I
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0;
                                                                   US-10-690-984-11

Sequence 11, Application US/10690984

Sequence 11, Application US/10690984

PUDLICATION: US20050090671A1

GENERAL INFORMATION:
APPLICANT: Chang, Ta-Chau
APPLICANT: Chang, Cheng-Chung
APPLICANT: Wu, Jin-Yi
TITLE OF INVENTION: QUARRUPLEX STABILIZER
FILE REFERENCE: 08919-112001
CURRENT APPLICATION NUMBER: US/10/690,984
CURRENT FILING DATE: 2003-10-22
NUMBER OF SEQ ID NOS: 13

SOGTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 11

LENGTH: 28
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; Patent No. US20020164786Al
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                                                                                                                                                                                                                                                                                                           APPLICANT: Bates, Paula J
APPLICANT: Bates, Paula J
APPLICANT: Bates, Paula J
APPLICANT: Mi, Yingchang
TITLE OF INVENTION: DISBASES
FILE REFERENCE: 09799910-0034
CURRENT APPLICATION NUMBER: US/10/607,455
CURRENT APPLICATION NUMBER: 06.26
PRIOR APPLICATION NUMBER: 60/392,143
PRIOR FILING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.2
SEQ ID NO 28
LENGTH: 28
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US-10-683-480-28
j Sequence 28, Application US/10683480
j Sequence 28, Application US/10683480
j Publication No. US20050053607A1
j GENERAL INFORMATION:
j APPLICANT: BATES, PAULA J.
j APPLICANT: HILER, DONALD M.
j APPLICANT: TRENT, JOHN O.
j APPLICANT: WILLER, DONALD M.
j TITLE OF INVENTION: A NEW METHOD FOR THE DIAGNOSIS OF
j TITLE OF INVENTION: MALIGNANT DISEASES
j FILE REPRENCE: LOUG-102-CIP-US
j CURRENT FILING DATE: 2003-10-09
j PRIOR APPLICATION NUMBER: 10/118,854
j PRIOR FILING DATE: 2002-04-08
j NUMBER OF SEQ ID NOS: 38
j SOFTWARE: PATCHIN Ver. 3.2
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  0; Indels
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100.0%; Score 20; DB 7; L
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , OTHER INFORMATION: synthetic oligonucleotide US-10-607-455-28
  0; Mismatches
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US-10-607-455-28
Sequence 28, Application US/10607455; Publication No. US20040132049A1; GENERAL INFORMATION:
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     20; Conservative
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LENGTH: 28
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     Matches
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/766,253

FILING DATE: 19-Jan-2001

CLASSIFICATION: AUNKNOWN>
PRIOR APPLICATION: AUNKNOWN>
PRIOR APPLICATION NUMBER: US/09/46,017

FILING DATE: 1997-04-25

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

ATTORNEY AGENT INFORMATION:

NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002920US

TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 20; DB 3; Length 44; 100.0%; Pred. No. 1.2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cach, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Marcews, Walliam H.
TITLE OF INVENTION: No. US20030009019Alel Telomerase
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
Andrews, William H.
TITLE OF INVENTION: No. US20020187471A1el Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
                                                                                                           ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Two Embarcadero Center, 8th Floor
                                                                                                                                                                                     STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECTULE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA" SEQUENCE DESCRIPTION: SEQ ID NO: 42:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: United States of America ZIP: 94111-3834
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 42, Application US/09438486
Publication No. US20030009019A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 44 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                             CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20; Conservative
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STATE: California
COUNTRY: United Stat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-766-253-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                CITY: San Figure.

STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 26-Apr-2001
CLASSIFICATION NUMBER: US 08/846,017
APPLICATION NUMBER: US 08/846,017
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 10-OCT-1996
ATTORNY/AGENT INDORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,420
TELEPHONE: (415) 576-0200
TELEPRAX: (415) 576-0200
TELEPRAX: (415) 576-0300
INNORMATION POR SEG ID NO: 42:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 20; DB 3; Length 44; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels
                                                                            Nakamura, Toru-Chapman, Karen B.
Morin, Greeg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020164786Alel Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                    ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 );
DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-843-676-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 42, Application US/09766253
Publication No. US20020187471A1
GENERAL INFORMATION:
Lingner, Joachim Nakamura, Toru Chapman, Karen B.
Morin, Greeg B.
Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TITIGGGGTTTTGGGGGTTTT 20
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                               Cech, Thomas R.
Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%;
Matches 20; Conservative C
                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
       GENERAL INFORMATION:
APPLICANT: Cech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-09-766-253-42
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Andrews, William H.
TITLE OF INVENTION: No. US20030044953A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFRENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 42:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 20; DB 5; I
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    );
DESCRIPTION: /desc = "DNA"
;
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-053-758-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
          COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 42, Application US/10054295
Publication No. US20030044953A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingper, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030032075A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                            FILING DATE: 14-NOV-11.7.

CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 05-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION NUMBER: US 08/724,643
FILING DATE: 10-OCT-1996
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION NUMBER: 36,429
FILING DATE: 01-OCT-1996
CLASSIFICATION INFORMATION:
NAME: APPLICATION NUMBER: 36,429
FELERHORE/DOCKET NUMBER: 36,429
FELERHORE (415) 576-0200
FELERHORE CHARACTERISTICS:
FUNNTAL: 44 hare Dairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                APPLICATION NUMBER: US/09/438,486
FILING DATE: 12-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 42, Application US/10053758
Publication No. US20030032075A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
The Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
US-10-053-758-42
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Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SECUENCES: 633
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPRY disk

MEDIUM TYPE: RIOPRY disk

MEDIUM TYPE: RIOPRY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/325,810

FILING DATE: 20-Dec-2002

CLASSIFICATION: AUNKNOWN->

PRIOR APPLICATION: AUNKNOWN->

PRIOR APPLICATION NUMBER: US/09/402,181

FILING DATE: 20-Sep-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: US-APR-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: US-APR-1997

APPLICATION NUMBER: US 08/851,843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 44;
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                         FILING DATE: 18-APR-1997

FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 36,429

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 20; DB 5; I 100.0%; Pred. No. 1.2e+02; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEG ID NO: 42:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 568, Application US/10325810
Publication No. USZ00030204069A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TTTTGGGGTTTTGGGGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 44 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-325-810-568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-054-611-42
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US-10-054-611-42
Sequence 42, Application US/10054611
Sequence 43, Application US/10054611
Sequence 44, Applicat
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION MMBRR: US/10/054,611
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/854,050

FILING DATE: «Unknown: 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 10-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002930US

TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
BESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-054-295-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 576-0200
TELEFAR: (415) 576-0300
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
DATE: 18-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TTTTGGGGTTTTGGGGGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 44 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 20; Conservative
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Sequence 568, Application US/10877022

Publication No. US20040247613A1

GENERAL INFORMATION:
    Linguer, Joachim
    Nakamura, Toru
    Chapman, Karen B.
    Marin, Gregg B.
    Harley, Calvin B.
    Andrews, William H.
    TITLE OF INVENTION: Human Telomerase Catalytic Subunit NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:
    ADDRESSER TOWNSEND AND ELEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 20; DB 8; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: /note= "hairpin primer" SEQUENCE DESCRIPTION: SEQ ID NO: 568:
                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                         AFFLICATION NUMBER: US 09/840,017
AFFLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAX-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
FILING DATE: 01-OCT-1997
FILING DATE: 01-OCT-1997
FILING DATE: 01-OCT-1997
                                             US 08/846,017
                         FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 0
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TTTTGGGGTTTTGGGGTTTT 20
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                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 44 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPAX: (415) 576-0.
INFORMATION FOR SEQ ID NO: 568
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1..44
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-877-022-568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-877-124-568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 20
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Publication No. US20040242529A1

GENERAL INFORMATION:

Linguer, Joachim
Nakamura, Toru
Chapman, Karen B.
Morth, Gregg B.
Harley, Calvin B.
Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 20; DB 6; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1..44
; CTHER INFORMATION: /note= "hairpin primer"
; SEQUENCE DESCRIPTION: SEQ ID NO: 568:
US-10-325-810-568
                                                                                                                                                                                                NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION:
TELEPHONE: (415) 576-0200
TELEFA: (415) 576-0300
INFORMATION FOR SEQ ID NO: 568:
SEQUENCE CHARACTERISTICS:
                                                                FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/432,503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 02-Nov-1999
APPLICATION NUMBER: 08/974,549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TTTTGGGGTTTTGGGGTTTT 20
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                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 19
US-10-877-124-568
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Gaps

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                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                    STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1..44

GTHER INFORMATION: /note= "hairpin primer"

SEQUENCE DESCRIPTION: SEQ ID NO: 568:
US-10-877-146-568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 100.0%; Score 20, DB 8; L Similarity 100.0%; Pred. No. 1.2e+02; 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-Nov-1999
APPLICATION NUMBER: 08/974,549
FILING DATE: cloacnown
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APF-1997
APPLICATION NUMBER: US 08/866,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/851,843
                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/877,146
FILING DATE: 24-Jun-2004
CLASSIFICATION: <UNKNOWN>
                              and Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION TELEPHONE: (415) 576-020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 41, Application US/09843676 Patent No. US20020164786A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TTTTGGGGTTTTGGGGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 20; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 22
US-09-843-676-41
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Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 20; DB 8; Length 44; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels
                           Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 01-0CT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-0CT-1997
ATORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 31,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: 1..44
; OTHER INFORMATION: /note= "hairpin primer"; SEQUENCE DESCRIPTION: SEQ ID NO: 568:
US-10-877-022-568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
FILING DATE: 14-AUG-1997
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
                                                                                                                                                 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-NOv-1999
APPLICATION NUMBER: US/09/4,549
FILING DATE: vUnknown>
APPLICATION NUMBER: US 08/44,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/86,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/81,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/851,650
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/877,022
FILING DATE: 24-Jun-2004
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/911,312
OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 568, Application US/10877146
Publication No. USZ0050013825A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Oacthim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELETRY: (415) 576-0300
INFORMATION FOR SEQ ID NO: 568:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TITIGGGGTTTTGGGGTTTT 20
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Matches 20; Conservative
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US-10-877-146-568
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                                                                                                                           SITABEL: 140 BEMARICAGETO CENTER, CENTER, CALIFORNIA COUNTRY: United States of America COUNTRY: United States of America COUNTRY: United States of America CONPUTER: Lab PC Compatible COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/09/766,253 FILING DATE: 19-Jan-2001 CLASSIFICATION AUMBER: US/08/66,017 FILING DATE: 199-O4-25 FILING DATE: 199-O4-25 FILING DATE: 190-O4-25 FILING DATE: 01-OCT-1996 ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-438-486-41
; Sequence 41, Application US/09438486
; Publication No. US20030009019A1
; Beblication No. US20030009019A1
; Publication No. US20030009019A1
; APPLICANT: Cech, Thomas R.
APPLICANT: Lingmer, Joachim
APPLICANT: Maxmura, Toru
; APPLICANT: Maxmura, Karen B.
APPLICANT: Marzley, Calvin
; APPLICANT: Andrews, William H.
; TILLE OF INVENTION: No. US20030009019A1e1 Telomerase
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
              TITLE OF INVENTION: No. US20020187471A1el Telomerase NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Apple, Randolph T. REGISTRATION NUMBER: 36,429 REFERENCE/DOCKET NUMBER: 015389-002920US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 20; DB 3; I
100.0%; Pred. No. 1.2e+02;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California COUNTRY: United States of America ZIP: 94111-3834 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           );
SEQUENCE DESCRIPTION: //desc = "DNA"
;
US-09-766-253-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
Andrews, William H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
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LENGTH: 46 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TTTTGGGGTTTTGGGGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 576
TELEFAX: (415) 576-0
INFORMATION FOR SEQ ID NO: 41:
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Best Local Similarity 100.
Matches 20; Conservative
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100.0%; Score 20; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
            APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamuza, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020164786Alel Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIPICATION: 536
                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR CHASTICATION DATA:

APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
PILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
APPLICATION NUMBER: US 08/724,643
APTORNEY/AGBNT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ 11 NO: 41:
                                                                                                                                                                                                                                                                                                                                                        COUNTRY: United States of America ZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 41. Application US/09766253
Publication No. US20020187471A1
GENERAL INFORMATION:
APPLICANT: Cech. Thomas R.
Lingner, Joachim Nakamura, Toru Chapman, Karen B.
Morin, Greeg B.
Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 TTTTGGGGTTTTGGGGTTTT 46
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LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                    STATE: California
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-843-676-41
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US-09-766-253-41
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Gaps

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Gaps
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100.0%; Pred. No. 1.2e+02;
iive 0; Mismatches 0; Indels
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Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: NO. US20030044953A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: IB-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                      APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECTLE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 41, Application US/10054295; Publication No. US20030044953A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TITIGGGGTTTTGGGGTTTT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 46 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 41: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 26
US-10-054-295-41
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Sequence 41, Application US/10053758

Publication No. US20030032075A1

GENERAL INFORMATION:

Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin

TITLE OF INVENTION: No. US20030032075A1e1 Telomerase
NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:

STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 20; DB 3; Length 46; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/438,486
FILING DATE: 12-NOV-1999
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION: 536
CLASSIFICATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION: 536
CLASSIFICATION: 536
CLASSIFICATION: 536
CLASSIFICATION: 536
CLASSIFICATION: 536
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APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/724,643
APPLICATION NUMBER: US 015389-002931US
REPERENCE/DOCKET NUMBER: 015389-002931US
TELEPAN: (415) 576-0300
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: NUCLEIC acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 rrrrccccrrrrccccrrrr 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; P
Matches 20; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-438-486-41
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TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California COUNTRY: USA ZIP: 94111-3834 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: ISM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                         NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 20; DB 5; 1
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181
FILING DATE: 29-5ep-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
                       FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,810
FILING DATE: 20-Dec-2002
CLASSIFICATION: <unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/854,050
                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

BESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-054-611-41
                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 567, Application US/10325810
Publication No. US200030204069A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachlim
Nakamura, Toru
Chapman, Karen B.
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Harley, Calvin B.
                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TITIGGGGTTTTGGGGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%;
Matches 20; Conservative 0
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US-10-325-810-567
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Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030059787A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                  NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 41:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 20; DB 5; L
100.0%; Pred. No. 1.2e+02;
                                                                                      FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: «Unknown»
PPLING DATE: 25-APR-1997
FILING DATE: 25-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,611
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
                                           PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/854,050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 41, Application US/10054611
Publication No. US20030059787A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
  DATE: 18-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TTTTGGGGTTTTGGGGTTTT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 46 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 20; Conservative
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US-10-054-611-41
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Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 46;
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                                                                       APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 05-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
APPLICATION NUMBER: US 08/911,312
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,503
FILING DATE: 10-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: SO PCT/US97/17885
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: SO PCT/US97/17885
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: NO PCT/US97/17885
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: 01-OCT-1997
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COTHER INFORMATION: /note= "hairpin primer"

SEQUENCE DESCRIPTION: SEQ ID NO: 567:
US-10-877-124-567
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100.0%; Pred. No. 1.2
:ive 0; Mismatches
            08/844,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 567, Application US/10877022; Publication No. US20040247613A1; GENERAL INFORMATION:
            APPLICATION NUMBER: US 0 FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TTTTGGGGTTTTGGGGTTTT 20
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INFORMATION FOR SEQ ID NO: 567:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 TITIGGGGTTTTGGGGTTTT
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Matches 20; Conservative
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| Sequence 567, Application US/205040
| Publication No. US20040245529A1
| GENERAL INFORMATION:
| Lingner, Joachim | Nakamura, Toru | Chapman, Karen B. | Harley, Calvin B. | Harley, Calvin B. | Harley, Calvin Human Telomerase Catalytic Subunit | NUMBER OF SEQUENCES: 72 | CORRESPONDENCE ADDRESSE: Townsend and Townsend and Crew LLP | STREET: Two Embarcadero Center, Eighth Floor | CITY: San Francisco | STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/877,124
FILING DATE: 24-Jun-2004
CLASSIFCATION: <underween volume of the compation of the compatible of the companion of the c
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LOCATION: 1..46
OTHER INFORMATION: /note= "hairpin primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 567:
                                                                                                                                                                                                                                                                                                                                                                   NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 567:
SEQUENCE CHARACTERISTICS:
ILENGTH: 45 base pairs
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
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FILING DATE: 02-Nov-1999
APPLICATION NUMBER: 08/974,549
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                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-877-124-567
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                                                                                                                                          ZIP: 94111-3834
COMPUTER READABLE FORM:
MADLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                       Townsend and Crew LLP
Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: /note= "hairpin primer";
SEQUENCE DESCRIPTION: SEQ ID NO: 567:
                                                                                                                                                                                                                                                                           APPLICATION DATA:

APPLICATION NUMBER: US/10/877,146
FILING DATE: 24-Jun-2004
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: US/99/432,503
FILING DATE: 02-Nov-1999
APPLICATION NUMBER: US/99/4,549
FILING DATE: 13-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 13-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 10-APR-1997
APPLICATION NUMBER: US 08/911,312
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-CCT-1997
TTORNEY/AGENT INFORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 20; DB 8; 1
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (415) 576-0200
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US-09-843-676-37
Sequence 37, Application US/09843676
; Patent No. US20020164786A1
                            ADDRESSEE: Townsend and STREET: Two Embarcadero
                         Townsend and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TITIGGGTTTTGGGGTTTT 20
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INFORMATION FOR SEQ ID NO: 567:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
                                                                     CITY: San Francisco
STATE: California
COUNTRY: USA
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
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Harley, Calvin B.
Hadrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 46;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA
APPLICATION NUMBER: US/10/877,022
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LOCATION: 1..46
OTHER INFORMATION: /note= "hairpin primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 567:
                                                                                                                                   PRIOR APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-NOV-1999
APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-NOV-1999
APPLICATION NUMBER: US 08/844,419
FILING DATE: 4URNOWN-
APPLICATION NUMBER: US 08/846,017
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 01-OCT-1997
ATTORNEY/AGRATI INFORMATION: UNMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGRATI INFORMATION: UNMBER: WO PCT/US97/17885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 20; DB 8; I
100.0%; Pred. No. 1.2e+02;
tive 0; Mismatches 0;
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US-10-877-146-567
Sequence 567, Application US/10877146
Publication No. US20050013825A1
GENERAL INFORMATION:
JAMPHINGRAT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Crey B.
                                                                                          FILING DATE: 24-Jun-2004
CLASSIFICATION: <Unknown>
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INFORMATION FOR SEQ ID NO: 567:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 46 base pairs
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Best Local Similarity 100.
Matches 20; Conservative
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COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 6-Apr-2001
CLASSIFICATION S36
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/44,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: ANALY AGENT INFORMATION:
NAME: ANALY AGENT INFORMATION:
NAME: ANALY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 48;
                      TITLE OF INVENTION: No. US20020164786A1el Telomerase NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 20; DB 3; Length 48
100.0%; Pred. No. 1.2e+02;
tive 0; Mismatches 0; Indels
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Andrews, William H.
TITLE OF INVENTION: No. US20020187471Alel Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSES: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
FREFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                      STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLGGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
     Andrews, William H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 37, Application US/09766253
Publication No. US20020187471A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TTTTGGGGTTTTGGGGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Triregedrificederrir 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                       ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
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US-09-766-253-37
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                                                                                                                 MOTIN, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020164786Alel Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STRET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002930US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEPHONE: (415) 576-0300

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/854,050
                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA" SEQUENCE DESCRIPTION: SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 40, Application US/09843676
Patent No. US20020164786A1
GENERAL INFORMATION:
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
                    Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TTTTGGGGTTTTGGGGTTTT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100...
Loca 20; Conservative
                         APPLICANT: Cech,
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-843-676-40
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Length 48;
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APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Naxamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
APPLICANT: Andrews, William H.
APPLICANT: ANDREWS, William H.
APPLICANT: ANDREWS, William H.
          PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTOREY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California COUNTRY: United States of America ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION NAMBER: US/09/438,486 FLING DATE: 12-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 20; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIPICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 37, Application US/09438486; Publication No. US20030009019A1 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TTTTGGGGTTTTGGGGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: other 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-766-253-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 36
US-09-438-486-37
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Lingner, Joachim
Nakamura, Toru
Chaman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020187471Aiel Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRIN APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION: AUDKNOWN>
PRIOR APPLICATION: AUDKNOWN>
PRIOR APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNY/AGENT INPERMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 20; DB 3; Length 48; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELECOMMUNICATION INFORMATION:
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: California
COUNTRY: United States of America
ZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/766,253 FILING DATE: 19-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 40, Application US/09766253
Publication No. US20020187471A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TTTTGGGGTTTTGGGGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 576-
INFORMATION FOR SEQ ID NO: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 35
US-09-766-253-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-766-253-37
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Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: NO. US20030032075Alel Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 20; DB 3; I 100.0%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTET READABLE FORM:

MEDIUM TYPE: RIOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Ver

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/053,758

FILING DATE: 18-Jan-2002

CLASSFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/654,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 01-OCT-1996
                                                                                                                                                                                                015389-002931US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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               PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: APPLE, Randolph T.
REFERENCE/DOCKET NUMBER: 05.429
REFERENCE/DOCKET NUMBER: 015389-0029;
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 37, Application US/10053758
Publication No. US20030032075A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TTTTGGGGTTTTGGGGTTTT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-438-486-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 38
US-10-053-758-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 20; DB 3; Length 48; llarity 100.0%; Pred. No. 1.2e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Greeg B.
APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
TITLE OF INVENTION: No. US2003009019Alel Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/438,486
FILING DATE: 12-000-1999
FILING DATE: 12-000-1999
FILING PAPLICATION NUMBER: US 08/851,843
FILING APPLICATION DATA:

APPLICATION NUMBER: US 08/851,843
FILING DATE: 05-000-1997
CLASSIFICATION S36
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/846,017
FILING APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
               CLASSIFICATION 536
PRIOR APPLICATION 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/724,643
FILING DATE: 01-0CT-1996
CLASSIFICATION: 536
ATTORNEY AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002931US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: California
COUNTRY: United States of America
ZIP: 9411-1834
COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
DESCRIPTION: /desc = "DNA"
US-09-438-486-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 37
US-09-438-486-40
Sequence 40, Application US/09438486
Publication No. US20030009019A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TITIGGGGTTITGGGGTTIT 20
18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
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Best Local Similarity
Matches 20; Conserv
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Andrews, William H.
TITLE OF INVENTION: No. US20030044953Alel Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 20; DB 5; 1
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/054,295
FLING DATE: 18-Jan-2002
CLASSIFICATION: 336
PRIOR APPLICATION DATA:
APPLICATION DATE: 08/854,050
FILING DATE: *CURROWN-APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                             TOPOLOGY: linear
MOLECTULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cech, Thomas R. Lingner, Joachim Nakamura, Toru Chapman, Karen B. Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 37, Application US/10054295 Publication No. US20030044953A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              1 TITIGGGGTTTTGGGGTTTT 20
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                                                               LENGTH: 48 base pairs
                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                  INFORMATION FOR SEQ ID NO: 40
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94111
COMPUTER READABLE FORM:
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US-10-053-758-40
is Sequence 40, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.;
; Applicand Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030032075A1e1 Telomerase
                                                                                                                                                                                                                                                                                                                                                                                     Length 48;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
           REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 20; DB 5; I 100.0%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/654,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/646,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: California COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                          LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 576-0200
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Randolph T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
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                                                                                                          TELEFAX: (415) 576-0.
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
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Length 48;
  Indels
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TITLE OF INVENTION: No. US20030059787A1el Telomerase NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
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100.0%; Pred No. 1.2e+02;
Micmatches 0;
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APPLICATION NUMBER: 08/854,050
FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APF-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
ATTORNEY/AGENT INFORMATION:
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States of America
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// MOLECULE TYPE: other nucleic acid
// DESCRIPTION: /desc = "DNA"
// SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-054-611-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (415) 576-0200
                                                                                                                                                       RESULT 42
US-10-054-611-37
US-10-054-611-37
; Sequence 37, Application US/10054611; Publication No. US20030059787A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.;
Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION TELEPHONE: (415) 576-020
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                                                                                       29 Trirggggrrrrggggrrrr 48
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Chapman, Karen B.
Morin, Gregg B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
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STATE: California
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INFORMATION FOR SEQ ID NO: 37
20; Conservative
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nes 20; Conservative
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  Matches
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Matches
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                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Andrews, William H.

TITLE OF INVENTION: No. US20030044953Alel Telomerase NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
RADRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0200
                                                                                                         Score 20; DB 5;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 20; DB 5; I
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/754,643
FILING DATE: 01-OCT-1996
                                                                                                       Query Match 100.0%; Score 20; DE Best Local Similarity 100.0%; Pred. No. 1.2 Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

BESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-054-295-40
                    DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
other nucleic acid
                                                                                                                                                                                                                                                                                            RESULT 41
US-10-054-295-40
; Sequence 40, Application US/10054295
; Publication No. US20030044953A1
; GENERAL INFORMATION:
. APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                           : Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
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                                                                                                                                                                                              1 TTTTGGGGTTTTGGGGTTTT 20
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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MEDIUM TYPER: Floppy disk
COMPUTER: IN PC Compatible
COMPUTER: IN PC COMPATIBLE TILING DATA:
APPLICATION NUMBER: US/10/325,810
FILING DATE: 20-Dec-2002
CLASSIFICATION NUMBER: US/09/402,181
FILING DATE: 29-Sep-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,312
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,312
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: US 08/911,312
                                                                               Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 20; DB 6; Length 48; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                            ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                יחבר אחבר אבייה באבר /note= "hairpin primer";
US-10-325-810-564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Ausenhus, Scott L. REGISTRATION NUMBER: 42,271 REFERENCE/DOCKET NUMBER: 015389-002620US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TTTTGGGGTTTTGGGGTTTT 20
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                                                                Harley, Calvin B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415) 576-03
INFORMATION FOR SEQ ID NO: 564:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
Nakamura, Toru
                                                                                                                                                                                                                                            CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1..48
OTHER INFORMATION:
                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
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                                                                                                                                                                                                                                  Harley, Calvin
Andrews, William H.
IITLE OF INVENTION: NO. US20030059787A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAWE: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ 1D NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 20; DB 5; I
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: United States of America ZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,611
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
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Publication No. US;0030204069A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
                                              Sequence 40, Application US/10054611
Publication No. US20030059787A1
GENERAL INFORMATION:
                                                                                                                   Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
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LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: California
                                                                                                                      APPLICANT: Cech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-325-810-564
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SEQUENCE CHARACTERISTICS
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US-10-877-022-564
US-10-877-124-564
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRNT APPLICATION DATA:
APPLICATION NAMBER: US/10/877,124

FILING DATE: 24-Jun-2004

CLASSIFICATION: < Unknown>
                                                                                                                                                                                                                                Morin, Greeg B.
Harley, Calvin B.
Andrews, William H.
INVENTION: Human Telomerase Catalytic Subunit
                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco CATTE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION: 1..48
OTHER INFORMATION: /note= "hairpin primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 564:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 14-AUG-1997
APPLICATION WUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
FILING DATE: 01-OCT-1997
FILING DATE: 01-OCT-1997
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APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-NOV-1999
APPLICATION NUMBER: 08/974,549
FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APF-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APF-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APF-1997
APPLICATION NUMBER: US 08/851,843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
                                                             Sequence 564, Application US/10877124; Publication No. US20040242529A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                    APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 564:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
               RESULT 45
US-10-877-124-564
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Publication No. US20040247613A1

GENERAL INFORMATION:
Information Tech, Thomas R.
Information Tech, Thomas R.
Information Town Thomas R.
Information Town Thomas R.
Information Town Thomas R.
Morin, Gregg B.
Harley, Calvin B.
Harley, Calvin H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS: 727

CORRESPONDENCE ADDRESS: 727

CORRESPONDENCE TOWNSEND and Townsend and Crew LLP
                       Length 48;
                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
                       Score 20; DB 8;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

REPLICATION NUMBER: US/10/877,022
FILING DATE: 24-Uun-2004
CLASSIFICATION COMPANDED: US/10/877,022
FILING DATE: 24-Uun-2004
CLASSIFICATION STAR:
APPLICATION NUMBER: US/09/432,503
FILING DATE: -CURROWN-
APPLICATION NUMBER: US/09/41,549
FILING DATE: -CURROWN-
APPLICATION NUMBER: US/08/44,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 12-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 08/851,843
100.0%; Scc. No. 1.-100.0%; Pred. No. 1.-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                         1 TITIGGGGTTTTGGGGTTTT 20
                                                                                                                                                                    29 ririfederirirecerrir 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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STATE: California
                                                                     20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                    Query Match
Best Local Similarity
Matches 20; Conserv
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Gaps
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TITLE OF INVENTION: No. US20020164786Alel Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                 ; LOCATION: 1..48
; OTHER INFORMATION: /note= "hairpin primer"
; SEQUENCE DESCRIPTION: SEQ ID NO: 564:
US-10-877-146-564
             ATORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 564:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 20; DB 8; 1
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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COUNTRY: United States of America
ZIP: 94111
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APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 39, Application US/09843676; Patent No. US20020164786A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
FILING DATE: 01-OCT-1997
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                                                                                                                                                                                                           LENGTH: 48 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TTTTGGGGTTTTTGGGGTTTT
                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                               FEATURE
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Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTIONS: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
                                                                                                                                                                                                                                                  Score 20; DB 8; Length 48; Pred. No. 1.2e+02; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/10/877,146
FILING DATE: 24-Jun-2004
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Two Embarcadero Center, Eighth Floor CIIY: San Francisco STATE: California
                                                                                                                              NAME/KEY:
LOCATION: 1..48
CTHER INFORMATION: /note= "hairpin primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 564:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/851,843
FLIING DATE: 06-MAX-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAX-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-Nov-1999
APPLICATION NUMBER: 08/974,549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/911,312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM FYEE: Floppy disk
COMPUTER: FLOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 564, Application US/10877146 Publication No. US20050013825A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                        TTTTGGGGTTTTT 48
                                                                                                                                                                                                                                                                                                                                       1 TITIGGGGTTTTGGGGTTTT 20
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Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                  Query Match 100.0%; S
Best Local Similarity 100.0%; P
Matches 20; Conservative 0;
  LENGTH: 48 base pairs
                     TYPE: nucleic acid
STRANDEDNESS: single
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                                                             TOPOLOGY: linear
                                                                                   MOLECULE TYPE: DNA
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                                                                                                                          NAME/KEY:
                                                                                                                                                                                                           US-10-877-022-564
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US-10-877-146-564
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DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-766-253-39
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 39, Application US/09438486 Publication No. US20030009019A1 GENERAL INFORMATION:
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                 Query Match
Best Local Similarity
Matches 20; Conserv
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Publication No. US20020187471A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin

Andrews, William H.

TITLE OF INVENTION No. US20020187471A1e1 Telomerase

NUMBER OF SEQUENCES: 171

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                       Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 19-7an-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
APTICATION NUMBER: US 08/724,643
ATTORNEY/AGENT INFORMATION:
NAME: APPLE Randolph T.
REFERENCE/DOCKET NUMBER: 36,429
TELECOMMUNICATION INFORMATION:
                          REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 20; DB 3; 1
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0;
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    TOPOLGGY: linear
    MOLECULE TYPE: other nucleic acid
    BESCRIPTION: /desc = "DNA"
    SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-843-676-39
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                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
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                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
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STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO: 39:
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US-09-766-253-39
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0
    Length 50;
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APPLICANT: Linguer, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Karen B.
APPLICANT: Morin, Gregs B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. US2003000919A1el Telomerase
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 12-NOV-1999
CLASSIFICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 10-APR-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 10-APR-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 10-APR-1997
CLASSIFICATION NUMBER: 01-007-1996
CLASSIFICATION NUMBER: 01-007-1096
CLASSIFICATION NUMBE
100.0%; Score 20; DB 3; L
ilarity 100.0%; Pred. No. 1.2e+02;
Conservative 0; Mismatches 0;
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; DESCRIPTION: /desc = "DNA"
US-09-438-486-39
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Score 20; DB 3; Length Pred No. 1 20+02;	Mismatche
100.0%;	
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itch al Sim	20;
Query Match Rest Local Similarity	Matches

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Search completed: February 16, 2006, 02:34:00 Job time : 294.248 secs

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                                                        February 16, 2006, 02:03:53; Search time 186.446 Seconds (without alignments) 98.157 Million cell updates/sec
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-10-310-914A-238162 Sequence -10-310-914A-238201 Sequence -10-310-914A-23825 Sequence -10-310-914A-626236 Sequence -10-310-914A-1143345 Sequence	2.0 23 7 US-10-310-914A-238702 Sequence 2.0 24 7 US-10-310-914A-565981 Sequence 2.0 25 7 US-10-310-914A-238163 Sequence	2.0 26 7 US-10-310-914A-138182 Sequence 2.0 31 7 US-10-310-914A-228203 Sequence 1.0 19 7 US-10-310-914A-455340 Sequence	1.0 20 7 US-10-310-914A-208723 Sequence 1.0 20 7 US-10-310-914A-328480 Sequence 1.0 20 7 US-10-310-914A-328480 Sequence	1.0 20 7 US-10-914A-935090 Sequence	1.0 20 7 US-10-310-914A-1222900 Sequence 1.0 20 7 US-10-310-914A-1222903 Sequence	1.0 21 7 US-10-310-914A-111276 Sequence 1.0 21 7 US-10-310-914A-322150 Sequence	21 7 US-10-310-914A-328481 Sequence	1.0 21 7 US-10-310-914A-348738 Sequence 1.0 21 7 US-10-310-914A-540890 Sequence	1.0 21 7 US-10-310-914A-621471 Sequence	1.0 21 7 US-10-310-914A-849471 Sequence 8454/1, 1.0 22 7 US-10-310-914A-84474 Sequence 84474,	1.0 22 7 US-10-310-914A-208738 Sequence 1.0 22 7 US-10-310-914A-445665 Sequence	1.0 22 7 US-10-310-914A-465262 Sequence 1.0 22 7 US-10-310-914A-549696 Sequence	1.0 22 7 US-10-310-914A-621472 Sequence 1.0 22 7 US-10-310-914A-803700 Sequence	22 7 US-10-310-914A-845459 Sequence 23 7 US-10-310-914A-208735 Sequence	1.0 23 7 US-10-310-914A-2208749 Sequence	1.0 23 / US-10-310-914A-3221/6 Sequence	1.0 23 7 US-10-310-914A-465292 Sequence 1.0 23 7 US-10-310-914A-467819 Sequence	1.0 23 7 US-10-310-914A-467906 Sequence 1.0 23 7 US-10-310-914A-526398 Sequence	1.0 23 7 US-10-310-914A-845463 Sequence	1.0 24 7 US-10-310-914A-111296 Sequence	1.0 24 7 US-10-310-914A-348737 Sequence	1.0 24 7 US-10-310-914A-431969 Sequence 1.0 24 7 US-10-310-914A-465293 Sequence	1.0 24 7 US-10-310-914A-465676 Sequence 1.0 24 7 US-10-310-914A-490858 Sequence	1.0 24 7 US-10-310-914A-526411 Sequence	1.0 24 7 US-10-310-914A-621491 Sequence	1.0 24 7 US-10-310-914A-621493 Sequence 1.0 24 7 US-10-310-914A-845464 Sequence	1.0 24 7 US-10-310-914A-1059987 Sequence	1.0 25 7 US-10-310-914A-111266 Sequence	) 25 7 US-10-310-914A-208725 Sequence	1.0 25 7 US-10-310-914A-526412 Sequence	1.0 25 7 US-10-310-914A-540891 Sequence 1.0 25 7 US-10-310-914A-621517 Sequence	25 7 US-10-310-914A-1107886 Sequence	25 11 US-11-121-849-555567 Sequence	25 11 US-11-136-527-15522 Sequence 25 11 US-11-136-527-15552 Sequence 25 11 US-11-136-557-15593
.4 72.0 21 7 US-10-310-914A-238162 Sequence .4 72.0 22 7 US-10-310-914A-238201 Sequence .4 72.0 22 7 US-10-914A-238252 Sequence .4 72.0 22 7 US-10-310-914A-626236 Sequence .4 72.0 22 7 US-10-310-914A-626237 Sequence .4 72.0 22 7 US-10-310-914A-526237 Sequence	4.4 72.0 23 7 US-10-310-914A-238202 Sequence 4.4 72.0 24 7 US-10-310-914A-565981 Sequence 4.4 72.0 25 7 US-10-310-914A-238163 Sequence	4.4 72.0 26 7 US-10-310-914A-138182 Sequence 4.4 72.0 31 7 US-10-310-914A-228203 Sequence 4.2 71.0 19 7 US-10-310-914A-455340 Sequence	4.2 71.0 20 7 US-10-310-914A-208723 Sequence 4.2 71.0 20 7 US-10-310-914A-328480 Sequence 6.2 71 0 7 11G-10-310-014A-328480 Sequence	4.2 71.0 20 7 US-10-310-914A-621470 Sequence	4.2 71.0 20 7 US-10-310-914A-1222900 Sequence 4.2 71.0 20 7 US-10-310-914A-1222903 Sequence	4.2 71.0 21 7 US-10-310-914A-111276 Sequence 4.2 71.0 21 7 US-10-310-914A-322150 Sequence	4.2 71.0 21 7 US-10-310-914A-328481 Sequence	4.2 71.0 21 7 US-10-310-914A-348738 Sequence 4.2 71.0 21 7 US-10-310-914A-540890 Sequence	4.2 71.0 21 7 US-10-310-914A-621471 Sequence 4.2 71.0 21 7 US-10-310-914A-845458 Sequence	4.2 71.0 21 7 US-10-314A-845471 Sequence 845471, 4.2 71.0 22 7 US-10-310-914A-84474 Sequence 84474,	4.2 71.0 22 7 US-10-310-914A-208738 Sequence	4.2 71.0 22 7 US-10-310-914A-465262 Sequence 4.2 71.0 22 7 US-10-310-914A-549696 Sequence	4.2 71.0 22 7 US-10-310-914A-621472 Sequence 4.2 71.0 22 7 US-10-310-914A-803700 Sequence	4.2 71.0 22 7 US-10-310-914A-845459 Sequence 4.2 71.0 23 7 US-10-310-914A-208735 Sequence	4.2 71.0 23 7 US-10-310-914A-208749 Sequence	4.2 71.0 23 7 US-10-310-914A-322176 Sequence	4.2 71.0 23 7 US-10-310-914A-465292 Sequence 4.2 71.0 23 7 US-10-310-914A-467819 Sequence	4.2 71.0 23 7 US-10-310-914A-467906 Sequence	4.2 71.0 23 7 US-10-310-914A-845463 Sequence	4.2 71.0 24 7 US-10-310-914A-111296 Sequence	4.2 71.0 24 7 US-10-310-914A-348737 Sequence	4.2 71.0 24 7 US-10-310-914A-431969 Sequence 4.2 71.0 24 7 US-10-310-914A-465293 Sequence	4.2 71.0 24 7 US-10-310-914A-465676 Sequence	4.2 71.0 24 7 US-10-310-914A-526411 Sequence	4.2 71.0 24 7 US-10-310-914A-621491 Sequence	4.2 71.0 24 7 US-10-310-914A-621493 Sequence 4.2 71.0 24 7 US-10-310-914A-845464 Sequence	4.2 71.0 24 7 US-10-310-914A-1059987 Sequence	4.2 71.0 25 7 US-10-914A-111266 Sequence	4.2 71.0 25 7 US-10-310-914A-208725 Sequence	4.2 71.0 25 7 US-10-310-914A-526412 Sequence	4.2 71.0 25 7 US-10-310-914A-540891 Sequence 4.2 71.0 25 7 US-10-310-914A-621517 Sequence	4.2 71.0 25 7 US-10-310-914A-1107886 Sequence	4.2 71.0 25 11 US-11-121-849-555567 Sequence	4.2 71.0 25 11 US-11-136-527-15522 Sequence 7.1 7.1 0 25 11 US-11-136-527-15522 Sequence 7.1 0 25 11 US-11-136-527-15633 Sequence 7.1 0 25 11 US-11-136-537-15633

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Sequence 596008, Application US/10310914A
Publication No. US/20060003322A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: uses thereof
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| Publication No. US2006000332A1
| Publication No. US2006000332A1
| Publication No. US2006000332A1
| GENERAL INFORMATION.
| APPLICANT: Bentwich, Kvuzat
| APPLICANT: Bentwich, Rouzat
| APPLICANT: Bentwich, Rouzat
| APPLICANT: Bentwich, Rouzat
| TITLE OF INVENTION: uses thereof
| TITLE OF INVENTION: uses thereof
| FILE REFERENCE: 06087.0200.CPUS01
| CURRENT APPLICATION NUMBER: US/10/310, 914A
| CURRENT APPLICATION NUMBER: US/2002-12-06
| NUMBER OF SEQ ID NOS: 1388402
| SOFTWARE: PatentIn version 3.3
| SEQ ID NO 185978
| TYPE: RNA
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Pred. No. 1.2e+02;
0; Mismatches 2; Indels
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; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-67
               TILE REPERENCE: C1039.70060US01
CURRENT APPLICATION NUMBER: US/11/127,654
CURRENT APPLICATION NUMBER: US/11/12,653
CURRENT FILING DATE: 2005-05-12
PRIOR FILING DATE: 2002-03-29
PRIOR FILING DATE: 2002-03-29
PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 1040
SOFTWARE: Patentin version 3.2
LENGTH: 20
  TITLE OF INVENTION: INFLAMMATORY DISEASES
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100.0%;
Best Local Similarity 100.0%;
Matches 20; Conservative 0;
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90.0%;
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US-10-310-914A-596008
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Sequence 861266,
Sequence 1058052,
Sequence 1100961,
Sequence 1155612,
Sequence 1182491,
Sequence 255, App
Sequence 150268,
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Sequence 150272,
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Sequence 429786,
Sequence 592413,
Sequence 622065,
Sequence 727232,
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Sequence 158172,
Sequence 164308,
Sequence 350862,
Sequence 352379,
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Sequence 817616,
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Sequence 35
Sequence 54
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US-10-310-914A-429807

US-10-310-914A-727253

US-10-310-914A-727253

US-10-310-914A-347390

US-10-310-914A-347390

US-10-310-914A-5431346

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US-10-310-914A-766181

US-10-310-914A-766181

US-10-310-914A-1109961

US-10-310-914A-1109961

US-10-310-914A-11038052

US-10-310-914A-11058052

US-10-310-914A-11038052
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Sequence 67, Application US/11127654
Publication No. US20050250726A1
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Berg, Daniel J.
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC US-11-127-654-67

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US-10-310-914A-138169/C

US-10-310-914A-138169/C

Sequence 138169, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Bentwich, Isaac

APPLICANT: Boinformatically detectable group of novel regulatory genes and

TITLE OF INVENTION: USS thereof

TITLE OF INVENTION: USS thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT PILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 138169

TYPE: RNA

TYPE: RNA

CORGANISM: Human

SOCIANS HUMA
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwaich, Isaac
APPLICANT: Bentwaich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
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TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
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Publication No. US20060003322A1

FURBERLA INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
APPLICANTON WUMBER: US/10/10,10,914A
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT FAPLICATION WUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SEQ ID NO 138179
LENGTH: 22
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Pred. No. 1.7e+02;
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Best Local Similarity 94.4
Matches 17; Conservative
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Best Local Similarity 94.4
Matches 17; Conservative
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US-10-310-914A-138179/c
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; ORGANISM: Human
US-10-310-914A-138168
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ORGANISM: Human
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UG-10-310-914A-596068/C

UG-10-310-914A-596068/C

UG-10-310-914A-596068/C

Sequence 596068, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Shiler, Kvuzat

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: uses thereof

TITLE OF INVENTION: uses thereof

TITLE OF INVENTION: USES 10000 CPUS01

CURRENT PRILICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PATENTING PATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402
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Pred. No. 1.2e+02;
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                                                                                                                                                                 Score 16.8; DB 7;
Pred. No. 1.2e+02;
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Pred. No. 1.2e+02;
                                                                                                                                  84.0%; Scor.
90.0%; Pred. No. 1...
0; Mismatches
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US-10-310-914A-138168/c
; Sequence 138168, Application US/10310914A
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90.0%;
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Best Local Similarity 90..
Best Local Similarity 90..
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Best Local Similarity 90.0
Matches 18; Conservative
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Best Local Similarity 90.0
Matches 18; Conservative
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US-10-310-914A-596011/c
                    ; ORGANISM: Human
US-10-310-914A-185978
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ORGANISM: Human
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ORGANISM: Human
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LENGTH: 25
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APPLICANT: Bentwich, Isaac
APPLICANT: Biler, Kvuzat
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION VUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 138196
LENGTH: 24
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Publication No. US20060003322A1
Publication No. US20060003322A1
Publication No. US2006000332A1
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
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Publication No. US20060003322A1
Publication No. US20060003322A1
RUBERTION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
FILE REFERENCE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 138229
LENGTH: 25
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Pred. No. 1.7e+02;
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94.4%;
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94.4%;
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LENGTH: 24
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Best Local Similarity 94.4
Matches 17; Conservative
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Matches 17; Conservative
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US-10-310-914A-227183/c
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  GENERAL INFORMATION:
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; ORGANISM: Human
US-10-310-914A-138229
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                                                                                                                                                                                                                                                                        Sequence 138228, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT PILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: Patentin version 3.3
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Publication No. US20060003322A1
SEQUENCE INFORMATION:
APPLICANT: Bentwich, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
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Pred. No. 1.7e+02;
0; Mismatches 1; Indels
                                          Length 22;
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                                        82.0%; Score 16.4; DB 7;
94.4%; Pred. No. 1.7e+02;
tive 0; Mismatches 1;
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Pred. No. 1.7e+02;
0; Mismatches 1;
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                                                                                                                             3 TTGGGGTTTTGGGGTTTT 20
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Best Local Similarity 94.4%;
Matches 17; Conservative C
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Best Local Similarity 94.4%;
Matches 17; Conservative (
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                                      Query Match
Best Local Similarity 94.4
Matches 17; Conservative
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US-10-310-914A-138228/c
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US-10-310-914A-138180/c
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US-10-310-914A-138196/c
US-10-310-914A-138179
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LENGTH: 22
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LENGTH: 23
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Sequence 271479, Application US/10310914A
Publication No. US20060003322A1
Publication No. US2006000332A1
Publication No. US2006000332A1
Publication No. US2006000332A1
Publication No. US200600032A1
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
FILE REFERENCE: 06087.0200.CPUS01
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 271479
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TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION METHODS AND METHODS AND METHODS AND METHOD TITLE OF INVENTION METHODS AND METHOD OF A STRAIN DISPOSED ON AND TITLE OF INVENTION NUMBER: US/11/170,693

CURRENT APPLICATION NUMBER: US/11/170,693

CURRENT FILING DATE: 2005-06-29

PRIOR APPLICATION NUMBER: 09/945,952

PRIOR APPLICATION NUMBER: 01/945,952

PRIOR APPLICATION NUMBER: 11/074,995

PRIOR APPLICATION NUMBER: 11/074,995

PRIOR PRIOR DATE: 2005-06-24

NUMBER OF SEQ ID NOS: 73

SEQ ID NO 39

LENGTH: 20

LENGTH: 20
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Pred. No. 3e+02;
0; Mismatches 2; Indels
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Pred. No. 3e+02;
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US-10-914A-1342346/c
; Sequence 1342346, Application US/10310914A
; Sequence 1342346, Application US/10310914A
; GENERAL INFORMATION:
; APPLICANT: Bentwah, Isaac
                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:

NAME/KEY: misc feature

LOCATION: (1)...(20)

COTHER INFORMATION: Forward Primer
US-11-170-693-39
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Best Local Similarity 89.5%;
Matches 17; Conservative
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Best Local Similarity 89.5
Matches 17; Conservative
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ORGANISM: Human
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US-10-914A-227197/C
US-10-310-914A-227197/C
Sequence 227197, Application US/10310914A
Sequence 227197, Application US/10310914A
Sequence 227197, Application US/2060003322A1
Sequence 227197, Application No. US2060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: USES thereof
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SEQ ID NO S: 1388402
SEQ ID NO 227197
LENGTH: 27
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Publication No. US20060003322A1
GENERAL INFORMATION:
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APPLICANT:
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APPLICATION WIGHER:
ITILE OF INVENTION:
CURRENT APPLICATION WIGHER:
CURRENT FILING DATE:
2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SOFTWARE: Patentin version 3.3
SEQ ID NO 138236
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              82.0%; Score 16.4; DB 7; Length 25; 94.4%; Pred. No. 1.8e+02;
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94.4%; Pred. No. 1.8e+02;
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Pred. No. 1.8e+02;
                                                             0; Mismatches
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94.4%;
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Best Local Similarity 94.4'
                                                             17; Conservative
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US-10-310-914A-138236/c
                                        Best Local Similarity
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US-11-170-693-39/c
                  Query Match
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                                                             Matches
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Sequence 1143293, Application US/10310914A
Publication No. US20060003322A1
Publication No. US2006000332A1
Publicantion No. US2006000332A1
RENERAL INFORMATION, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: Uses thereof
TITLE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION WHOBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1443293
LENGTH: 23
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Publication No. US20060003322A1

GENERAL INFORMATION.

APPLICANT: Bentwich, Isaac

TITLE OF INVENTION: uses thereof

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SEQ ID NO 844567

LENGTH: 24
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US-10-310-914A-271527/c
US-10-310-914A-571527/c
Sequence 271527, Application US/10310914A
Sequence 271527, Application No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kuzat
APPLICANT: Shiler, Kuzat
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
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89.5%; Pred. No. 3.1e+02;
tive 0; Mismatches 2;
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     2 TITGGGGTTTTGGGGTTTT 20
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Best Local Similarity 89.5
Matches 17; Conservative
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US-10-310-914A-1143293/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: RNA
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Publication No. US20060003322A1

GENERAL INFORMATION:
FILLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Uses thereof
FILLE REPERENCE: 06087.0200.CPUSOI;
CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILLING DATE: 2002-112-06
NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: Patentin version 3.3

SEQ ID NO 626125

LENGTH: RNA
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APPLICANT: Bentwitch, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE OF INVENTION: uses thereof
FILE OF INVENTION: uses 1200.CPUS01
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 626126
LENGTH: 23
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Pred. No. 3.1e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                        Length 22;
                                                                                                                                                                                                                                                                                  Query Match 79.0%; Score 15.8; DB 7; Length 2 Best Local Similarity 89.5%; Pred. No. 3e+02; Matches 17; Conservative 0; Mismatches 2; Indels
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION UNMER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1342346
LENGTH: 22
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; Publication No. US20060003322A1
; GENERAL INFORMATION:
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89.5%;
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Best Local Similarity 89.5
Matches 17; Conservative
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Best Local Similarity 89.5
Matches 17; Conservative
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US-10-310-914A-626125/c
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US-10-310-914A-626126/c
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                                                                                                                                                                                                            ORGANISM: Human
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                                                                                                                                                                                    TYPE: RNA
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US-10-310-914A-565951/C

Sequence 565951, Application US/10310914A

Sequence 565951, Application US/10310914A

Sequence 565951, Application US/10310914A

Sequence 565951, Application US/103102A1

SEQUENCE SEQUE
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; Beduence 60025, Application US/11175859
; Publication No. US2060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REPERENCE: 3690.1
; CURRENT FILING DATE: 2005-07-05
; RIOR APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SEQ ID NO 60025
; LENGTH: 50
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Pred. No. 3.3e+02;
0; Mismatches 2;
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Pred. No. 3.1e+02;
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1 UUUUGGGAUUUCGGGGUUU 19
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Best Local Similarity 89.5%;
Matches 17; Conservative
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Best Local Similarity 89.5
Matches 17; Conservative
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ORGANISM: homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: RNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-11-175-859-60025
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US-11-175-859-60025
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Sequence 271489/c
Sequence 271489, Application US/10310914A
Sequence 271489, Application US/10310, 14A
TITLE OF INVENTION: Beiniformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PATENTIN version 3.3
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Publication No. US20060003322A1

GENERAL INFORMATION;
APPLICANT: Bentwich, Isaac

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: USES thereof

TITLE OF INVENTION: USES thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310, 914A

CURRENT PILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: Patentin version 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                    Score 15.8; DB 7;
Pred. No. 3.1e+02;
0; Mismatches 2;
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        CURRENT APPLICATION NUMBER: US/10/310,914A CURRENT FILING DATE: 2002-12-06 NUMBER OF SEQ ID NOS: 1388402 SOFTWARE: Patentin version 3.3 SEQ ID NO 271527 LENGTH: 25
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36.8%;
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Best Local Similarity 89.5%;
Matches 17; Conservative
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Best Local Similarity 36.00
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Best Local Similarity هادر المحافظة المحافظة
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US-10-310-914A-844568
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US-10-310-914A-844568
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                                                                                                                                                                                                                                                     TYPE: RNA
ORGANISM: Human
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Sequence 626141, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL Shiler, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 626141
LENGTH: 20
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Publication No. US20060003322A1
Publication No. US20060003322A1
GENERAL INFORMATION:
TERERIA PERICANT: Shiler, Kvuzat
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: Uses thereof
TITLE REFERENCE: 06087.0200.CPUS01
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
LENGTH: 21
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
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Pred. No. 4.4e+02;
0; Mismatches 1; Indels
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Pred. No. 4.4e+02;
0; Mismatches 1;
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94.1%;
                               19 TGGGGTTTTGGGGGTTT 3
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Best Local Similarity 94.1%;
Matches 16; Conservative
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Best Local Similarity 94.1
Matches 16; Conservative
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US-10-310-914A-138178
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Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich.
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: USes thereof FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
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| Publication No. US20060003322A1
| Publication No. US2006000332A1
| GENERAL INPORMATION:
| APPLICANT: Bentwich, Isaac
| APPLICANT: Bentwich, Isaac
| APPLICANT: Briler, Kvuzat
| TITLE OF INVENTION: Bloinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: Uses thereof
| FILE REFERENCE: 06087.0200.CPUS01
| FILE REFERENCE: 06087.0200.CPUS01
| CURRENT APPLICATION UNGBER: US/10/310,914A
| CURRENT FILING DATE: 2002-12-06
| NUMBER OF SEQ ID NOS: 1388402
| SOFTWARE: Patentin version 3.3
| SEQ ID NO 144338
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CURRENT APPLICATION NUMBER: US/10/310,914A CURRENT FILING DATE: 2002-12-06
                          CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
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Matches 16; Conservative
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Best Local Similarity 94.1
Matches 16; Conservative
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Best Local Similarity 94.1
Matches 16; Conservative
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US-10-310-914A-1143338/c
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US-10-310-914A-626221/c
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; ORGANISM: Human
US-10-310-914A-1143338
                                                                                                                                                                                                          US-10-310-914A-626220
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US-10-310-914A-626221
                                                                                                                                                                                  ORGANISM: Human
                                                                                                   SEQ ID NO ,626220
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LENGTH: 19
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4 TGGGGTTTTGGGGTTTT 20

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Sequence 1143370, Application US/10310914A

Sequence 1143370, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, 1saac
APPLICANT: Bentwich Isaac
SOFTWARE: Patentin version 3.3
SEQ ID NO 1143370
LENGTH: 25
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APPLICANT: Halapi, Eva

APPLICANT: Halapi, Eva

APPLICANT: Halapi, Eva

TITLE OF INVENTION: METHODS OF DIAGNOSIS AND TREATMENT FOR

TITLE OF INVENTION: ASSCIATION
FILE REFERENCE: 2345.2044-003

CURRENT APPLICATION NUMBER: US/11/043,752

CURRENT APPLICATION NUMBER: US/11/043,752

CURRENT APPLICATION NUMBER: G0/487,012

PRIOR PILING DATE: 2004-07-14

PRIOR FILING DATE: 2004-07-14

PRIOR FILING DATE: 2003-07-14

PRIOR FILING DATE: 2003-07-14

PRIOR FILING DATE: 2003-07-14

PRIOR FILING DATE: 2004-04-05

NUMBER OF SEQ ID NOS: 4126

SEQ ID NO 216

LEMETH: 20

LEMETH: 20
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85.0%; Pred. No. 5.3e+02;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.0%; Score 15.4; DB 7; 94.1%; Pred. No. 4.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 216, Application US/11043752
Publication No. US20060014165A1
GENERAL INFORMATION:
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Matches 16; Conservative
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     24 TGGGGTTTTGGGGGTTT
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Best Local Similarity 85.0
Matches 17; Conservative
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US-10-310-914A-1143370/c
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US-10-310-914A-84509/c
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ORGANISM: Human
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US-10-310-914A-626295/C

US-10-310-914A-626295/C

Sequence 626295, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Kvuzat
APPLICANT: Bentwich, Kvuzat
APPLICANT: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06
CURRENT FILING DATE: 2002-12-06
SOFTWARE: PatentIn version 3.3

SOFTWARE: PatentIn version 3.3
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Publication No. US20060003322A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: uses through detectable group of novel regulatory genes and FILE REPERENCE: 06097.0200.CPUSOI
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
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94.1%; Pred. No. 4...
0; Mismatches
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 138235
LENGTH: 25
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Best Local Similarity 94.1
Matches 16; Conservative
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Matches 16; Conservative
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US-10-310-914A-626296/c
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US-10-310-914A-626295
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RESULT 41

US-10-310-914A-675377/C

Sequence 675377, Application US/10310914A

Sequence 675377, Application US/10310914A

Sequence 675377, Application US/10310914A

Sequence 675377, Application US/10310914A

Sequence 675377

APPLICANT: Bentwich, Isaac

APPLICANT: Bentwich, Isaac

APPLICANT: Bentwich, Isaac

APPLICANT: Bentwich, Isaac

TITLE OF INVENTION: Uses thereof

CURRENT APPLICATION WUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 675377

LENGTH: 21

LENGTH: 21
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Sequence 1222901, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL Shiler, Kvuzat
APPLICANT:
APLICANT:

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Pred. No. 5.3e+02;
0; Mismatches 3;
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Pred. No. 5.3e+02;
0; Mismatches 3;
Score 15.2; DB 7;
Pred. No. 5.3e+02;
                                                                  0; Mismatches
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US-10-310-914A-238142/c
; Sequence 238142, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
                                                                                                                                     1 TITIGGGTTTTGGGGTTTT 20
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Query Match 76.0%;
Best Local Similarity 85.0%;
Matches 17; Conservative
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Best Local Similarity 85.0%;
Matches 17; Conservative
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Best Local Similarity 85.0%;
Matches 17; Conservative
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US-10-310-914A-1222901
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US-10-310-914A-455408/C

Sequence 455408, Application US/10310914A

Publication No. US2006003322A1

Publication No. US200600332A1

APPLICANT: Bentwich, Isaac

APPLICANT: Bentwich, Isaac

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

TITLE OF INVENTION: Uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT PILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 455408

T.ENGTH: 21
       APPLICANT: Shiler, tesast
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
TITLE REFERENCE: 06087,0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 84509
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Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: USS thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
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85.0%; Pred. No. 5.3e+02;
tive 0; Mismatches 3;
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Best Local Similarity 85.0
Matches 17; Conservative
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Matches 17; Conservative
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US-10-310-914A-622070/c
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CRGANISM: Human
US-10-310-914A-622070
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                                                                                                                                                                                                                                                                                                                                                                          TYPE: RNA
ORGANISM: Human
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LENGTH: 21
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US-10-310-914A-282917/c

US-10-310-914A-282917/c

Sequence 282917 Application US/10310914A

Sequence 282917 Application US 0000003322A1

GENERAL INFORMATION

APPLICANT: Bentwich, Isaac

APPLICANT: Bentwich, Isaac

TITLE OF INVERTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVERTION: Uses thereof

TITLE OF INVERTION: Uses thereof

TITLE OF INVERTION: Uses thereof

CURRENT PELING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 282917
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Publication No. US2006000332A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Biler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087, 0200, CPUS01
CURRENT APPLICATION WUMBER: US/10/310,914A
CURRENT PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 465697
LENGTH: 23
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76.0%; Score 15.2; DB 7;
85.0%; Pred. No. 5.4e+02;
iive 0; Mismatches 3;
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Pred. No. 5.4e+02;
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Sequence 501657, Application US/10310914A

PUDIfication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac
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85.0%;
    Query Match 76.0
Best Local Similarity 85.0
Matches 17; Conservative
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Best Local Similarity 85.0
Matches 17; Conservative
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US-10-310-914A-465697/c
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; ORGANISM: Human
US-10-310-914A-465697
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ORGANISM: Human
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US-10-314A-465689/c

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US-10-310-914A-465689/c

US-10-310-914A-465689/c

Sequence 465689, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Shiler, Kuzat

TITLE OF INVENTION: uses thereof

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT PELING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 465689
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US-10-310-914A-1222898/
Sequence 122898, Application US/10310914A
Sequence 122898, Application US/10310914A
Sequence 122898, Application US/10310914A
Sequence 122898, Application US/10310914A
GENERAL INFORMATION:
APPLICANT: Bantwich, Isaac
APPLICANT: Bantwich, Shiler, Kuzat
APPLICANT: Bantwich Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.cPUS01
CURRENT APPLICATION UNDERF: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SOFTWARE: PatentIn version 3.3
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
LENGTH: 22
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Pred. No. 5.4e+02;
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85.0%; Pred. No. s...
0; Mismatches
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Best Local Similarity 85.03
Matches 17; Conservative
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Matches 17; Conservative
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ORGANISM: Human
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ORGANISM: Human
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REPERENCE: 06087.0200.CPUSO1
FILE REPERENCE: 06087.0200.CPUSO1
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 501657
LENGTH: 23
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Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: Uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION UNMERE: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: Patentin version 3.3

SEQ ID NO 651609
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US-10-310-914A-675445/c
US-10-310-914A-675445/c
Sequence 675445, Application US/10310914A
Sequence 67545, Application US/10310914A
Sequence 67545, Application US/10310914A
Sublication No. US-20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kuzat
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
CURRENT PELICATION: USES 100 NO.CPUS01
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 655445
LENGTH: 23
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76.0%; Score 15.2; DB 7; Length 23;
Best Local Similarity 85.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels
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Best Local Similarity
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US-10-310-914A-651609/c
                                                                                                                                                                                                                                                           ; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-501657
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; ORGANISM: Human
US-10-310-914A-651609
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Best Local Similarity 85.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps
Qy 1 TTTGGGGTTTT 20
Db 22 TGTTGGGGTTTT 3
Search completed: February 16, 2006, 02:52:56
Job time: 188.446 secs
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COB74726 Sequence AX514115 Sequence AX520264 Sequence AX104312 Sequence AX104329 Sequence AX104329 Sequence AX355395 Sequence AX355395 Sequence AX547382 Sequence CS087338 Sequence CS087338 Sequence CS087335 Sequence CS087347 Sequence CS087377 Sequence CS087377 Sequence CS087377 Sequence CS087377 Sequence CS08737 Sequence AX65513 Sequence CS08737 Sequence CS08737 Sequence AX65513 Sequence AX65613 Sequence AX65613 Sequence AX65713 Sequence AX14146 Sequence AX13908 Sequence AX141412 Sequence AX141412 Sequence AX141412 Sequence AX141412 Sequence AX141412 Sequence AX141412 Sequence AX141414 Sequence AX141413 Sequence AX141414 Sequence AX14144 Se	AX.08932 Sequence AX.104327 Sequence AX.104717 Sequence AX.104775 Sequence AX.104777 Sequence AX.104777 Sequence AX.104775 Sequence AX.105103 Sequence AX.105237 Sequence AX.105237 Sequence AX.105237 Sequence AX.105237 Sequence AX.105237 Sequence AX.1052408 Sequence
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Core version 5.1.7  1993 - 2006 Biocceleration Ltd.  19 sw model  5, 17:51:58 ; Search time 455.843 Seconds (without alignments) 2369.293 Million cell updates/sec  39999 19  ext 1.0  42172563 residues  chosen parameters: 2097806  chosen parameters: 2097806  sw maries  10 summaries  results predicted by chance to have a  1 to the score of the result being printed, of the total score distribution.	Description AX10388 Sequence AX355419 Sequence AX355420 Sequence AX355420 Sequence AX355420 Sequence AX355431 Sequence AX355431 Sequence AR135030 Sequence AR135030 Sequence AR135030 Sequence AX104032 Sequence AX104032 Sequence AX342438 Sequence
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Patent: US 6008200-A 1 28-DEC-1999;
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Immunostimulatory nucleic acids
Breant: WO 0122972-A 82 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US); Coley Pharmaceutical
GmbH (DB)
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Methods for enhancing antibody-induced cell lysis and treating
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Bratzler, R. L. Inhibition of angiogenesis by nucleic acids Patent: WO 02053141-A 80 11-JUL-2002; Coley Pharmaceutical Group, Inc. (US) Location/Qualifiers
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UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
Location/Qualifiers
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AX103890
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AX355420
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PAT 12-JAN-2002
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munuostimulatory nuclei acids
Patent: WO 0122972-A 24 05-AFR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
Vectors and methods for immunization or therapeutic protocols Patent: US 6821957-A 63 23-NOV-2004; University of Iowa Research Foundation; Iowa City, IA Location/Qualifiers
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Immunomodulatory oligonucleotides
Patent: EP 1167377-A 1 02-JAN-2002;
THE UNIVERSITY OF JOWA RESEARCH FOUNDATION
                                                                                                                                      74.7%; Score 14.2; DB 6;
84.2%; Pred. No. 3.2e+04;
iive 0; Mismatches 3;
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/db_xref="taxon:32630"

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    forganism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

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other sequences; artificial sequences.
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Sequence 224 from Patent W00122972.
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/organism="unknown"
/mol_type="genomic DNA"
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Best Local Similarity 84.2
Matches 16; Conservative
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AX342378
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Unclassified.
1 (bases 1 to 20)
1 (bases 1 to 20)
Krieg,A.M., Davis,H.L., Wu,T. and Schorr,J.
Vectors and methods for immunization or therapeutic protocols
Patent: US 6339068-A 63 15-JAN-2002;
Location/Qualifiers
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Unclassified.
(Dases 1 to 20)
Krieg,A.M., Davis,H.L., Wu,T. and Joachim,S.
                                                                                                                                                                           Unknown.
Unclassified.
Unclassified.
I (Exieg. A.M., Klinman, D. and Steinberg, A.D.)
Immunomodulatory oligonucleotides
L. Patent: US 6194388-A 1 27-FEB-2001;
Location/Qualifiers
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Pred. No. 3.2e+04;
0; Mismatches 3;
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Sequence 63 from patent US 6821957.
AR607454
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/mol_type="unassigned DNA"
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Sequence 63 from patent US 6339068.
AR182891
                                                                            AR135030 20 bp
Sequence 1 from patent US 6194388
AR135030 GI:14123935
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AR182891
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AR135030
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/db_xref="taxon:32630"
/note="Synthetic oligonucleotide
chimeric phosphorothioate/phosphodiester backbone with
phosphorothioate at 5' and 3' ends"
                                                                                                                                       Methods for enhancing antibody-induced cell lysis and treating
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                                                                                                                                                                    Patent: WO 0197843-A 449 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
Location/Qualifiers
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/note="Synthetic Sequence"
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other sequences; artificial sequences.
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Sequence 18 from patent US 6566500.
AR337615
AR337615.1 GI:33724021
 Seguence 449 from Patent WO0197843.
                                                                                                                          Weiner, G. and Hartmann, G.
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AX355421.1 GI:18620089
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Pred. No. 3.2e+04;
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 Pred. No. 3.2e+04;
0; Mismatches 3; Indels
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Patent: BP 1167379-A 1 02-JAN-2002;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                             Immunomodulatory oligonucleotides
Patent: EP 1167379-A 1 02-JAN-2002;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
Location/Qualifiers
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    .20
    forganism="synthetic construct"
|mol type="unassigned DNA"
|db_xref="taxon:32630"

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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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synthetic construct
other sequences; artificial sequences.
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synthetic construct
other sequences; artificial sequences.
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Sequence 1 from Patent EP1167379.
AX342405
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Seguence 1 from Patent EP1167378.
AX342438
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Best Local Similarity 84.2%;
Matches 16; Conservative
84.28;
Best Local Similarity 84.2
Matches 16; Conservative
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Matches 16; Conserv
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AX342405
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AX355421
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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                                        Score 13.4; DB 6; Length 30;
Pred. No. 7.9e+04;
0; Mismatches 1; Indels
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Datection of genetic polymorphisms
Patent: WO 02052044-A 6462 04-JUL-2002;
Riken (JP)
                                                                                                                                                                                                                                                                                                                                                                                                                   Nakamura, Y., Sekine, A., Iida, A. and Saito, S. Detection of genetic polymorphisms
Patent: WO 02052044-A 313 04-UUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 70.5%; Score 13.4; DB 6; Best Local Similarity 82.4%; Pred. No. 7.9e+04; Matches 14; Conservative 1; Mismatches 2;
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Sequence 6462 from Patent W002052044.
AX520264 GI:23570800
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/note="cysMR"
                                             Query Match
Best Local Similarity 93.3%;
Matches 14; Conservative
                                                                                                               1 GGGGTGACGTTCAGG 15
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AX514115/c
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the generation or modification of metabolic pathways
Patent: WO 2004076659-A 21 10-SBP-2004;
Metabolic Explorer (FR)
Location/Qualifiers
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Zink, O.
                                                                                                                                                                                                                                                    Gaps
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                                                             proteinaceous compounds
Patent: US 6566500-A 18 20-MAY-2003;
Board of Regents, The University of Texas System; Austin, TX
Location/Qualifiers
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Ulanovsky,L. and Raja,M.C.
Nucleic acid amplification using modular branched primers
Patent: US 6197556-A 5 06-MAR-2001;
Location/Qualifiers
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            1 (bases 1 to 39) Vitetta,E.S., Ghetie,V.F., Smallshaw,J. and Baluna,R.G. Compositions and methods for modifying toxic effects of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.5%; Score 13.4; DB 6; Length 22; 93.3%; Pred. No. 8e+04; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                73.7%; Score 14; DB 6; Length 39; 100.0%; Pred. No. 3.9e+04; ive 0; Mismatches 0; Indels
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/organism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"
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/organism="unknown"
/wol_type="unassigned DNA"
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Sequence 5 from patent US 6197556.
AR137717.1 GI:14479226
                                                                                                                               1. .39
/organism="unknown"
/mol_type="genomic DNA"
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CQ874726.1 GI:52747896
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synthetic construct
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Unclassified.
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Unclassified
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AR137717
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/db xref="taxon:32630"
/noFe="Syntheric oligonucleotide
chimeric phosphorothioate/phosphodiester backbone with
phosphorothioate at 5' and 3' ends"
                                                                                                          Weiner, G. and Hartmann, G. Methods for enhancing antibody-induced cell lysis and treating
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83.3%; Pred. No. 1e+05;
iive 0; Mismatches 3; Indels
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Patent: WO 0197843-A 423 27-DEC-2001,
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
Location/Qualifiers
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UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
Location/Qualifiers
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/organism="synthetic construct"
/mol type="unassigned DNA"
/db xref="taxon:32630"
/note="Synthetic oligonucleotide
phosphorodithioate backbone"
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83.3%; Pred. No. 1e+05;
iive 0; Mismatches 3;
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                                                                          other sequences; artificial sequences
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Sequence 521 from Patent WO02053141.
AX547382
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AX355395
AX355395.1 GI:18620063
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Immunostimulatory nucleic acids
Patent: WO 0122972-A 524 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
                                                                                                                                                                                                                                                     Krieg, A.M., Schetter, C. and Vollmer, J.C.
Immunostimulacory nucleic acids
Patent: WO 1022972-A 521 05-ABR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US); Coley Pharmaceutical
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    .20
    forganism="synthetic construct"
|mol type="unassigned DNA"
|db_xref="taxon:32630"

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Sequence 521 from Patent WO0122972.
AXI04329
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Sequence 524 from Patent WO0122972.
AX104332. GI:13920529
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 GGGGTGACGTTCAGGGG 17
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69.5%; Score 13.2; DB 6; Length 32;
Best Local Similarity 83.3%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 3; Indels
                                                                                                                              Length 32;
1. .32
/organism="synthetic construct"
/mol_type="unassigned DNA"
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/note="bescription of artificial sequence: Oligonucleotide"
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Novel anti-IGF-IR antibodies and uses thereof
Patent: WO 03059551-A 97 24-JUL-2003;
PIERRE FABRE MEDICAMENT (FR)
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/noTe="Oligonucleotide"
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Humanization of antibodies
Patent: WO 2005042743-A 463 12-MAY-2005,
                                                                                                                            Score 13.2; DB 6
Pred. No. 1e+05;
0; Mismatches
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1 Similarity 83.3%;
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1 Similarity 83.3%; Pred. No. 1e+05;
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                                         Inhibition of angiogenesis by nucleic acids Inhibition of angiogenesis by nucleic acids Patent: WO 02053141-A 521 11-JUL-2002; Coley Pharmaceutical Group, Inc. (US)
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/mol_type="unassigned DNA"
/db xref="texon:32630"
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PAT 25-MAY-2005
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Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
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Patent: WO 02008453-A 180 31-JAN-2002;
Phase-1 Molecular Toxicology (US)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/noTe="Primers"
                                                                                                                                                            Dall-Acqua,W., Damschroder,M. and Wu,H.
Humanization of antibodies
Patent: WO 2005042743-A 505 12-MAY-2005;
Medimmune, Inc. (US)
        Sequence 505 from Patent WO2005042743. CS087377
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                                                                                                                            other sequences; artificial sequences.
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/organism="Canis familiaris"
/mol_type="unassigned DNA"
/db_xref="taxon:9615"
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CQ827797.1 GI:49456213
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                                                               CS087377.1 GI:66712826
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Canis familiaris
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AX455113/c
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 Pred. No. 9.9e+04;
0; Mismatches 3; Indels
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Humanization of antibodies
Patent: WO 2005042743-A 466 12-MAY-2005;
Medimmune, Inc. (US)
Location/Qualifiers
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/mol type="unassigned DNA"
/db_xref="taxon:32630"
/nofe="primers"
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Humanization of antibodies
Patent: WO 2005042743-A 504 12-MAY-2005;
MedImmune, Inc. (US)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primers"
                                                                                                                                                           Sequence 466 from Patent WO2005042743.
CS087338
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Sequence 504 from Patent WO2005042743.
CSO87376.1 GI:66712825
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synthetic construct
other sequences; artificial sequences.
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83.3%;
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                    15; Conservative
   Best Local Similarity
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CS087338
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Disease risk estimating method using sequence polymorphisms in
specific region of chromosome 19
Patent: WO 2004003229-A 57 08-3AN-2004;
Aarhus University (DK); Arbejdamilj Instituttet (National
Institute of Occupational Health) (DK)
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Method for purifying keratinocyte growth factors
Patent: EP 1334981-A 26 13-AUG-2003;
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                                                              Query Match
67.4%; Score 12.8; DB 6;
Best Local Similarity 87.5%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 2;
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|mol_type="unassigned DNA"
|db_xref="taxon:32630"
|noFe="Probe"
/db_xref="taxon:9606"
/note="CD90 antisense primer"
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synthetic construct
other sequences, artificial sequences.
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Sequence 57 from Patent WO2004003229.
CQ760615.1 GI:44904118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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Sequence 26 from Patent EP1334981.
AX814043
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unclassified sequences.
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SOURCE
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CQ760615/c
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AX814043
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Kamboj,R. and Nutt,S.
Glutamate receptor (or EAA receptor) polynucleotides and their uses
Patent: US 6136544-A 29 24-0CT-2000;
Location/Qualifiers
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      de Bari, C., Luyten, F. and Dell'Accio, F.
Compositions comprising muscle progenitor cells and uses thereof
Patent: WO 2004012503-A 47 12-FBB-2004;
Tigenix N.V. (BE)
Location/Qualifiers
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                                                                                                                            /organism="synthetic construct"
/mol_type="unassigned DNA"
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/nofe="primer"
                       Jam, C.
Replication protein
Patent: WO 2004051269-A 20 17-JUN-2004;
Yorkshire Cancer Research (GB)
Location/Qualifiers
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Sequence 47 from Patent WO2004012503.
CQ775024
 other sequences; artificial sequences
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AR135661
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    .20
    /organism="Homo sapiens"

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ses 14; Conservative
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Koziel,M.G., Desai,N.M., Lewis,K.S., Warren,G.W., Evola,S.V.,
Wright,M.S., Launis,K.L., Rothstein,S.J., Bowman,C.G., Dawson,J.L.,
Dunder,E.M., Pace,G.M. and Suttie,J.L.
Synthetic DNA sequence having enhanced insecticidal activity in
maize
              PAT 29-SEP-1999
                                                                                                                                                1 (bases 1 to 32)
Kozial, MG., Desai, N.M., Lewis, K.S., Warren, G.W., Evola, S.V.,
Crossland, L.D., Wright, M.S., Merlin, E.J., Launis, K.L., Bowman, C.G.,
Dawson, J.L., Dunder, E.M., Pace, G.M. and Suttie, J.L.,
Synthetic DNA sequence having enhanced activity in maize
Patent: US 5859336-A 43 12-JAN-1999;
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

    .32
/organism="unknown"
/mol_type="unassigned DNA"

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       32 bp
Sequence 43 from patent US 5859336.
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AR098486
AR098486.1 GI:12807743
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                                                                                                                                                                                                                    Nex,B.R., Vogel,U., Rockenbauer,E. and Bukowy,Z.K.
Disease risk estimating method using sequence polymorphisms in a specific region of chromosome 19 agatent: WO 2004,003229-A 139 08-JAN-2004;
Aarhus University (DK); Arbeidsmilj Instituttet (National Institute of Occupational Health) (DK)
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Human single nucleotide polymorphisms
Patent: w0 0166800-A 1698 13-SEP-2001;
WHITEHERD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
                                                                                                                                                                                                                                                                                                                                                                                                             /organism="synthetic construct"
/mol_type="unassigned DNA"
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/note="probe"
                                                                                                            Sequence 139 from Patent WO2004003229.
CQ760697
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Sequence 1698 from Patent WO0166800.
AX249619
AX249619.1 GI:15864242
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/organism="Homo sapiens"
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CQ760697.1 GI:44904200
GGTGACGTTCAGGGGG 18
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AX249619/C
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Koziel, M.G., Desai, N.M., Lewis, K.S., Kramer, V.C., Warren, G.W., Chola, S.V., Crosaland, L.D., Wright, M.S., Merlin, E.J., Launis, K.L. and Rothstein, S.J. Synthetic dna sequence having enhanced insecticidal activity in
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Patent: WO 02052044-A 822 04-JUL-2002;
                                                                                                                             67.4%; Score 12.8; DB 6; llarity 87.5%; Pred. No. 1.6e+05; Conservative 0; Mismatches 2;
 1. .32
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="teaxon:32630"
/noTe="primer P5(a)"
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Patent: BP 1213356-A 43 12-JUN-2002;
Syngenta Participations AG (CH)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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AX453908
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Koziel, M.G., Desai, N.M., Lewis, K.S., Kramer, V.C., Warren, G.W., Pavola, S.V., Crossland, L.D., Wright, M.S., Merlin, E.J., Launis, K.L., Rothstein, S.J., Bowman, C.G., Dawson, J.L., Dunder, E.M., Pace, G.M. and Suttie, J.L., Bowman, C.G., Bowson, J.L., Dunder, E.M., Pace, G.M. maize to DNA sequence having enhanced insecticidal activity in maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Koziel, M.G., Desai, N.M., Lewis, K.S., Kramer, V.C., Warren, G.W., Evola, S.V., Crossland, L.D., Wright, M.S., Merlin, E.J., Launis, K.L. and Rothstein, S.J.
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Koziel, M., Desadi, N., Pace, G.M., Suttie, J., Carozzi, N., Boyce, C.,
Dawson, J.L., Dunder, B., Wright, M., Launis, K., Rothstein, S.J.,
Lewis, K., Warren, G. and Evola, S.
Transgenic malze seed and method for controlling insect pests
Patent: US 6720488-4 31 31-ARP-2004;
Syngenta Investment Corporation, Wilmington, DB
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Pred. No. 1.6e+05;
0; Mismatches 2; Indels
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                                                                                                          IS 5625136-A 43 29-APR-1997;
Location/Qualifiers
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Patent: EP 1209237-A 43 29-MAY-2002;
Syngenta Participations AG (CH)
Location/Qualifiers
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Sequence 43 from patent US 6720488.
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Sequence 43 from Patent EP1209237.
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87.5%;
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Unclassified.
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Matches 14; Conserv
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AR494995/c
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REFERENCE AUTHORS

KEYWORDS

SDOG

JOURNAL

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PAT 05-OCT-2002

AUTHORS

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Planomicrobium okeanokoites
Planomicrobium okeanokoites
Bacteria; Firmicutes; Bacillales; Planococcaceae; Planomicrobium.
1 (bases 1 to 50)
Sugisaki, H. and Kanazawa, S.
New restriction endonucleases from Flavobacterium okeanokoites
(FokI) and Micrococcus luteus (MluI)
Gene 16 (1-3), 73-78 (1981)
6282705
Original source text: F.okeanokoites DNA, clone pAO43.
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Planomicrobium okeanokoites
Planomicrobium okeanokoites
Bacteria, Firmicutes, Bacillales, Planococcaceae, Planomicrobium.
1 (bases I to 50)
Sugisaki, H. and Kanazawa, S.
New restriction endonucleases from Flavobacterium okeanokoites
(FokI) and Micrococcus luteus (MluI)
Gene 16 (1-3), 73-78 (1981)
6282705
Original source text: Fromeanokoites DNA, clone pAO43.
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Location/Qualifiers
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Flavobacterium okeanokoites Fokl cleavage site F2/F7.
M18006.1 GI:148700
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Flavobacterium okeanokoites FokI cleavage site F7/F1.
M18007 M10381
M18007.1 GI:148701
                             ch 67.4%; Score 12.8; DB 6; Length 41; 1 Similarity 77.8%; Pred. No. 1.6e+05; 14; Conservative 1; Mismatches 3; Indels
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/organism="Planomicrobium okeanokoites"
/mol_type="genomic DNA"
/db_xref="taxon:244"
26 bp_upstream of Fokl site.
                                                                                                             1 GGGGTGACGTTCAGGGGG 18
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Db 35 GTGATGTTCAGGGAGG 50
Search completed: February 15, 2006, 18:55:32
Job time : 469.843 secs
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Acd31559 E-cell st
Acd31559 Immunosti
Adc36591 Immunosti
Adc36581 Immunosti
Add36581 Immunosti
Add36581 Unmethyla
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Adv87198 B cell-st
Adv8719 Human sur
Adv86375 Human sur
Adv87187 Adpa-1 i
Adv35074 Kappa VL
Adv35077 PCR primer I
Adv81380 Human Ci
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Adv813894 Synthetic
Adv813894 Synthetic
Adv813894 Synthetic
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Ach36464 Polynucle
Ach86398 Allergic
                                                     February 15, 2006, 17:25:23; Search time 143.207 Seconds (without alignments) 884.241 Million cell updates/sec
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         GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 300 summaries
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50 6 ABZ04742 19 4 AAF998401 19 4 AAF9984571 19 6 ABS78562 19 9 ADB372352 19 9 ADB372352 19 9 ADB372352 19 9 ADB372352 20 2 AAV47684 20 3 AAB799499 20 4 AAF99855 20 4 AAF99764 20 6 ABS78425 20 6 ABS78439 20 6 ABS78425 20 6 ABS	10 ADGG 11 ADGGG 11 ADGG 11 ADGGG 11 ADGGG 11 ADGG 11 ADGG 11 ADGGG 11 ADGGG 1
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Vaccine, cytostatic, virucidal, bactericidal, fungicidal, anti-parasitic, immunostimulatory; tumour; viral infection; bacterial infection; tungal infection; parasitic infection; cancer; asthma, infections disease; allergy, immune deficiency; phosphorothioate; ss.

Immunostimulatory nucleic acid #71.

(first entry)

12-JUN-2001

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Adc12469 Human sec Add056024 Human sec Add056024 Human sec Add03606 Human sec Add034858 Human sec Add34859 Human sec Adc73038 Human sec Adf73478 Human sec Adf73954 Human sec Adf73954 Human sec Adf168847 Human sec Adf168848 Human sec Adf168848 Human sec Adf168848 Human sec Adc78545 Human sec Adc78545 Human sec Adc78545 Human sec Adc78548 Human sec Adc78644 Human sec Adc78644 Human sec Adc78644 Human sec Adc78644 Human sec Adc78648 Human sec Adc78644 Human sec Adc78648 Human sec Adc78648 Human sec Adc78644 Human sec Ad
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Vaccinating against tumors, infectious diseases, allergies and asthmausing immunostimulatory Py-rich and TG nucleic acids.

Krieg AM, Schetter C, Vollmer J;

WPI; 2001-273485/28

(IOWA ) UNIV IOWA RES FOUND (COLE-) COLEY PHARM GMBH.

25-SEP-1999; 99US-0156113P. 27-SBP-1999; 99US-0156135P. 23-AUG-2000; 2000US-0227436P.

25-SEP-2000; 2000WO-US026383

WO200122972-A2.

Synthetic.

05-APR-2001

Disclosure; Page 40; 338pp; English.

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The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immuno response. The present sequence is one such immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, heemophilus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Th2 to a Th1 immune response and to activate immune cells. Note: the present sequence may have a phosphorothioate backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth; tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Matches
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ABS77596
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ALIGNMENTS

AAF98955 standard; DNA; 19 BP. RESULT 1 AAF98955

AAF98955; SXXX

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The present invention relates to methods for treating or preventing cancer, involving administering to a subject having or at risk of developing cancer immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies. The methods are useful for treating or preventing cancer such as basal cell carcinoma, bladder cancer, brain and central nervous system (CNS) cancer, breast cancer, cervical cancer, colon and rectum cancer, connective tissue cancer, envisal cancer, elung cancer, Hidney cancer, larynx cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian cancer, stomach cancer, bresticular cancer, rhabdomyosarcoma, skin cancer, stomach cancer, testicular cancer, and uterine cancer. The present sequence is an immunostimulatory oligonucleotide described in the
                                                                                                                                                                  cancer, such as basal cell carcinoma, comprises
                                                                                                                                                                                                              administering immunostimulatory nucleic acids that induce expression or cell surface antigens and antibodies to a subject having or at risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunostimulatory, antiinflammatory, dermatological; antipsoriatic; antiulcer; gene therapy, vaccine; non-allergic inflammatory disease; psoriasis; eczema; allergic contact dermatitis; latex dermatitis; inflammatory bowel disease; ulcerative colitis; crohn's disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 19; DB 6; Length 19; 100.0%; Pred. No. 18; 0; Indels iive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                        Disclosure; Page 208; 312pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunostimulatory nucleic acid #74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exemplification of the invention
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  22-JUN-2000; 2000US-0213346P.
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                                              (IOWA ) UNIV IOWA RES FOUND
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                                                                                                                                                                                        Treating or preventing
                                                                                              Hartmann G;
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Best Local Similarity
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                                                                                                                                                                                                                                                            developing cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2003050268-A1.
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                                                                                                 Weiner G,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            administering at least one antiangiogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, nervascular glaucoma, retrolental fibroplasia, nubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophilac joints, angiofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.
rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to inhibiting angiogenesis in a subject,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibody-induced cell lysis; cancer; immunostimulatory; CD20; angiogenesis; metastasis; cytostatic; ss.
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                                                                      scleroderma, hypertrophic scar
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                                                                                                                                                                                                                                                                                                                                                      (COLE-) COLEY PHARM GROUP INC
                                                                                                                                                                                                                                                            14-DEC-2001; 2001WO-US048458.
                                                                                                                                                                                                                                                                                                          14-DEC-2000; 2000US-025534P
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Best Local Similarity 100.
Matches 19; Conservative
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                                                                                                                                                                  WO200253141-A2.
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                                                                                                                      Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.
                                                                  The invention describes a method of treating non-allergic inflammatory disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases, such as psoriasis, eczema, allergic context dermatitis, latex dermatitis or inflammatory bowel disease e.g., ulcerative colltis or Crohn's disease. This sequence represents an immunostimulatory nucleic acid
 eczema
                                                                                                                                                                                                                                Gaps
        allergic contact dermatitis, latex dermatitis or inflammatory bowel disease by administering an immunostimulatory nucleic acid.
Treating non-allergic inflammatory diseases, such as psoriasis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ds; allergy; asthma; poly-G nucleic acid; aerosol formulation; hypo-responsive subject; immunostimulatory.
                                                                                                                                                                                                     100.0%; Score 19; DB 9; Length 19; 100.0%; Pred. No. 18;
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Pred. No. 18;
                                                                                                                                                                                                                             0; Indels
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                                             Disclosure; Page 10; 229pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 6; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               Immunostimulatory nucleic acid #71
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100.0%;
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                                                                                                                                                                                                                                                                                                                                        ADB36457 standard; DNA; 19
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                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                              19; Conservative
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(PETE/) PETERSEN D
                                                                                                                                                                                                                  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS2003087848-A1
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ADB36457
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Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suppressing allergies, including asthma, rhinitis, urticaria and atopic dermatitis, in a subject, comprises administering a first and second dose of an immunostimulatory nucleic acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        ss; antiasthmatic; antiallergic; dermatological; antiinflammatory; antibacterial; virucide; immunoglobulin E antagonist; allergy; immunostimulator; asthma; rhinitis; urticaria; dermatitis; bacterial infection; viral infection.
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Pred. No. 18;
Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                    Allergic response suppressor oligonucleotide #80.
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Best Local Similarity 100.0%;
Matches 19; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BRATZLER R L.
PETERSEN D M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-833006/82.
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(FOUR/) FOURON Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2004235774-A1
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                                                                                                                                                                                                                                                                                                                          10-FEB-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                               ADU89396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BRAT/)
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The invention relates to inhibiting angiogenesis in a subject, comprising administering at least one antiangiogenic nucleic acid molecule. Also included is a kit comprishing a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with soild tumour growth, tumour metastasis, precancerous lesion, rheumatchid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, cornneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, intestinal adhesions, atherosclerosis, acleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                       Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.
metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
                 diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound granulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibody-induced cell lysis; cancer; immunostimulatory; CD20; angiogenesis; metastasis; cytostatic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 17.4; DB 6;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunostimulatory nucleic acid SEQ ID NO: 448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 21; 276pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGGGTGACGTTCAGGGGGG 19
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                                                                                                                                                                                                                                                                                                                              (COLE-) COLEY PHARM GROUP INC.
                                                                                                                                                                                                                                                         14-DEC-2001; 2001WO-US048458.
                                                                                                                                                                                                                                                                                              14-DEC-2000; 2000US-0255534P.
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Best Local Similarity 94.7%;
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-566690/60
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                                                                                                                                                                                                                     11-JUL-2002
                                                                                                                                                Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (pyrich) for thymidine (T) rich. The method is used to vaccinate subjects against tumnou antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, hemophilus, campylobacter, clostridium, Escherichia coll and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a first to a Thl immune response and to activate immune cells. Note: the present sequence may have a phosphorothioate backbone
                                                                                                                           Vaccine, cytostatic, virucidal; bactericidal, fungicidal, anti-parasitic, immunostimulatory, tumour, viral infection; bacterial infection; fungal infection; parasitic infection; cancer; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vaccinating against tumors, infectious diseases, allergies and asthmausing immunostimulatory Py-rich and TG nucleic acids.
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                                                                                                                                                                                     Infectious disease; allergy; immune deficiency; phosphorothioate;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.6%; Score 17.4; DB 4; Length 19; 94.7%; Pred. No. 1.1e+02; live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19 BP; 1 A; 2 C; 12 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Angiogenesis inhibitory oligonucleotide #82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 40; 338pp; English.
                                                                                             Immunostimulatory nucleic acid #73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vollmer J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GGGGTGACGTTCAGGGGGG 19
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27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
                                                                                                                                                                                                                                                                                                                                  25-SEP-2000; 2000WO-US026383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Krieg AM, Schetter C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-273485/28
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                                                         12-JUN-2001
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                                                                                                                                                                                                                         Synthetic.
                      AAF98957;
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Gaps

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The invention relates to a method of treating or preventing allergy or asthma which comprises administering to a subject a poly-G nucleic acid in an aerosol formulation. The methods and compositions of the present invention are useful for diagnosing and/or treating asthma and allergy especially in a hypo-responsive subject. The present sequence represents an immunostimulatory nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.
                                                                                                                                                                                         The invention describes a method of treating non-allergic inflammatory disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases, such as pportlasts, eczema, allergic context dermatifis, latex dermatitis or inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease. This sequence represents an immunostimulatory nucleic acid
                                                           Treating non-allergic inflammatory diseases, such as psoriasis, eczema, allergic contact dermatitis, latex dermatitis or inflammatory bowel disease by administering an immunostimulatory nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ds; allergy; asthma; poly-G nucleic acid; aerosol formulation; hypo-responsive subject; immunostimulatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.6%; Score 17.4; DB 9; Length 19; 94.7%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19 BP; 1 A; 2 C; 12 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                      Disclosure; Page 10; 229pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunostimulatory nucleic acid #73.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGGGTGACGTTCAGGGGGG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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PETERSEN D M.
FOURON Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-657977/62.
                   WPI; 2003-521815/49.
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(FOUR/)
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                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to methods for treating or preventing cancer, involving administering to a subject having or at risk of developing cancer immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies. The methods are useful for treating or preventing cancer such as basal cell carcinoma, bladder cancer, brain and central nervous system (CNS) cancer, brain and central nervous system (CNS) cancer, breast cancer, cervical cancer, colon and rectum cancer, connective tissue cancer, oesophageal cancer, colon and rectum cancer, larynx cancer, larynx cancer, larynx cancer, larynx cancer, pancreatic cancer, prostate cancer, hadden, only hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin cancer, sequence is an immunostimulatory oligonucleotide described in the exemplification of the invention
                                                                                                                                                                                                                                              Treating or preventing cancer, such as basal cell carcinoma, comprises administering immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies to a subject having or at risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.6%; Score 17.4; DB 6; Length 19; 94.7%; Pred. No. 1.1e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19 BP; 1 A; 2 C; 12 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 209; 312pp; English.
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                     22-JUN-2001; 2001WO-US020154.
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                                                                22-JUN-2000; 2000US-0213346P.
                                                                                                           (IOWA ) UNIV IOWA RES FOUND
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                                                                                                                                                        Hartmann G;
                                                                                                                                                                                                   WPI; 2002-154611/20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                   developing cancer.
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                                                                                                                                                          Weiner G,
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Best Loca Matches

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Gaps

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Indels

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Ligand binding; restriction enzyme; nucleic acid determination; pharmaceutical; BamHI; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modulating polynucleotide ligand binding site affinity using determination of the flanking duplex sequences.
                                                                                                                                                                                     Polynucleotide sequence including binding site for BamHI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 40; 62pp; English.
                                               AAZ95948 standard; DNA; 40 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TMTE-) IM TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lane MJ, Benight AS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-116369/10.
                                                                                                                                                                                                                                                                                                                                                           409963077-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-JUN-1998;
                                                                                                                                           10-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                           09-DEC-1999,
                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                           AAZ95948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
RESULT 13
                      AAZ95948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method of suppressing a symptom of an allergic response in a subject by administering a first and second dose of an immunostimulatory nucleic acid that comprises a nucleotide sequence comprising 5'-cg-3', and where the second dose is administered from 1 day to 8 weeks after the first dose. The methods and compositions of the present invention are useful for the treatment or prevention of asthma and allergy, including rhinitis, urticaria and atopic dermatitis, using an immunostimulatory nucleic acid alone or in combination with other medicaments. They can also be used in preventing bacterial and viral infections. This sequence represents an oligonucleotide used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suppressing allergies, including asthma, rhinitis, urticaria and atopic dermatitis, in a subject, comprises administering a first and second dose of an immunostimulatory nucleic acid.
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ss; antiasthmatic; antiallergic; dermatological; antiinflammatory; antibacterial; virucide; immunoglobulin E antagonist; allergy; immunostimulator; asthma; rhinitis; urticaria; dermatitis; bacterial infection; viral infection.
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                        Length 19;
                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence 19 BP; 1 A; 2 C; 12 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Allergic response suppressor oligonucleotide #82.
                      Score 17.4; DB 9;
Pred. No. 1.1e+02;
                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 82; 235pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Petersen DM, Fouron Y;
                                                                                                                       GGGGTGACGTTCAGGGGGG 19
                                                                                                                                                                   GGGGTGTCGTTCAGGGGGG 19
                                                                                                                                                                                                                                                                                        ВЪ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.6%;
94.7%;
                        91.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-APR-2004; 2004US-00831778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-FEB-2000; 2000US-0179991P.
02-FEB-2001; 2001US-00776479.
                                                                                                                                                                                                                                                                                        ADU89398 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                       10-FEB-2005 (first entry)
                        Query Match
Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 94.7
hes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BRAT/) BRATZLER R L. (PETE/) PETERSEN D M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-833006/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PETE/) PETERSEN !
(FOUR/) FOURON Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2004235774-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bratzler RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5-NOV-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                       ADU89398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                         RESULT 12
ADU89338

ID ADU89338

XX ADU8
XX AD
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Faldasz BD;

99WO-US012516. 98US-0087905P. 99US-00324672.

(first entry)

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The invention provides a method for determining the sequence of polynucleotide flanking regions that modulate ligand binding characteristics of an adjacent binding site. The method comprises: (i) providing a number of different binding site. The method comprises: (i) providing a number of different duplex polynucleotides, each having the sequence flanking the binding site; (ii) exposing the duplex to a ligand selective for the binding site; (iii) isolating duplexes which bind or not bind the ligand, and (iv) determining the nucleotide composition of the flanking duplex sequence by sequencing the duplex sequence adjacent to the binding site. The invention is used to modulate the ligand-binding characteristics of any nucleotide sequence. The invention is less costly and more efficient than prior art techniques that moderate ligand binding using small molecule pharmaceuticals. Sequences AA25762-296170 represent polynucleotide sequences including the binding site for the restriction enzyme BamHI and used in the course of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunostimulatory oligodeoxyribonucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.8%; Score 14.4; DB 3; Length 40; 93.8%; Pred. No. 3.1e+03; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 40 BP; 9 A; 9 C; 15 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunostimulatory; oligodeoxyribonucleotide; ODN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 GTGACGTTCAGGGGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 gradacarrandadada 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV27677 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1998
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ID AAV.
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AC AAV.
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DT 01-(
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Gaps

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1 GGGGTGACGTTCAGGGGGG 19 GGGGTGTCGTTCAGGGGGG 19

Matches

(OTTA-) OTTAWA CIVIC HOSPITAL LOEB RES INST. (IOWA ) UNIV IOWA RES FOUND. (QIAG-) QIAGEN GMBH.

98WO-US010408 97US-0047209P 97US-0047233P

20-MAY-1998; 20-MAY-1997; 20-MAY-1997;

WO9852581-A1.

26-NOV-1998

Wu T;

Schorr J,

Davis HL, Krieg AM,

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AAV27641-751 represent immunostimulatory oligodeoxyribonucleotides (ODNs) of the invention. The ODNs contain at least one unmethylated CpG dinucleotide, and have the formula: 5' NIXICGX2N2 3', where at least one nucleotide separates consecutive CpGs, X1 is adenine, guanine, or thymine, X2 is cytosine or thymine, N is any nucleotide and N1+N2 is 0-26 bases with the provision that N1 and N2 does not contain a CCGG tetramer or more than one CGG or CGG trimer OR 5' NIXICACGX3X4N 3', where at least one nucleotide separates consecutive CpGs, X1 and X2 are selected from GpT, GpG, GpA, ApT and ApA, X3and X4 are selected from TpT or CpT, N is any nucleotide and N1+N2 is 0-26 bases with the provision that N1 and N2 does not contain a CCGG tetramer or more than one CCG or CGG trimer. The ODNs activate lymphocytes in a subject and redirect a subject's immune response from a Th2 to a Th1 (e.g. by inducing monocytic cells and other CC cells to produce Th1 cytokines, including IL-12, IFN agamma and GM-CSF). The ODNs can be used to treat or prevent an asthmatic disorder, a utoimmune diseases, in desensitisation therapy, as an artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                    New immunostimulatory nucleic acid molecules - which contain at least one unmethylated CpG dinucleotide, used for treating e.g. tumours, infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CpG-N motif; immunostimulation; antigen; CpG-S motif; immunisation; ODN; viral antigen; bacterial antigen; parasite; therapeutic; growth factor; toxin; tumour suppressor; cytokine; apoptotic protein; interferon; hormone; clotting factor; ligand; receptor; oligodeoxynucleotide; ss.
                disease;
              Th2; Th1; cytokine; treatment; prevention; asthma; autoimmune disease; desensitisation therapy; artificial adjuvant; antibody generation; ss
unmethylated CpG dinucleotide; activate; lymphocyte; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
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Pred. No. 3.7e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                               Disclosure, Page 25; 109pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GGGGTGACGTTCAGGGGGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGTCAACGTTCAGGGGGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV74249 standard; DNA; 20 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.7%;
84.2%;
                                                                                                                                         97WO-US019791
                                                                                                                                                                      96US-00738652
                                                                                                                                                                                                 (IOWA ) UNIV IOWA RES FOUND.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                    or autoimmune disease.
                                                                                                                                                                                                                              Kline JN;
                                                                                                                                                                                                                                                         WPI; 1998-272127/24.
                                                                                                                                           30-OCT-1997;
                                                                                                                                                                       30-OCT-1996;
                                                                                  WO9818810-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-MAR-2003
15-MAR-1999
                                                                                                              07-MAY-1998
                                                        Synthetic.
                                                                                                                                                                                                                                Krieg AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV74249;
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                                                                                                                                                                                                      method for enhancing the immunostimulatory effect of an antigen encoded by nucleic acid contained in a nucleic acid construct. The method in involves determining the CpG-N and CpG-S motifs present in the construct, removing neutralising CpG (CpG-N) motifs and optionally inserting stimulatory CpG (CpG-S) motifs in the construct, thereby producing a nucleic acid construct having enhanced immunostimulatory efficacy. The method can be used for immunisation against viral antigens, e.g. from hepatitis B virus (HBV), bacterial antigens or an antigen derived from a parasite. They can also be used for expression of a therapeutic polypeptide, e.g. growth factors, tumour suppressors, cytokines, apoptotic proteins, interferons, hormones, clotting factors, ligands and receptors. (Updated on 20-MAR-2003 to correct PA field.)
                                                                                                                                                                                          AAV74237-V74253 are oligodeoxynucleotide (ODN) primers used to describe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B cell; stimulant; immune response; B cell activation; cancer; vaccine; immunostimulatory molecule; infection; therapy; 88.
                                              Use of neutralising CpG and stimulating CpG motifs in DNA vectors - for enhancing the immunostimulatory effect of an antigen or enhancing the expression of a therapeutic polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 14.2; DB 2; Length 20;
Pred. No. 3.7e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 1 A; 1 C; 12 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16. .20
/*tag= a
/note= "phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B-cell stimulating oligonucleotide, ODN1585.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                               Example 1; Page 64; 109pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGGGTGACGTTCAGGGGGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 gegricacertrreseses 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
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Best Local Similarity 84.2%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ48834 standard; DNA; 20
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/*tag=
nor
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WPI; 1999-059712/05
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25-SEP-1999; 99US-0156113P.
27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
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                                                                                                     (IOWA ) UNIV IOWA RES
                                                                                                                                         Krieg AM, Klinman D,
                                                                                                                                                               WPI; 2001-217934/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200122972-A2.
                                                        07-FEB-1995;
          US6194388-B1
                                27-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF99097;
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                                                                                                                                                                                                           This sequence represents a B cell stimulatory oligonucleotide. The invention relates to compositions comprising an oligonucleotide (I) with unmethylated guanine and cytosine nucleotides and an antigen in a carrier. The oligonucleotides can be administered to a subject in a composition with an antigen in a carrier to enhance an immune response by and can be used to treat, prevent or ameliorate an immune system and can be used to treat, prevent or ameliorate an immune system deficiency e.g. cancer or viral, fungal, bacterial or parasitic infection. They can also be administered as a vaccine adjuvant to stimulate the response of a host to a vaccine. The compositions can be used to treat humans or vertebrate animals including dogs, cats, sheep pigs, cows, goats, chickens, mice and monkeys. Preceding chemotherapy with the immunostimulatory oligonucleotides should be useful for
                                                                                                                                                    Immunostimulatory oligonucleotides which enhance B cell activation useful for treating an immune system deficiency e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligodeoxyribonucleotide; ODN; cytosine-guanine dinucleotide; CpG; immunostimulatory; therapy; immune system deficiency; tumour; cancer; antibacterial; antiparasitic; fungicide; antiviral; cytostatic; leukaemia; systemic lupus erythematosus; sepsis; autoimmune disease; immunoinhibitory; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                       increasing the responsiveness of malignant cells to subsequent chemotherapy. The 8-40 nucleotide size of the oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                             th 74.7%; Score 14.2; DB 3; Length 20; Similarity 84.2%; Pred. No. 3.7e+03; 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunostimulatory oligodeoxyribonucleotide (ODN) 1585.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mod_base= OTHER
/note= "Phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= b
/mod_base= OTHER
                                                                                                                                                                                          Claim 10; Col 10; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGGGTGACGTTCAGGGGGG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                               facilitates uptake into cells
                                 95US-00386063
                                                         94US-00276358
                                                                                (IOWA ) UNIV IOWA RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD02961 standard; DNA; 20
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                                                                                                                             WPI; 2000-086224/07.
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modified_base
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                                 07-FEB-1995;
                                                         15-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAY-2001
           28-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                        Krieg AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD02961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches
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The present invention relates to immunomodulatory oligodeoxyribonucleotides (ODMs) containing methylated or unmethylated represents a compositions having unmethylated CpG dinucleotides. Immunostimulatory ODN compositions having unmethylated CpG dinucleotides are useful for activating lymphocytes and for treating, preventing or ameliorating an immune system deficiency e.g. tumour or cancer or viral, fungal, bacterial or parasitic infection and leukaemia. Neural ODN that contains a methylated CpG dinucleotide are useful for treating diseases such as systemic lupus erythematosus, sepsis and autoimmune diseases. Immunoinhibitory ODN Gontaining CpG dinucleotides that are not in the stimulatory motif and activity. The present sequence is an immunostimulatory
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                                                                                                                                                                                                                                                                                                                                                                         Immunostimulatory composition useful for stimulating immune response in subject, comprises antigen and immunostimulatory nucleic acid comprising oligonucleotides having unmethylated cytosine-guanine dinucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88
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immunostimulatory, tumour, viral infection, bacterial infection,
fungal infection, parasitic infection, cancer, asthma,
infectious disease, allergy, immune deficiency, phosphorothioate,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 14.2; DB 4; Length 20; Pred. No. 3.7e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                 Steinberg AD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ODN) 1585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 10; Col 10; 20pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGGGTGACGTTCAGGGGGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          activity. The present sequence oligodeoxyribonucleotide (ODN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВР
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95US-00386063
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Best Local Similarity 84.2
Matches 16; Conservative
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                                                                                                                                                                                                                      response. The method comprises administering an immunostimulatory uncleic acid to a non-rodent subject in sufficient quantity to stimulate an immunostimulatory nucleic acid. The present sequence is one such immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects adding tumour antigens, viral antigens (e.g. herpesviridae, retroviridae, and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is staphylococcus, preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Th2 to a Th1 immune response and to activate immune cells. Note: the
                                                                                                                            Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.
                                                                                                                                                                                                            present invention relates to a method for stimulating an immune
                                                                                                                                                                                                                                                                                                                                                                                                                        present seguence may have a phosphorothioate backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20 BP; 1 A; 1 C; 12 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                            Claim 101; Page 42; 338pp; English.
                                                                Vollmer J;
             UNIV IOWA RES FOI COLEY PHARM GMBH
                                                              Schetter C,
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                                                                Krieg AM,
             (IOWA )
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74.7%; Score 14.2; DB 4; Length 20; 84.2%; Pred. No. 3.7e+03; ive 0; Mismatches 3; Indels
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                              Conservative
                Local Similarity
les 16; Conserva
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  Query Match
                              Matches
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Angiogenesis inhibitory oligonucleotide #224.
ABS77740 standard; DNA; 20 BP
            (first entry)
            13-DEC-2002
                                                      Synthetic
      ABS77740;
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tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound granulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar. Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;

WO200253141-A2

11-JUL-2002

14-DEC-2001; 2001WO-US048458

14-DEC-2000; 2000US-0255534P.

(COLE-) COLEY PHARM GROUP INC

Bratzler RL;

WPI; 2002-566690/60

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                                                                                                         The invention relates to inhibiting angiogenesis in a subject, comprising administering at least one antiangiogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lession, rheumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic
Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating or preventing cancer, such as basal cell carcinoma, comprises administering immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies to a subject having or at risk of developing cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibody-induced cell lysis; cancer; immunostimulatory; CD20; angiogenesis; metastasis; cytostatic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 14.2; DB 6; Length 20; Pred. No. 3.7e+03;
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                                                                  Claim 2; Page 23; 276pp; English.
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84.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                            acid of the invention
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BERG D J.
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                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
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                                                                                                              ACD99530;
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Matches
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                                             ACD99530
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                   breast cancer, cervical cancer, colon and rectum cancer, connective tissue cancer, desophageal cancer, eye cancer, Hidney cancer, larynx cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian cancer, spancreatic cancer, prostate cancer, rhabdomyosarcoma, skin cancer, stomach cancer, testicular cancer, and uterine cancer. The present sequence is an immunostimulatory oligonucleotide described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to treating a subject infected with HIV comprising administering a CpG nucleic acid (e.g. an adjuvant type CpG obligonuclectide, an immunostimulatory CpG oligonuclectide or a B cell stimulatory CpG oligonuclectide). The CpG are used as gene therapy vaccines to treat a subject infected with HIV. The present sequence is a
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bone cancer, brain and central nervous system (CNS) cancer
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                                                                                                                                                                                                                                                                           Score 14.2; DB 6; Length 20; Pred. No. 3.7e+03;
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                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B-cell stimulatory, CpG containing oligonucleotide #1.
                                                                                                                                                                                                                               Sequence 20 BP; 1 A; 1 C; 12 G; 6 T; 0 U; 0 Other;
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                                                                                                                                                                                  exemplification of the invention
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95US-00386063.
99US-00415142.
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84.28;
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Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                   Local Similarity 84.2
es 16; Conservative
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Immunostimulatory oligonucleotide; unmethylated CpG dinucleotide; immunoinhibitory oligonucleotide; oellular transcripton factor; viral activity; lymphocyte activation; B cell; natural killer cell; NK; immune system deficiency; viral infection; immune disease; SLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention describes a method of treating non-allergic inflammatory disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases, such as psoriasis, eczema, allergic context dermatitis, latex dermatitis or inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease. This sequence represents an immunostimulatory nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                   Immunostimulatory, antiinflammatory, dermatological, antipsoriatic; antiulcer; gene therapy, vaccine; non-allergic inflammatory disease; psoriasis; eczema; allergic contacticis dermatitis; latex dermatitis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating non-allergic inflammatory diseases, such as psoriasis, ecz allergic contact dermatitis, latex dermatitis or inflammatory bowel disease by administering an immunostimulatory nucleic acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lymphocyte (B cell) activating oligonucleotide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y match 74.7%; Score 14.2; DB 9; Local Similarity 84.2%; Pred. No. 3.7e+03; hes 16; Conservative 0; Mismatches 2
                                                                                                                                                                                             Immunostimulatory nucleic acid #216.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 14; 229pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GGGGTGACGTTCAGGGGGG 19
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BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAR-2002; 2002US-00112653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAR-2001; 2001US-0279642P.
ACD99530 standard; DNA; 20
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                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Krieg AM, Berg DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KRIEG A M.
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systemic lupus erythematosus, sepsis, viral infection, immunosuppressive, immunostimulating, immunomodulating, antibacterial, antiinflammatory; dermatological, virucide, phosphorothioate backbone, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        asthma which comprises administering to a subject a poly G nucleic acid in an aerosol formulation. The methods and compositions of the present invention are useful for diagnosing and/or treating asthma and allergy especially in a hypo-responsive subject. The present sequence represents an immunostimulatory nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                                                           Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method of treating or preventing allergy or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitogenic oligonucleotide ODN1585 used in B-cell stimulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 14.2; DB 9; Length 20;
Pred. No. 3.7e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lymphocyte; B cell; natural killer cell; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 20 BP; 1 A; 1 C; 12 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *tag= a
/mod_base= OTHER
/note= "Phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Phosphorothioate backbone"
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                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 8; 221pp; English.
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                                                                                        02-FEB-2001; 2001US-00776479
                                                                                                                                    03-FEB-2000; 2000US-0179991P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 74.7%;
Best Local Similarity 84.2%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                    Bratzler RL, Petersen DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADO58881 standard; DNA; 20
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                                                                                                                                                                              BRATZLER R L.
PETERSEN D M.
                                                                                                                                                                                                                                                                                                                 WPI; 2003-657977/62.
                                                                                                                                                                                                 (PETE/) PETERSEN I
(FOUR/) FOURON Y.
    US2003087848-A1
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modified_base
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                                              08-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         systemic lupus erythematosus (SLE), sepsis, or cancer. The coligonucleotides are safe to use since they do not initiate an immune reaction when administered to a subject in vivo. ACAG2324-ACAG2352 represent the immunomodulatory oliuponucleotides of the invention. Note: The present sequence given as SEQ ID No:1 in the Sequence listing differs from that given on page 6 (ACAG2351) and page 17 (ACAG2352) of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel immunostimulatory oligonucleotide comprising 2-100 nucleotides and containing at least one unmethylated CpG dinucleotide, useful for activating a subject's B cells or natural killer cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to immunostimulatory oligonucleotides containing at least one unmethylated CpG dinucleotide, and immunoinhibitory oligonucleotides which are capable of interfering with the activity of viral or cellular transcription factors. The immunostimulatory oligonucleotides are useful for activating a subject's lymphocytes (B cells or natural killer (NK) cells). They are useful for treating, preventing or ameliorating an immune system deficiency. The immunoinhibitory oligonucleotides are useful for treating or preventing viral infection in a subject. They are also useful for treating or yeroenting or viral infection in a subject. They are also useful for treating or immune system deficiency in a subject. The immunoinhibitory oligonucleotides can be used in a pharmaceutical composition which may be used for vaccinating an subject. The oligonucleotides may be used for treating an immune disease such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
systemic lupus erythematosus; sepsis; cancer; immunomodulatory; immunostimulant; dermatological; antiinflammatory; cytostatic; antibacterial; virucide; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.7%; Score 14.2; DB 9; Length 20; 84.2%; Pred. No. 3.7e+03; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunostimulatory nucleic acid #213.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 13; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GGGGTGACGTTCAGGGGGG 19
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                                                                                                                                                                                                                        99US-00415142
                                                                                                                                                                                                                                                                    95US-00386063
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                                                                                                                                                                                                                                                                                                                 (KRIE/) KRIEG A M.
                                                                                                                                  US2003026782-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specification
                                                                                                                                                                                                                      08-OCT-1999;
                                                                                                                                                                                                                                                                    07-FEB-1995;
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                                                                                                                                                                            06-FEB-2003
                                                                                        Synthetic
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                                                                                                                                                                                                                                                                                                                                                             Krieg AM;
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Best Loc Matches

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Gaps

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21-OCT-2003; 2003US-00690495.

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                                                                                                                                                                                                                                                              The present invention provides oligonucleotides comprising unmethylated CpG dinucleotides. The invention is useful to activate lymphocytes specifically to activate B cells and natural killer cells, for treating diseases associated with an immune system activation such as systemic lupus erythematosus, sepsis and viral infections. The invention is useful
                                                                                                                                                                                                                                                                                                                                         as an immunosuppressive, immunosimulating, immunomodulating, antibacterial, antiinflammatory, dermatological and virucidal agent. The present sequence is a mitogenic oligonucleotide used in the stimulation of B-cells. This sequence is used in the invention.
                                                                                                                                                                         New immunomodulatory oligonucleotides containing at least one unmethylated CpG dinucleotide, useful for treating diseases including systemic lupus erythematosus and sepsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
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/note= "Phophorothioate linkage"
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/note= "Phophorothioate linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B-cell stimulatory CpG oligonucleotide ODN1585.
                                                        US DEPT HEALTH & HUMAN SERVICES. COLEY PHARM GROUP INC.
                                                                                       CPG IMMUNOPHARMACEUTICALS INC.
                                                                                                                     Krieg AM, Klinman D, Steinberg AD;
                                                                                                                                                                                                                                        Claim 5; SEQ ID NO 1; 19pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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/note= "CpG island"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16..20
/*tag= c
/mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGGGTGACGTTCAGGGGGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGTCAACGTTCAGGGGGG 20
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 95US-00386063.
              99US-00415142.
                                          IOWA ) UNIV IOWA RES FOUND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antisense gene therapy
                                                                                                                                                  WPI; 2004-356245/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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modified base
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07-FEB-1995;
08-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                          (USSH )
(COLE-)
(CPGI-)
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ADQ36558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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The invention relates to a new oligonucleotide which: (a) comprises about CC 2-100 nucleotides and containing at least one unmethylated CpG dinucleotide, or (b) is capable of interfering with the activity of viral or cellular transcription factors and containing a consensus immunication or melicial or cellular transcription factors and containing a consensus immunoinhibitor CpG motif represented by the formula (1): 5/GCXnCCG3/
CW ancleotide and no 1-50. Also included are an oligonucleotide and a capable composition comprising the oligonucleotide and a largering means, calls (by contacting the calls with the oligonucleotide and a subject (by pharmaceutical carrier, activating a subject's B cells or natural killer cells (by contacting the colloquicleotide) treating, contrating or ameliorating) an immune system deficiency in a subject, when a vaccine, treating a disease associated with an immune collomic or auchioaction in a subject (by administering the composition in conjunction with a pharmaceutical carrier), an improved method for in vivo diagnoses using oligonucleotide probes comprising methylating CpG containing oligonucleotide probes comprising methylating CpG containing oligonucleotide probes comprising or method for in vivo diagnoses using oligonucleotide probes comprising or method for in vivo diagnoses using oligonucleotide probes comprising an immune system deficiency, such as systemic lupus erythematosus, sepsis, tumour, cancer, or viral, fungal, bacterial or parasitic infection.

C compositions comprising the logionucleotide are useful for treating a subject.

The immunoshibitory oligonucleotide is useful for treating or preventing or viral infection in a subject. The oligonucleotide is useful for creating are useful for creating or preventing or viral infection in a subject. The oligonucleotides may also be used in composition with a vaccine to boost a subject's immune system to effect a conjunction with a vaccine to boost a subject's immune system to else on the malignant cells to subminish or for 
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                                                                                                                                                                                                                                                                                                           New oligonucleotides containing unmethylated CpG dinucleotide, useful for
                                                                                                                                                                                                                                                                                                                               treating, preventing or ameliorating an immune system deficiency, e.g. tumor, cancer, or viral, fungal, bacterial or parasitic infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; SEQ ID NO 1; 14pp; English.
                                                                                                                                                                                                                            Steinberg AD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GGGGTGACGTTCAGGGGG 19
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95US-00386063.
99US-00415142.
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nes 16; Conservative
                                                                                                                                                                                     STEINBERG A D.
                                                                                                                                                                                                                            Klinman D,
                                                                                                                                                                                                                                                                    WPI; 2004-552597/53
                                                                                                                                           KRIEG A M.
KLINMAN D.
                                                           15-JUL-1994;
                                                                              07-FEB-1995;
08-OCT-1999;
                                                                                                                                                                                                                              Krieg AM,
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(STEI/)
                                                                                                                                              KRIE/)
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Matches
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ADR20014

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The invention relates to oligonuclectides containing at least one unmethylated CpG dinuclectide. The invention relates to an oligonuclectide delivery complex comprising an oligonuclectide of the invention and a targeting means, a method of activating a subject's B cells or natural killer cells by contacting the cells with an immens system deficiency in a subject, vaccinating a subject by administering the composition in conjunction with a vaccine, a method of treating a disease associated with an immune system activation in a subject by administering a neutral oligonuclectide alone or in conjunction with a pharmaceutical carrier, and a method of performing a neutral oligonuclectide alone or in conjunction with a pharmaceutical carrier, and a method of performing antisense therapy comprising methylating CpG containing oligonuclectides are useful for treating diseases associated with immune system activation, such as systemic lupus erythematosus and sepsis. Compositions comprising systemic lupus erythematosus and sepsis. Compositions comprising a subject's B cells or natural killer cells, for treating a subject the invention are useful for activating a subject of an immune system deficiency or for vaccinating a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunoinhibitory oligonucleotides are useful for treating or preventing a viral infection in a subject. The oligonucleotides may also be used in conjunction with a vaccine to boost a subject's immune system to effect a better response from the vaccine, or for increasing the responsiveness of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cells to subsequent chemotherapy. This sequence represents an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New oligonucleotides containing unmethylated CpG dinucleotide, useful activating a subject's B cells or natural killer cells, as vaccine, or for treating, preventing or ameliorating an immune system deficiency.
                                                                                     immune system deficiency, immune system activation; systemic lupus erythomatosus; sepsis; viral infection; chemotherapy; cytostatic; virucide; fungicide, antibacterial; antiparasitic; immunosuppressive; antiinflammatory; dermatological; ss.
                                                              Unmethylated CpG dinucleotide; B cell; natural killer cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unmethylated CpG dinucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (COLE-) COLEY PHARM GROUP INC.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Steinberg AD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; SEQ ID NO 1; 14pp; English
                       Unmethylated CpG dinucleotide #1.
                                                                                                                                                                                                                                                                                                                                                                                              07-FEB-1995; 95US-00386063.
08-OCT-1999; 99US-00415142.
21-OCT-2003; 2003US-00690495.
                                                                                                                                                                                                                                                                                                                              26-FEB-2004; 2004US-00789051
                                                                                                                                                                                                                                                                                                                                                                            94US-00276358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IOWA ) UNIV IOWA RES FOUND.
(COLE-) COLEY PHARM CECTET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klinman D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-552569/53
                                                                                                                                                                                                                                           JS2004142469-A1.
                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1994;
                                                                                                                                                                                                                                                                                    22-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Krieg AM,
                                                                                                                                                                                                 Synthetic
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Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

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o,
                            Gaps
                            ö
Score 14.2; DB 12; Length 20;
Pred. No. 3.7e+03;
0; Mismatches 3; Indels (
 74.7%;
84.2%;
                          16; Conservative
  Query Match
Best Local Similarity
                            Matches
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1 GGGGTGACGTTCAGGGGGG 19
                                 GGGTCAACGTTCAGGGGGG 20
                                 N
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cellular transcription factor; immunoinhibitory, CpG, phosphorothioate backbone; B cell activation; matural killer cell activation; immune system deficiency; systemic lupus erythematcous; sepsis; antisense; methylation; antiinflammatory; dermatological; immunosuppressive; virucide; ss; /mod_base= OTHER /note= "phosphorothioate linkage" /note= "phosphorothioate linkage" B-cell stimulating oligonucleotide ODN 1585. Location/Qualifiers /mod_base= OTHER ADR20014 standard; DNA; 20 BP. 94US-00276358. 95US-00386063. 99US-00415142. 26-FEB-2004; 2004US-00788191 21-OCT-2003; 2003US-00690495 Ø Д 16. .20 *tag= /*tag= US2004152656-A1 modified base modified base 15-JUL-1994; 07-FEB-1995; 21-OCT-2004 05-AUG-2004 Synthetic. primer. Key 

USSH ) US SEC HEALTH AND HUMAN SERVICES COLEY PHARM GROUP INC (IOWA ) UNIV IOWA RES FOUND COLE-)

Steinberg AD; Krieg AM, Klinman D,

WPI; 2004-624263/60.

New oligonucleotide comprises at least one unmethylated CpG dinucleotide, useful for stimulating an immune response or for treating diseases associated with immune system activation, e.g. systemic lupus erythematosus or sepsis.

Claim 5; SEQ ID NO 1; 19pp; English.

This invention describes novel oligonucleotides capable of interfering with the activity of viral or cellular transcription factors and containing a consensus immunoinhibitory CpG motif having the formula: CCGXAGCG3', where X is a nucleotide and n is 0-50 and a phosphorothioate backbone modification. The invention also describes an oligonucleotide delivery complex comprising the oligonucleotide and a targeting means e.g. a pharmaceutical carrier. The oligonucleotide and targeting means e.g. a pharmaceutical carrier. The oligonucleotide and targeting a subject's Beels or natural Killer cells; reating, preventing or ameliorating a disease associated with an immune system activation in a subject (systemic lupus erythematosus or sepsis); performing antisense therapy comprising methylating CpG containing oligonucleotide prior to administration to a subject; and treating oligonucleotide probes comprising methylating CpG containing oligonucleotides prior to administration to a subject; and treating or preventing a viral infection in a subject. The targeting means is selected from cholesterol, virosome, lipid, or a target cell specific binding agent. The coligonucleotides described in the invention have antiinflammatory,

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cc and containing at least one unmethylated CpG dinuclectide. The oligonuclectide is capable of interfering with the activity of viral or cellular transcription factors and containing a consensus immunoinhibitory CpG motif having the formula: 5'GCGXnGCG3', where X is a nucleotide and n is 0-50. Also included are an oligonucleotide delivery complex (comprising the oligonucleotide above and a targeting means), a comparamentical composition (comprising the oligonucleotide above and a cargeting means), a comparamentical carrier), activating a subject's B cells, activating a subject's natural killer cells, treating (preventing or ameliorating) and subject's natural killer cells, treating (preventing or ameliorating) and issue deficiency in a subject, vaccinating or subject, treating a clisance therapy (comprising methylating CpG containing or performing antisense therapy (comprising methylating CpG containing oligonucleotides prior to administration to a subject), in vivo diagnoses cusing oligonucleotides prior to administration to a subject in vivo diagnoses conjugnucleotides prior to administration to a subject and treating or preventing a viral infection in a subject. The oligonucleotide is useful for treating diseases associated with immune system activation including systemic lupus erythematosus or sepsis, or for treating, preventing, or coligonucleotide is also useful for treating or preventing viral coligonucleotide is also useful as a vaccine. The present sequence is an immune coligonucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    systemic lupus erythematosus; sepsis; tumour; cancer; viral infection; bacterial infection; fungal infection; cytostatic; virucidal; antibacterial; fungicidal; antiinflammatory; dermatological; immunosuppressive; vaccine; gene therapy; phosphorothicate backbone; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitogenic CpG oligonucleotide ODN1585 used in B-cell activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunomodulatory; CpG dinucleotide; immune system deficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.7%; Score 14.2; DB 13; Length 20; 84.2%; Pred. No. 3.7e+03; Live 0; Mismatches 3; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/mod_base= OTHER
/note= "Phosphorothioate backbone"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Phosphorothioate backbone
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/mod_base= OTHER
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07-FEB-1995; 95US-00386063.
08-OCT-1999; 9US-00415142.
21-OCT-2003; 2003US-00690495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGTCAACGTTCAGGGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 84.2
nes 16; Conservative
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modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ss; immunostimulatory oligonucleotide; CpG dinucleotide; transcription factor; immunoinhibitory CpG motif; B cell; natural killer cell; immune system deficiency; antisense therapy; viral infection; immune response; systemic lupus erythematosus; sepsis;
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                                                                                                                                                                                                                  Gaps
dermatological, immunosuppressive and virucide activity. ADR20014-ADR20040 represent the oligonucleotides describes in the disclosure the invention.
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                                                                                                                                                         Score 14.2; DB 13; Length 20;
Pred. No. 3.7e+03;
0; Mismatches 3; Indels (
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                                                                                                                  Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note = "Phosphorothioate linkage"
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(USSH ) US SEC HEALTH AND HUMAN SERVICES.
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/note= "CpG dinucleotide'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Krieg AM, Klinman D, Steinberg AD,
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95US-00386063.
99US-00415142.
                                                                                                                                                                                                                                                                                                                                                                                                                                     BP
                                                                                                                                                                   74.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ADR28877 standard; DNA; 20
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/mod_base=
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nes 16; Conservative
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07-FEB-1995;
08-OCT-1999;
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                                                                                                                                                                        Query Match
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AD5228677

AD7228677

AD722877

AD72297

AD722
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o O

Gaps

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The invention provides novel oligonucleotides containing unmethylated CpG dinucleotides and therapeutic utilities based on their ability to dinucleotides an immune response in a subject. Oligonucleotides of the invention are useful for treating, preventing or ameliorating an immune system deficiency or a tumour, cancer, viral, bacterial or fungal infection. They are useful for treating diseases associated with immune system activation including systemic lupus erythematosus or sepsis. They are also useful as vaccines to boost subject's immune system. The invention is also useful in gene therapy. The present sequence is a CpG oligonucleotide used to stimulate B-cells Note: This sequence is acted to be the same as that shown as SEQ ID NO: I in page 18 of the specification. However these sequences differ.
                                                                                                                                                                                                                         New oligonucleotide comprises at least one unmethylated CpG dinucleotide,
                                                                                                                                                                                                                                          useful for treating, preventing, or ameliorating an immune system deficiency or a tumor, cancer, viral, bacterial, or fungal infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CpG dinucleotide; gene therapy a; vaccine; cancer; viral infection; fungal infection; bacterial infection; parasitic infection; systemic lupus erythematosus; sepsis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CpG immunomodulatory oligo, ODN 1585 used in B cell stimulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 14.2; DB 13; Length 20;
Pred. No. 3.7e+03;
0; Mismatches 3; Indels
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15. .20
/*tag= b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
                                                                     (IOWA ) UNIV IOWA RES FOUND.
(COLE-) COLEY PHARM GROUP INC.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                               Steinberg AD;
                                                                                                                                                                                                                                                                                                 Claim 5; SEQ ID NO 1; 19pp; English.
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07-FEB-1995; 95US-00386063.
08-OCT-1999; 99US-00415142.
21-OCT-2003; 2003US-00690495.
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Best Local Similarity 84.2%;
Matches 16; Conservative
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/*tag=
                                                                                                                                               Klinman D,
                                                                                                                                                                                    WPI; 2004-603584/58.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32-SEP-2004
                                                                                                                                                 Krieg AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADR88228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADR88228
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                                                                                                                                                                                                                                                                        The present invention provides oligonucleotides comprising is useful immunomodulatory unmethylated CpG dinucleotide. The invention is useful for treating, preventing and ameliorating immune system deficiencies such as systemic lupus erythematosus and sepsis, tumour, cancer, viral, bacterial and fungal infections. The invention acts as an cytostatic, virucidal, antibacterial, fungicidal, antinflammatory, dermatological and immunosuppressive agent. The invention is also useful in the production of vaccines and in gene therapy. The present sequence is a mitogenic CpG oligonucleotide used in B-cell activation. Note: This sequence is stated to be SEQ ID NO: 1 in the sequence differs from the sequence designated as SEQ ID NO: 1 in the
                                                                                                                                                               New oligonucleotide comprises at least one unmethylated CpG dinucleotide, useful for treating, preventing, or ameliorating an immune system deficiency or a tumor, cancer, viral, bacterial, or fungal infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immune response; immune system deficiency; tumour; cancer;
viral infection; systemic lupus erythematosus; sepsis; vaccine;
gene therapy; bacterial infection; fungal infection; phosphorothioate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.7%; Score 14.2; DB 13; Length 20; 84.2%; Pred. No. 3.7e+03; ive 0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CpG oilgonucleotide ODN 1585 used to stimulate B-cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/mod_base= OTHER
/note= "Phosphorothioate nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Phosphorothioate nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
               (IOWA ) UNIV IOWA RES FOUND.
(COLE-) COLEY PHARM GROUP INC.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 1; 20pp; English.
                                                                                         Steinberg AD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GGGTCAACGTTCAGGGGGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGGTGACGTTCAGGGGGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADR45002 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-FEB-2004; 2004US-00789353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94US-00276358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16. .20
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                                                                                         Klinman D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                              WPI; 2004-603582/58
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                                                                                         Krieg AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADR45002;
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Gaps

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Suppressing allergies, including asthma, rhinitis, urticaria and atopic dermatitis, in a subject, comprises administering a first and second dose
                                                                                                                                                                                                                                                    The invention relates to immunomodulatory oligonucleotides containing an unmethylated CpG dinucleotide. The oligonucleotide of the invention is useful in preparing a composition for treating a disease associated with an immune system activation, e.g. systemic lupus erythematosus, sepsis or viral infection. It is also useful to prepare vaccine. The present sequence is an immunomodulatory oligonucleotide used to stimulate B
                                                                                                                                                    New oligonucleotide comprising 2-100 nucleotides and containing an unmethylated CpG dinucleotide, useful in preparing a composition for treating a disease, e.g., systemic lupus erythematosus, sepsis or viral
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ss; antiasthmatic; antiallergic; dermatological; antiinflammatory; antibacterial; virucide; immunoglobulin E antagonist; allergy; immunostimulator; asthma; rhinitis; urticaria; dermatitis; bacterial infection; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                               Score 14.2; DB 13; Length 20;
Pred. No. 3.7e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Allergic response suppressor oligonucleotide #224.
                                                                                                                                                                                                                                                                                                                                                                     Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
                                      (IOWA ) UNIV IOWA RES FOUND.
(COLE-) COLEY PHARM GROUP INC.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fouron Y;
                                                                                                 Steinberg AD;
                                                                                                                                                                                                                            Claim 5; SEQ ID NO 1; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GGGGTGACGTTCAGGGGGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gecrcaacerrcaededed 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-FEB-2000; 2000US-0179991P.
02-FEB-2001; 2001US-00776479.
08-OCT-1999; 99US-00415142.
21-OCT-2003; 2003US-00690495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-APR-2004; 2004US-00831778.
                                                                                                                                                                                                                                                                                                                                                                                                ch 74.7%;
1 Similarity 84.2%;
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADU89540 standard; DNA; 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                 Krieg AM, Klinman D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BRAT/) BRATZLER R L.
(PETE/) PETERSEN D M.
(FOUR/) FOURON Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-833006/82.
                                                                                                                            WPI; 2004-667684/65.
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2004235774-A1
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                                                                                                                                                                                                    infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 34
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                                                                                                                                                                      New immunomodulatory oligonucleotides for preventing, treating or ameliorating diseases associated with immune system deficiency or activation, e.g. cancer, viral infection, systemic lupus erythematosus or
                                                                                                                                                                                                                                                                    The present invention relates to an oligonucleotide containing at least one unmethylated CpG dinucleotide. The invention is useful in gene therapy and for preparing vaccine. The invention is also useful for preventing, treating or ameliorating diseases associated with immune system deficiency or activation such as cancer, viral, fungal, bacterial or parasitic infection, systemic lupus erythematosus or sepsis. The present sequence is a CpG immunomodulatory oligonucleotide used in B cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunomodulator; immune system; systemic lupus erythematosus; sepsis; viral infection; vaccine; B cell; virucide; phosphorothioate backbone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 14.2; DB 13; Length 20; Pred. No. 3.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mod_base= OTHER
/note= "Phosphorothioate backbone"
15. .20
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/note= "Phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ODN1, oligonucleotide used to stimulate B cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                       (IOWA ) UNIV IOWA RES FOUND.
(COLE-) COLEY PHARM GROUP INC.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                   Steinberg AD
                                                                                                                                                                                                                                              Claim 5; SEQ ID NO 1; 19pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGGGTGACGTTCAGGGGGG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                 74.78;
84.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGTCAACGTTCAGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94US-00276358
95US-00386063
    95US-00386063
              09-OCT-1999; 99US-00415142.
21-OCT-2003; 2003US-00690495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-2004; 2004US-00788199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADS17223 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *tag=
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                                                                                                                   Krieg AM, Klinman D,
                                                                                                                                            WPI; 2004-634548/61
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1994;
07-FEB-1995;
    07-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
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                                                                                                                                                                                                                                                                                                                                                                              stimulation.
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ADS17223
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JS2005009774-A1
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07-FEB-1995;
09-OCT-1999;
21-OCT-2003; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                          ADV97282;
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                                      The invention relates to a method of suppressing a symptom of an allergic response in a subject by administering a first and second dose of an immunostimulatory nucleic acid that comprises a nucleotide sequence comprising 5'-cg-3', and where the second dose is administered from 1 day to 8 weeks after the first dose. The methods and compositions of the present invention are useful for the treatment or prevention of asthma and allergy, including rhinitis, uritearia and atopic dermatitis, using an immunostimulatory nucleic acid alone or in combination with other medicaments. They can also be used in preventing bacterial and viral infections. This sequence represents an oligonucleotide used in the
                                                                                                                                                                                                                                                                                                                                                                                                            Immune modulation; immunity; immunogenicity; immune disorder; tumor; cancer; cytostatic; neoplasm; systemic lupus erythematosus; SLE; antiinflammatory; dermatological; immunosuppressive; sepsis; infection; virucide; fungal infection; fungicide; bacterial infection; antibacterial; parasitic infection; autoimmune disease; rheumatoid arthritis; antiarthritic; antirheumatic; multiple sclerosis; neuroprotective; antisense therapy; hybridization;
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                          Mitogenic CpG oligonucleotide ODN1585 used in B-cell stimulation.
                                                                                                                                                                                                                      ö
                                                                                                                                                                                              Score 14.2; DB 13; Length 20; Pred. No. 3.7e+03; 0; Mismatches 3; Indels
                                                                                                                                                                           Sequence 20 BP; 1 A; 1 C; 12 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "Phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COLEY PHARM GROUP INC.
US DEPT COMMERCE & NAT INST STANDARDS.
                   Disclosure; SEQ ID NO 224; 235pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiviral vaccine; phosphorothioate; ss.
an immunostimulatory nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= b
/mod_base= OTHER
                                                                                                                                                                                                                                            1 GGGGTGACGTTCAGGGGGG 19
                                                                                                                                                                                                                                                                  GGGTTGACGTTTTGGGGGG 20
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95US-00386063.
99US-00415142.
                                                                                                                                                                                                                                                                                                                         ADW28066 standard; DNA; 20 BP
                                                                                                                                                                                                74.78;
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                                                                                                                                                                                                                                                                                                                                                                    24-MAR-2005 (first entry)
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                                                                                                                                                                                                          Local Similarity 84.2
les 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16. .20
                                                                                                                                                     method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2005004062-A1
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07-FEB-1995;
09-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified
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                                                                                                                                                                                                                                                                                                                                               ADW28066;
                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                   RESULT 35
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                                                                                                              Use of an immunostimulatory oligonucleotide for boosting an immune response of a subject, or for stimulating an immune response in a subject, where increases in IFN-gamma and IL-12 expression are indicators of the immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ss; immune modulation; pharmaceutical; immunomodulator; cytostatic; viruodie; fundicide; antibacterial; antiparastic; antiinflammatory; dermatological; immunosuppressive; antiarthritic; antirheumatic; neuroprotective; immunostimulant; immune disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 20;
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/note= "unmethylated CpG dinucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .3
/*tag= a
//mod base= phosphorothioate backbone
9. .10
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/mod_base= phosphorothioate backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 14.2; DB 14;
Pred. No. 3.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 1; 19pp; English.
Steinberg AD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GGGGTGACGTTCAGGGGGG 19
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95US-00386063.
99US-00415142.
2003US-00690495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADV97282 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-APR-2005 (first entry)
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Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .20
Krieg AM, Klinman D,
                                                       WPI; 2005-065257/07
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Klinman D,
 Klinman D,
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modified base
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09-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                         05-MAY-2005
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(USDC ) US
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  Krieg AM,
                                                                                                                                                                                                                                                                                                                                                                                  ADX84981;
                                               Treating
                                                                                                                                                                                                                                                                                                                                   RESULT 38
                                                                                                                                                                                                                                                                                                                                                ADX8498
                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                              요
                                                                                                                                                                             The invention relates to a novel pharmaceutical composition (A) for oral administration comprising an immunostimulatory nucleic acid (1) (8-100 nucleotides in length) in a pharmaceutically acceptable carrier. The immunostimulatory nucleic acid is of the formula 5.x 1 x 2 CGX 3 x 4 3. (Where C and G are unmethylated). The carrier comprises an emulsion. A composition of the invention has immunomodulator, cytostatic, virucide, fungicide, antibacterial, antiparasitic, antihlammatory, dermatological, immunosuppressive, antiarthritic, antihlammatory, commonition is useful to treat/prevent/ammainitic, antihrheumatic, neuroprotective, and immunostimulant activity. A nucleic acid of the invention is useful to treat/prevent/ammainitic, bacterial or parasitic deficiency (e.g. tumors, cancers or viral, fungal, bacterial or parasitic infections) or a disease (e.g. systemic lupus erythematosus, sepsis, crheumatotid arthritis and multiple sclarosis) associated with immune system activation. The nucleic associate are useful as vaccine adjuvants to stimulate a subject's response to a vaccine, and for antisense therapies or as in vivo hybridization probes. The present sequence represents an immunosity and immunosity and immunosity immune immunosity.
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                                                                                              Oral composition, useful e.g. to treat/prevent/ameliorate an immune system deficiency or diseases associated with immune system activation, comprises an immunostimulatory nucleic acid in a pharmaceutically
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                               Score 14.2; DB 14; Length 20;
Pred, No. 3.7e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                  immunostimulatory oligonucleotide of the invention, ODN 1585
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B cell-stimulating oligonucleotide - SEQ ID 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIV infection; anti-HIV; B-lymphocyte; ss.
                                                                                                                                                             Disclosure; SEQ ID NO 1; 18pp; English.
                                                   Steinberg AD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGGGTGACGTTCAGGGGGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ĠĠĠŦĊAĄĊĠŤŤĊĄĠĠĠĠĠ 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
(IOWA ) UNIV IOWA RES FOUND.
(COLE-) COLEY PHARM GROUP INC.
(USSA ) US SEC OF ARMY.
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09-OCT-1999; 99US-00415142.
16-AUG-2001; 2001US-00931583.
                                                                                                                                                                                                                                                                                                                                                                                                                                   74.7%;
84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-AUG-2003; 2003US-00649584
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                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 84.2'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KRIEG A M.
KLINMAN D.
STEINBERG A D.
                                                  Krieg AM, Klinman D,
                                                                          WPI; 2005-080553/09.
                                                                                                                                    acceptable carrier.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified
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09-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-FEB-2005
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(STEI/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 37
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The invention comprises a method of treating HIV by administering a CpG nucleic acid (e.g. an adjuvant-type nucleic acid or an IFN-alpha-inducing CpG nucleic acid) and an anti-HIV therapy (e.g. an inhibitor of HIV replication). The method of the invention is useful for the treatment and prevention of HIV. The present DNA sequence represents an oligonucleotide that was used to stimulate B cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immune modulation; immunotherapy; antisense therapy; hybridization; interferon-gamma; cytokine; immune deficiency; immunostimulant; immune disorder; tumor; cancer; cytostatic; neoplasm; viral infection; virucide; infection; fungicide; bacterial infection; antibacterial; parasitic infection; antiparasitic; nucleic acid vaccine; leukemia; systemic lupus erythematosus; antiinflammatory; dermatological; immunosuppressive; sepsis; autoimmune disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                   subject infected with HIV comprises administering a CpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 74.7%; Score 14.2; DB 14; Length 20; Best Local Similarity 84.2%; Pred. No. 3.7e+03; Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CpG oligonucleotide ODN 1585 used to stimulate B cells.
                                                                                                                                               nucleic acid and an anti-HIV therapy to the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mod_base= OTHER
/note= "Phosphorothioate backbone"
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                                                                                                                                                                                                            Disclosure; SEQ ID NO 1; 37pp; English
Steinberg AD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 gegrczacerrcaegege 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADX84981 standard; DNA; 20 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-00386063.
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                                                      WPI; 2005-172294/18
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Steinberg AD;

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The invention relates to a method for increasing interferon (IFN)-gamma in a subject. The method involves administering an immunostimulatory oligonucleotide/delivery complex to modulate immune response of the subject. The invention is useful for treating diseases associated with immune system deficiency e.g. tumor or cancer or viral, fungal, bacterial or parasitic infections; as vaccine; for treating leukemia, systemic lupus erythematosus, sepsis and autoimmune diseases. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New modified proteinaceous composition, useful for treating e.g., tumors.
                                          Use of immunostimulatory oligonucleotide delivery complex comprising oligonucleotide linked to biodegradable delivery complex for increasing interferon-gamma levels and treating diseases associated with immune system deficiency e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ricin; (x) Asp(y); primer; mutant; mutagenesis; ss; vascular leak syndrome; VLS; cancer; immunotoxin; IT; cytokine; RTA; aphasia; myalgia; fatigue; hypotension; rhabdomyolysis; MAb; ribosome inactivating protein; RIP; vaccine; graft vs. host disease; GVHD; non-Hodgkin's lymphoma; Hodgkin's lymphoma; cytostatic; immunosuppressive; myloma; tumour; monoclonal antibody.
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                                                                                                                                                                                                                                                                                                                               74.7%; Score 14.2; DB 14; Length 20; 84.2%; Pred. No. 3.7e+03; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                     is the CpG oligonucleotide used to stimulate B cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer, D75N, used to mutate the RTA (x) Asp(y) motif.
                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baluna RG;
                                                                                                                        Disclosure; SEQ ID NO 1; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smallshaw JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; SEQ ID NO 18; 52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGGTGACGTTCAGGGGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-OCT-2002; 2002US-00282935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-2000; 2000US-00538873
22-SEP-2000; 2000US-00668419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADC24305 standard; DNA; 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VITETTA E S.
GHETIE V F.
SMALLSHAW J E.
              WPI; 2005-172254/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-744874/70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BALUNA R G.
                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2003143193-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADC24305;
                                                                                                                                                                                                                                                                                                                                  Query Match
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The invention discloses a new modified proteinaceous composition which

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Computers a protein marking a hypersy, sequence computers a protein alters the ability of a (x)App(y) sequence to induce Vascular Leak Syndrome (VLS). The present invention relates to the filed to physical provides immunofoxins (TTS) and cancer biology. The invention provides immunofoxins (TTS) and cytokines, methods for producing them, which have been mutated to lack amino acid sequences which induce VLS or other side effects. Also calaimed is a ricin A chain toxin (RTA) with a reduced ability to promote toxicity in a patient, where at least one amino acid flanking the coxicity in a patient is further (x)Asp(y) sequence is altered. The toxicity in a patient is further of defined as VLS, aphasia, myadigia, fatigue, hypotension or rhabdomyolysis. The are hybrid molecules consisting of monoclonal antibodies (NAbs), or other cell binding ligands, which are biochemically or genetically linked to toxins, toxin subunits or ribosome inactivating proteins (RIPs) from plants, fungi or bacteria. The modified proteinaceous composition is useful for treating (e.g. vaccine) graft vs. host disease (GVHD), non-Hodgkin's and Hodgkin's lymphoma, myloma and some solid tumours. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus stearothermophilus template-dependent DNA polymerase for preparing cDNA molecule from RNA template comprises reverse transcriptase activity in the presence of magnesium ions and absence of manganese ions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR primer; DNA polymerase; reverse transcriptase; rabbit; tissue factor;
                                                                                                                                                                                                                                                                                                                                                           sequence presented is a primer which was used to mutate the RTA (x)Asp(y)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a purified thermostable template-dependent DNA polymerase from Bacillus stearchtermophilus comprising reverse transcriptase (RT) activity in the presence of magnesium ions at a concentration of 1 mM and in the substantial absence of manganese in The DNA polymerase is useful for preparing cDNA molecules from RNA perplates and for amplifying a nucleic acid. The present sequence is a PCR primer for rabbit tissue factor (RTF). This sequence was used to demonstrate the activity of the DNA polymerase of the present invention
a protein having a (x) Asp(y) sequence and at least one amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.7%; Score 14; DB 10; Length 39; 100.0%; Pred. No. 4.8e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 39 BP; 10 A; 10 C; 8 G; 11 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rabbit tissue factor PCR primer #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Page 22; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAY-2000; 2000WO-US013960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC89992 standard; DNA; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GGTGACGTTCAGGG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GETGACGTTCAGGG 13
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Matches 14; Conserv
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Claim 23; Page 195; 2785pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                            ABZ49680;
                                                                                                                                                                                                                                                                                                                                                           RESULT 42
                                                                                                                                                                                                                                                                                                                                                                       ABZ49680/
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                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     concoding enzymes associated with drug metabolism. The invention relates encoding enzymes associated with drug metabolism. The invention relates concoding enzymes associated with drug metabolism. The invention relates to methods and compositions for identifying individuals who have at least one polymorphism may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from ABZ4317-ABZ50807 using a variety of detection assays, including hybridisation assays, nucleic acid evaluating and screening drugs using genetic polymorphism data, particularly that relating to single nucleotide polymorphisms (SNPs), may be used in studying the relationship between DNA sequence variations and human diseases, conditions, and responses to drugs. SNPs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying individuals having a polymorphism, useful for determining the effectiveness or side effect of a drug or treatment protocol, comprises detecting at least one polymorphism in the drug metabolizing enzyme
                                                                                                                                                                                                                                                                       Human; drug metabolising enzyme; gene; drug metabolism; chromosome 22; polymorphic site; drug evaluation; drug screening; genotyping; genetic profiling; therapeutic customisation; adverse reaction; clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
                                                                                                                                                                                                                                                                                                                                                                                                /standard name= "Single nucleotide polymorphism (SNP)"
                                                             Gaps
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0
                                    72.6%; Score 13.8; DB 4; Length 30; 88.2%; Pred. No. 5.9e+03;
                                                           Indels
            Sequence 30 BP; 6 A; 5 C; 12 G; 7 T; 0 U; 0 Other;
                                                             0; Mismatches
                                                                                                                                                                                                                                               Human SULTX3 gene polymorphic site, #313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saito
                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                          BP.
                                                                                      3 GGTGACGTTCAGGGGGG 19
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02-MAY-2001; 2001JP-00135256.
27-AUG-2001; 2001JP-00256862.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-DEC-2001; 2001WO-JP011592
                                                                                                           13 GGCGATGTTCAGGGGGG
                                                                                                                                                                        ABZ43529 standard; DNA; 41
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                                                 Local Similarity 88.2
nes 15, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid.
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                                                                                                                                                                                                                                                                                                                                                              Key
variation
                                                                                                                                                                                                 ABZ43529;
                                      Query Match
                                                             Matches
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c such as repeating sequences. The detection and analysis of polymorphisms in genes encoding drug metabolising enzymes allows the customisation of drug therapies based upon the genetic profile of individual patients.

This would not only take the guesswork out of selecting the drug with the care the likelihood of adverse reactions, thereby increasing safety.

CC greatest therapeutic effect for a particular patient, but would also cereduce the likelihood of adverse reactions, thereby increasing safety.

CC approval processes. For example, individuals could be selected for capable of responding to a particular drug or drug class, and previously failed drug candidates could be revived if they were matched with more capable of responding to a particular drug or drug class, and previously failed drug candidates could be revived if they were matched with more compropriate patient populations. The methods, data and compositions of the invention may therefore lead to a an increase in the range of possible drug trials, the time taken for a drug to be approved, the length of time patients are on medication and the number of different companions, failed drug trials, the time taken for a drug to be approved, the length of time patients are on medication and the number of different companions a patient needs to take before finding an effective therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human SULTX3 gene polymorphic site, #6462.
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27-AUG-2001; 2001JP-00256862.
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88.2%;
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Best Local Similarity 88.2
Matches 15; Conservative
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99US-00264466. 91US-00810898.

08-MAR-1999;

20-DEC-1991;

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Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates concoding enzymes and compositions for identifying individuals who have at least to methods and compositions for identifying enzyme-encoding genes. The polymorphisms may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from ABZ43217-ABZ50887 using a variety of detection assays, including hybridisation assays, nucleic acid arrays and PCR-based methods. The invention also encompasses methods of evaluating and screening drugs using genetic polymorphism data, particularly that relating to single nucleotide polymorphisms (SNPs), may be used in studying the relationship between DNA sequence variations and human diseases, conditions, and responses to the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variations such as repeating sequences. The detection and analysis of polymorphisms (SNPs would not only take the guesswork out of selecting the drug with the such as repeating sequences. The detection and analysis of polymorphisms in genes encoding drug metabolising enzymes allows the customisation of cup therapies based upon the genetic profile of individual patients. This would not only take the guesswork out of selecting the drug discovery and arched for reduce the likelihood of adverse reactions, thereby increasing safety. Methods of the invention are also useful in the drug discovery and approval processes. For example, individuals could be selected for clinical trials only if their genetic profiles indicate that they are capable of responding to a particular drug or drug class, and previously the invention may therefore lead to a mincrease in the range of genetic possible drug candidates could be revived if they were matched with more any therefore lead to a mincrease in the number of adverse drug the invention any therefore lead to a mincrease of drug trages of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              medications a patient needs to take before finding an effective therapy
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72.6%; Score 13.8; DB 6; Length 41; 88.2%; Pred. No. 6e+03; ive 0; Mismatches 2; Indels Sequence 41 BP; 5 A; 23 C; 2 G; 11 T; 0 U; 0 Other; Query Match
Best Local Similarity 88.2.
Best Local 15; Conservative

1 GGGGTGACGTTCAGGGG 17 26 GGGGTGGGGTTCAGGGG 10 요

AAD07150 standard; DNA; 22 BP RESULT 43

AAD07150;

06-AUG-2001 (first entry)

Priming site 19379; PCR; polymerase chain reaction; amplification; branched modular primer; front module; FM; back module; BM; PCR primer; PCR primer PR2-379 for improving priming site 19379 specificity.

Bacteriophage lambda.

proofreading; ss.

Location/Qualifiers /*tag= a /mod_base= i /*tag= b /mod_base= i mutation mutation 

US6235889-B1

22-MAY-2001.

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primers used in methods for amplifying a nucleic acid segment. The branched modular primer comprises of front and back oligonucleotide modules. The front module (FM) and back module (BM) comprise of a stem segment having a sequence that is the same from module to module and an arm segment having a sequence that varies from module to module arm of the back and front modules are annealed to a template which contains the priming site. These modules are designed for priming sites in lambda phage DNA. The composition is useful for amplifying a nucleic acid profireading amplification primer PR2-379 used for improving Bacteriophage lambda reverse priming site 19379 specificity
                                                                                                                                                                                                                                                             New composition comprising front and back oligonucleotide modules, each module has a stem and an arm segment with varying or constant sequences, useful for amplifying nucleic acid segments such as in polymerase chain
                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to compositions for branched modular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 70.5%; Score 13.4; DB 4; Length 22; Local Similarity 93.3%; Pred. No. 9.1e+03; nes 14; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22 BP; 4 A; 3 C; 8 G; 5 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                               Disclosure; Col 18; 32pp; English.
                                                                             95US-00384699.
                                                                                                                                         (UYCH-) UNIV CHICAGO
                                                                                                                                                                                                                      WPI; 2001-366426/38.
                                                                                                  06-MAY-1997;
                                                                                                                                                                               Ulanovsky L;
                                                                                                                                                                                                                                                                                                                               reaction.
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5 TGACGTTCAGGGGGG 19 Best Loca Matches ò

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Gaps

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Gaps

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AAF74944 standard; DNA; 22 RESULT 44 AAF74944 ID AAF7

AAF74944;

BP

Bacteriophage lambda fragment PCR ampification primer SEQ ID NO:5. (first entry) 23-MAY-2001

Bacteriophage lambda, PCR primer, amplification, genome mapping, biomedical research; clinical diagnostic, ss.

Bacteriophage lambda

Synthetic.

US6197556-B1

36-MAR-2001

36-MAY-1997;

97US-00852001. 91US-00810898. 20-DEC-1991; 06-FEB-1995; 

(UYCH-) UNIV CHICAGO.

Ulanovsky L, Raja MC;

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(A) with modified metabolic pathways comprising: (a) genetic modification of a microorganism to inhibit production or consumption of a metabolite when it is grown on a defined medium, thus affecting its ability to grow; (b) growing the modified organism in the defined medium so that evolution can occur, optionally with addition of a co-substrate to allow evolution; and (c) selecting as (A) cells able to grow on the medium, optionally in presence of co-substrate. The evolved microorganisms (A), or evolved proteins (I) expressed by them, are useful in biotransformation processes, especially those involving NaDPH-dependent enzymes, particularly synthesis of amino acids (Met. Cys. Thr. Lys or Ile) but also synthesis of mucleic acids or lipids, and metabolism of sugars. (A) provide more efficient production of selected metabolism of sugars. (A) strains. This sequence represents a nucleic acid molecule used in the method of the invention.
                                        The invention relates to a method for preparing evolved microorganisms
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                                                                                                                                                                                                                                                                                                                        The present invention describes a method for amplifying a template nucleic acid segment (I), comprising annealing (I) to a branched primer having front (FOM) and back oligonucleotide modules with arm segments complementary to a site in (I), extending the arm of FOM to form an initial extension strand, annealing the strand to a reverse primer (RP), sectonding RP to form second initial extension strand, and amplifying the second strand. The method can be used for amplifying nucleic acid segments, useful in genome mapping, biomedical research and clinical diagnostics. The method eliminates the need for custom primer synthesis in methods to amplify nucleic acid segments. The modular combination of just a few oligonucleotides essentially mimics the performance of a conventional, custom-made primer by matching a sequence of a priming site in the template. AMPTA990 to AMPTA979 represent oligonucleotides espectation and appliances and a priming site and appliance of the complete of the proposition of the conventional of the complete of the conventional of the conventional of the convention of the conv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 used in the exemplification of the present invention. N.B. Any Ns given in the oligonucleotide sequences represent inosine bases
                                                                                Amplifying a template nucleic acid segment, involves annealing a combination of several branched and/or covered oligonucleotide modules selected from a pre-synthesized library, to the template DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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biotransformation; NADPH-dependent enzyme; nucleic acid metabolism;
lipid metabolism; sugar metabolism.
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V 93.3%; Pred. No. >...
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                                                                                                                                                                                                                                                     Disclosure, Col 18; 33pp; English.
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14-MAY-2003; 2003FR-00005768.
14-MAY-2003; 2003FR-00005769.
06-NOY-2003; 2003FR-00013054.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (META-) METABOLIC EXPLORER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-653418/63.
WPI; 2001-256370/26
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-SEP-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADR99754;
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ADR99754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for treating condition associated with survivin expression or overexpression, such as breast cancer, colon cancer, lung cancer, bladder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention comprises dsRNA oligomeric sequences which are targeted to the human survivin gene. The dsRNA oligomeric compounds of the invention are useful for inhibiting expression of the human survivin gene, and can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel double-stranded compound, modulating expression of human survivin,
                                                                                                                                                                                                                                                                                            survivin; antisense therapy; gene silencing; cancer; cytostatic; breast tumor; colon tumor; prostate tumor; lung tumor; bladder tumor; ovary tumor; renal tumor; pancreas tumor; non-hodgkin lymphoma; hepatocellular carcinoma; ss; siRNA; short interfering RNA; RNA interference.
                                Gaps
                                0
70.5%; Score 13.4; DB 13; Length 30; 93.3%; Pred. No. 9.2e+03; ive 0; Mismatches 1; Indels C
                                                                                                                                                                                                                                                                   Human survivin gene-specific siRNA sequence - SEQ ID 196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 25; SEQ ID NO 196; 159pp; English.
                                                                                                                                                        ADW46519/c
ID ADW46519 standard; RNA; 19 BP.
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13-APR-2004; 2004US-00823448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JUN-2004; 2004WO-US017490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-JUN-2003; 2003US-0475324P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Swayze E;
                                                                  1 GGGGTGACGTTCAGG 15
                                                                                       1 GGGTGACGGTCAGG 15
                                                                                                                                                                                                                                      (first entry)
                                   14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2005-081840/09.
    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ISIS-) ISIS PHARM (ELIL ) LILLY & CO
                                                                                                                                                                                                                                                                                                                                                                                                                          WO2005002507-A2.
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                      07-APR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-JAN-2005.
                                                                                                                                                                                                         ADW46519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bhat B,
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New evolved microorganisms with altered metabolic pathways, useful e.g. for production of amino acids, are selected as mutants able to grow on

Disclosure; SEQ ID NO 21; 113pp; French

for productior defined media.

2 GGGGUGAACUUCAGGUGG 19

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1 GGGGTGACGTTCAGGGGG

BP

AAF99395 standard; DNA; 20

RESULT 48

AAF99395

AAF99395;

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be used in the treatment of cancer, such as: hepatocellular cancer, breast cancer, colon cancer, prostate cancer, lung cancer, bladder cancer, ovarian cancer, renal cancer, glioblastoma, pancreatic cancer and non-Hodgkin's lymphoma. The present nucleic acid represents a human survivin-specific siRNA sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention comprises dsRNA oligomeric sequences which are targeted to the human survivin gene. The dsRNA oligomeric compounds of the invention are useful for inhibiting expression of the human survivin gene, and can be used in the treatment of cancer, such as: hepatocellular cancer, breast cancer, colon cancer, prostate cancer, lung cancer, bladder cancer, in the cancer, prostate cancer, lung cancer, bladder non-Hodgkin's lymphoma. The present nucleic acid represents a human survivin-specific siRNA sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          survivin; antisense therapy; gene silencing; cancer; cytostatic; breast tumor; colon tumor; prostate tumor; lung tumor; bladder tumor; ovary tumor; renal tumor; pancreas tumor; non-hodgkin lymphoma; hepatcocallular carcinoma; ss; siRNA; short interfering RNA;
                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                  Score 13.2; DB 14; Length 19; Pred. No. 1.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human survivin gene-specific siRNA sequence - SEQ ID 195.
                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                Sequence 19 BP; 4 A; 9 C; 3 G; 0 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19 BP; 3 A; 3 C; 9 G; 0 T; 4 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 GGGGTGAACTTCAGGTGG 1
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                                                                                                                                                                                                                                                                                      69.5%;
83.3%;
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13-APR-2004; 2004US-00823448
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGGGTGACGTTCAGGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADW46518 standard; RNA; 19
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                                                                                                                                                                                                                                                                                                                                                        15; Conservative
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(BLIL ) LILLY & CO ELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2005-081840/09.
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNA interference.
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ID ADW46518
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response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immuno response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophlus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Th2 to a Th1 immune response and to activate immune cells. Note: the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                     Vaccine, cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic; immunostimulatory; tumour; viral infection; bacterial infection; fungal infection; parasitic infection; cancer; asthma; infections disease; allergy; immune deficiency; phosphorothioate; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccinating against tumors, infectious diseases, allergies and asthma
using immunostimulatory Py-rich and TG nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present invention relates to a method for stimulating an immune
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Pred. No. 1.1e+04;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present sequence may have a phosphorothioate backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
                                                                                                        Immunostimulatory nucleic acid #511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 101; Page 48; 338pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vollmer J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
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                                                                                                                                                                                                                                                                                                                                  25-SEP-2000; 2000WO-US026383.
                                                                                                                                                                                                                                                                                                                                                                                                        23-AUG-2000; 2000US-0227436P.
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83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                          FOUND
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                                                                   (first entry)
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(COLE-) COLEY PHARM GMBH
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Best Local Similarity
                                                                                                                                                                                                                                                               WO200122972-A2.
                                                                                                                                                                                                                                                                                                                                                                     25-SEP-1999;
27-SEP-1999;
                                                                     12-JUN-2001
                                                                                                                                                                                                                                                                                                  05-APR-2001.
                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Krieg AM,
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RESULT 49

AAF99392

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Gaps

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Score 13.2; DB 14; Length 19; Pred. No. 1.1e+04; 3; Mismatches 3; Indels

Query Match 69.5%; Best Local Similarity 66.7%; Matches 12; Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immunostimulatory content immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. herpesviridae, retroviridae haemophilus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Th2 to a Th1 immune response and to activate immune cells. Note: the present sequence may have a phosphorothioate backbone
                                                                                                                                Vaccine, cytostatic, virucidal, bactericidal, fungicidal, anti-parasitic, immunostimulatory, tumour, viral infection; bacterial infection; fungal infection; parasitic infection; cancer, asthma; infections allergy, immune deficiency; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 1.1e+04;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Angiogenesis inhibitory oligonucleotide #524.
                                                                                                  Immunostimulatory nucleic acid #508.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 101; Page 48; 338pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vollmer J;
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                                                                                                                                                                                                                                                                                                                       25-SEP-2000; 2000WO-US026383
                                                                                                                                                                                                                                                                                                                                                       99US-0156113P
                                                                                                                                                                                                                                                                                                                                                                       27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
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 AAF99392 standard; DNA; 20
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                                                                 (first entry)
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(COLE-) COLEY PHARM GMBH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-273485/28
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                                                                                                                                                                                                                                                                                                                                                       25-SEP-1999;
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                                                                  12-JUN-2001
                                                                                                                                                                                                                                                                                      05-APR-2001
                                                                                                                                                                                                                      Synthetic
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                                 AAF99392
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administering at least one antiangiogenesis in a subject, Compitating administering at least one antiangiogenic mucleic acid molecule. Also included is a kit comprising a first container housing the antiangiogenic mucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis, diabetic retinopathy retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, anglofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.
Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth; tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection, neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 28; 276pp; English
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/Hong in the laboratory of Gerald M. Rubin (University of
/Hong in the laboratory of Gerald M. Rubin (University of
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Nishijima,I., Yu,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contract: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1159 row: 1 column: 12
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National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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                                                                                          1 (bases 1 to 50)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.
Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu,
Rogers, J. and Bradley, A.
Direct Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 14.2; DB 11;
Pred. No. 3.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPP308j13"
/clone_lib="MHPP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGGGTGACGTTCAGGGGGG 19
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Homo sapiens
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Matches 16; Conservative
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Gaps

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us-09-669-187a-80.szlm50.rst

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SM Danio rerio

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 41)

Ss Humphray, S. J., Huckle, E. and Durham, J.L.

Direct Submission

Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

humquery@sanger.ac.uk Unpublished

This sequence was generated from the T7 end of BAC 62P9 is

part of the Daniokey BAC Library created by R. Plasterk and N.V.

Keygene: Furnher details:

http://www.sanger.ac.uk/Projects/D_rerio/.
                                                                                                                                                                                                                                                                                                                                                                                                     ball 1477 41 bp DNA linear GSS 13-MAR-2003 Danio rerio genomic clone DKEY-62P9, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fully Cacus viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viridiplantae; Streptophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. I (bases I to 35).

Buell, C.R., Zheng, L., Cowles, A. and Cairney, J. Sequencing of ESTs from loblolly pine embryonic libraries Contact: C. Robin Buell
Plant Genomics Group
adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CO411608

35 bp mRNA linear EST 02-JUL-20
EST841993 Sequencing ESTs from loblolly pine embryos Pinus taeda
CDNA clone PIALM51 5' end, mRNA sequence.
CO411608
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Best Local Similarity 82.4%; Pred. No. 1.5e+05;
Matches 14; Conservative 0; Mismatches 3;
                                                                                                                            Query Match
69.5%; Score 13.2; DB 9;
Best Local Similarity 83.3%; Pred. No. 9.4e+04;
Matches 15; Conservative 0; Mismatches 3;
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/note="vector pindigoBAC-536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-62P9"
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Weator: PWD42nry, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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                                                                                                                                                                                                                                                                                                                                                                              46 bp DNA linear GSS 20-FEB-200 2M0134D20R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCZM0134D20 R, genomic survey sequence.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
(Stratagene) and Superscript II RT (Life Technologies) Note: this is a NIH_MGC Library. |"
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O
                                                                                                           Length 32;
                                                                                                                                                                2; Indels
                                                                                                        Score 13.8; DB 2;
Pred. No. 4.7e+04;
0; Mismatches 2;
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Insert Length: 10000 Std Error: 0.00
Plate: 0134 row: D column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plate: 0134 row: D column: 20
Seq primer: CACACAGAAAACAGTATGACC
Class: plasmid ends
High quality sequence stop: 46.
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/clone="UUGC2M0134D20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ838956.1 GI:13008864
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                                                                                                        ch 72.6%;
1 Similarity 88.2%;
15; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
                                                                                                              Query Match
Best Local Similarity
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Gaps

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EST 02-JUL-2004

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(bases 1 to 44)
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                        /clone="PIALMS1"
/lab host="E.coli DH10B-TonA"
/clone lib="Sequencing ESTS from loblolly pine embryos"
/clone lib="Sequencing ESTS from loblolly pine embryos"
/note="Organ: Zygotic Embryo and Megagametophyte; Somatic
Embryo; Vector: pCMV-SPORT 6.1; Site_1: Not1; Site_2:
EcoRV; tissue: Whole megagametophytes isolated from pine
seeds, Whole embryos excised from these megagametophytes;
whole somatic embryos and suspensor tissue from tissue
culture, isolated from call line Al2. Pooled RNA from
zygotic embryos, megagametophytes, and somatic embryos was
used for library construction. Pine conse were harvested
weekly from open-pollinated 7-56 mother trees, collections
occurred from 7/0/10 until 10/15/02. Whole
megagametophytes were first isolated from pine seeds, and
whole embryos excised from these megagametophytes each was
flash frozen. Embryo development was assessed using the
system of Pullman et al (Pullman GS, Johnson S, Peter G,
cairney J, Xu N. 2003. Loblolly Pine somatic
embryogenesis: development of a maturation medium and
resulting embryo quality. Plant Cell Reports 21:74-758
(http://link.springer.de/link/service/journals/00299/conte
nts/03/00586). For photographs see Ciavatta et al 2001.
(Ciavatta VT, Morillon R, Pullman GS, Chrispeels M,
cairney J. 2001. An aquaglyceroporin is abundantly
expressed early in the development of the suspensor and
the embryo proper of loblolly pine (Pinus taeda L.). Plant
Physiol. 127: 1556-1567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (http://www.plantphysiol.org/cgi/content/full/127/4/1556))
The Institute for Genomic Research
712 Medical Center Dr. Rockville, MD 20850, USA
8mail: rbuelledigr.org
This clone is available through TIGR. Please contact pine@tigr.org
for further information
Seq primer: ATT TAG GTA ACA CTA TAG.
Location/Qualifiers
                                                                                                                                                                                                                  /organism="Pinus taeda"
/mol_type="mRNA"
/cultivar="7-56 mother tree, open-pollinated tree from,
Lyons, Georgia, USA"
/db_xref="taxon:3352"
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                               clone="PIALM51"
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Best Local Similarity
Matches 15; Conserva
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KEYWORDS
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Hayashi, S.
Direct Submission
Submitted (27-AUG-2002) Shigeo Hayashi, RIKEN Center for
Submitted (27-AUG-2002) Laboratory for Morphogenetic Singaling;
Developmental Biology, Laboratory for Morphogenetic Singaling;
Chuo-ku, Minatojima-minamimachi 2-2-3, Kobe, Hyogo 650-0047, Japan (B-mail:shayashi@cdb.riken.go.jp, Tel:81-78-301-3184,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 28)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA986325 28-MAY-1996 aRNA linear EST 28-MAY-1996 uc79d12.xl Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:1431863 3' similar to TR:O14742 O14742 NUCLEOLAR PROTEIN. ;
                                                                                                                                                                                     Fax:81-78-301-3183)
This clone was isolated from genomic DNA flanking an insertion of the P element vector P{GaNB} of a Drosophila strain.

Location/Qualifiers
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HMI Mouse EST Project
WashU-HMI Mouse EST Project
Fax: 314 286 1800
Fax: 314 286 1810
Email: mouseestchewatson.wustl.edu
This clone is available royalby-free through LLNL , contact the
This Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 44;
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Possible reversed clone: similarity on wrong strand
Seg primer: primer name ambiguous
High quality sequence stop: 1.
Location/Qualifiers
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    .44
    organism="Drosophila melanogaster"

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                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="NP6643"
/db_xref="taxon:7227"
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/strain="C57BL"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /map="64F2"
/clone="NP6643-5-1"
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Best Local Similarity
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CC027439
CC027439.1 GI:29442296
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Best Local Similarity
Matches 14; Conserv
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Zea mays
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JOURNAL
COMMENT
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KEYWORDS
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                                                                                   /clone lib="Sugano mouse kidney mkia"
/clone lib="Sugano mouse kidney mkia"
/note="Organ: kidney, Vector: pME188-FL3; Site 1: DralII
(CACTGTGTG); Site_2: DralII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGGCCTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME188-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the CDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
University of Utah
Um. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ616333 37 bp DNA linear GSS 13-DEC-200 1M0446A08F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0446A08 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.

Giurognathi, Muroidea, Muridae, Murinae, Mus.

I (bases I to 37)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rose, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 64.2%; Score 12.2; DB 1; Length 28; Similarity 82.4%; Pred. No. 2.8e+05; 14; Conservative 0; Mismatches 3; Indels
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/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 37.
Location/Qualifiers
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/clone="UUGC1M0446A08"
clone="IMAGE:1431863"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
                                           /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 GGTGTGAAGTTCAGTGG
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Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
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Best Local Similarity
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ORGANISM
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pWAP2 (gil #742114[ph]AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Contact: Walbot V
Department of Biological Sciences
Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Epermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

    (Passes 1 to 42)

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Tel: 650 723 2227
Fax: 650 725 8221
Fax: 650 725 8221
Fax: 6x0 726 8221
Very probable ligation site of ends cut by single endonuclease.
Very probable ligation site of ends cut by single endonuclease.
Plate: 3591 15 1 row: 4
Class: transposon-tagged.
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/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BqlII;
RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3591 15 1 D10.1EL y 1 3591 - RescueMu Grid P Zea mays genomic, genomic survey sequence.
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/cultivar="mixed background W23/A188/B73/K55"
/db_xref="txxxed" background W23/A188/B73/K55"
/db_xref="txxxed" background W23/A188/B73/K55"
/tissue_type="loaf"
/dev_stage="adult"
/lab_host="DA108"
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Sciurognathi, Muroidea; Muridae; Glires; Rodentia; Sciurognathi, Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 45)

RS Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stockes, R., Tingey, A., von. Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von. Niederhausern, A. and Wright, D., Weiss, R., Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center University of Utah Genome Center University of Utah Genome Center University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
                            site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid P was grown at Molokai in 2002. DNB was extracted from leaf strips, double digested using BamHI and BgllI, and ligated to form circular plasmids. DH10B were transformed and then screened on LB plates with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.05 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were lidated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel
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45 bp DNA linear GSS 29-SEP-200
1M0008K13R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0008K13 R, genomic survey sequence.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
go to the web
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                                                                                                                                                                                                                                                                64.2%; Score 12.2; DB 9; Length 42; 82.4%; Pred. No. 2.9e+05; ive 0; Mismatches 3; Indels
      units. For more information on RescueMu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Exror: 0.00
Plate: 0008 row: K column: 13
Seg primer: CACACAGGAAACAGCTATGACC
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    .45
    /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"

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High quality sequence stop: 45.
Location/Qualifiers
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/clone="UUGC1M0008K13"
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                                                                                                                                                                                  ampicillin."
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Fax: 801 585 7177
Email: ddunn@genet
                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 14; Conserva
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AZ307335/c
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electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X.10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Laboratory Mouse DNA Resource
Laboratory Mouse DNA Resource
Laboratory Mouse DNA Resource
Laboratory Mouse Laboratory Resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
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1M0568H23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0568H23 F, genomic survey sequence.
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1 (basea; Lo 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Keilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts.
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/clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
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                                                                                                                                                                                                                                                                                           Query Match 64.2%; Score 12.2; DB 9; Length 45; Best Local Similarity 82.4%; Pred. No. 2.9e+05; Matches 14; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC1M0568H23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Err
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Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
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84112, USA
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AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus.

E 1 (bases 1 to 41)
S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
                                     EST 26-SEP-2003
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1M0056A13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0056A13 R, genomic survey sequence.
AZ331072
                                                                                                                                                                                                                        Xenopus laevis
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                               Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
Email: tshini@enes.nig.ac.jp
The information of this clone is available through the following
34 bp mRNA linear EST 26-SEP-2
BJ035059 NIBB Mochii normalized Xenopus neurula library Xenopus
laevis cDNA clone XL031m15 5', mRNA sequence.
BJ035059.1 GI:17414312
EST.
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/mol_type="mRNA"
/db xref="traxon:8355"
/clone="x1031m15"
/tissue_type="whole embryo"
/dev stage="stage 15"
/clone_lib="NIBB Mochii normalized Xenopus neurula
library"
                                                                                                                                                                                                                                                                                           Xenopodinae, Xenopus, Xenopus.
1 (bases 1 to 34)
Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
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86.7%; Pred. No. 4.5e+05;
tive 0; Mismatches 2;
                                                                                                                                                                                             Xenopus laevis (African clawed frog)
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Location/Qualifiers
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Mus musculus
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Best Local Similarity 86.7
Matches 13; Conservative
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84112, USA
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AZ331072/c
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                                     10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /done lib="Whole Heart Library (DOGESTS)"
/folome lib="Whole Heart; Vector: pBluescript II SK; Site 1:
EcoR; Site_2: Xhol; Library constructed using pBluescript
XR kit from Stratagene. Cloned cDNA was size selected
between 1-3 kb. Mark Haskins VWD, PhD, Pathology and
Medical Genetics, School of Veterinary Medicine,
University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA 19104-6051"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
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Pred. No. 4.3e+05;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baliay V.S., Nascimento, L.U. and McCombie, W.R. ESTs from Canis familiaris whole heart (dog) Unpublished (2004)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA Tel: 516 367 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="3 month old normal canine"
/lab_host="XL10 Gold"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Canis familiaris"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mccombie@cshl.org.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:
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CX012159.1 GI:56394570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Unknown"
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Canis familiaris
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86.7%;
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Best Local Similarity 86.7
Matches 13; Conservative
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Best Local Similarity
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mRNA

DEFINITION

RESULT 12

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CX012159

ACCESSION

VERSION KEYWORDS

SOURCE

AUTHORS TITLE JOURNAL COMMENT

REFERENCE

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FEATURES

13;

Matches

ORIGIN

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/db_xref="taxon:39946"
/clone="RG152"
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AQ074235.1 GI:3435354
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                                                 FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inductible C7/Dector DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (bases 1 to 50)

NOI/NIDR-Gap http://www.ncbi.nlm.nih.gov/ncicgap.

Noti/NIDR-Gap http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Dental Research,
Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

CDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Not-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG272395 50 bp mRNA linear EST 20-FEB-2001 nah29f02.x1 NCI_CGAP_HN21 Homo sapiens cDNA clone IMAGE:4232571 3',
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                             /lab host="B. Coli strain X110-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
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                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Exror: 0.00
Plate: 0056 row: A column: 13
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 41.
Location/Qualifiers
                                                                                                                                                                                                                                                          organism="Mus musculus"
                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0056A13"
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                                                                                                                                                                                                                                                                                                                                                                                                sex="Male"
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rel: 801 585 5606
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KEYWORDS
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AUTHORS
TITLE
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Oryza sativa (indica cultivar-group)

Oryza sativa (indica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

IE 1 (bases 1 to 20)

MCCouch, S.R., Kochert, G., Yu, Z.H., Wang, Z.Y., Khush, G.S.,

Coffman, W.R. and Tanksley, S.D.

Molecular mapping of rice chromosomes

Lateor. Appl. Genet. 76, 815-829 (1988)

Contact: Susan R. McCouch

Cornell University

Dept. Plant Breeding, Ithaca, NY 14853-1901, USA

Tel: 607 255 6483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ074235 20 BDNA linear GSS 14-SEP-2000 21 pUCB Patl Rice Etiolated Leaf Genomic Library Oryza Bativa (indica cultivar-group) genomic clone RG152, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://ars-genome.cornell.edu/cgi%2Dbin/WebAce/webace?db=ricegenes&class=Marker&object=RG152 DNA Sequencing was done by the DOE Plant Research Lab, Michigan State University. Informatics was done at the Computational Biology Centers, University of Minnesota.
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                                                                                                                                                                                                                                                                           /tissue_type="nasopharyngeal carcinoma"
/lab host="DH10B"
/clone_lib="NCI_CGAP_HN21"
/note="Organ: head/neck; Vector: pAMP1; mRNA made from head/neck tumor, cDNA made by oligo-dT priming.
licetionally cloned into UDG sites Size-selected on agarose gel, average insert size 300 bp. Primary library.cDNA Library Preparation: David B. Krizman, Ph.D."
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For mapping information, additional citations and other related
information concerning this probe, please refer to the RiceGenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Oryza sativa (indica cultivar-group)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.1%; Score 11.8; DB 2; Length 50; 86.7%; Pred. No. 4.6e+05; Live 0; Mismatches 2; Indels
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/db_xref="taxon:39946"
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                                                                                                                                                     /organism="Homo sapiens"
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/cultivar="IR36"
                                                                                                                                                                                                                                                     /clone="IMAGE:4232571"
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Insert Length: 1 Std Brror: 0
Seg primer: M13 -21 dye primer
Class: RFLP probe.
Location/Qualifiers
                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
info@image.llnl.gov
Seq primer: -400P from Gibco.
Location/Qualifiers
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1M0029L01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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/clone_lib="puC8 PstI Rice Etiolated Leaf Genomic Library" hote="Vector: puC8; Total leaf DNA was digested with the restriction enzyme PstI. DH5-alpha bacterial cells were then transformed with ligated plasmid. Random genomic clones were given consecutive numbers (RC+#)as they were prepared. The same numbers were then used to designate loci in the genome as detected by genetic mapping."
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Mus musculus
Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butherra, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
I (bases I to 25)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Ballay, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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/clone lib="Mouse 10kb plasmid UTGCIM library"
/note="Vector: PWD42Iv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                      61.1%; Score 11.6; DB 9; Length 20; 77.8%; Pred. No. 5.4e+05; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone UUGC1M0029L01 F, genomic survey sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/clone="UUGC1M0029L01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ddunn@genetics.utah.edu
Length: 10000 Std Errc
0029 row: L column: 01
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                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                      Similarity
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Plate:
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                                                                                                                                                                                                                                                                                                                 14;
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KEYWORDS
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SM Danio rerio

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Cypriniformes; Cyprinidae; Danio.

I (bases 1 to 28)

S clark, Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M.,

Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,

Underwood, K., Steptoc, M., Theising, B., Allen, M., Bowers, Y.,

Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,

Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,

Waterston, R. and Wilson, R.

Unpublished (1998)
electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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CDNA Library Arrayed by:
CDNA Library Preparation: Matthew Clark. CDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
Miscouri (web address: www.resgen.com) email contact:
(web address: www.resgen.com) email contact: info@resgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="26 somite embryos, adult livers, shield stage embryos" tage embryos" host="XL1-blue MRF" /clone_lib="Zebrafish WashU MPIMG EST"
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI497442
fb53f02.x1 Zebrafish WashU MPING EST Danio rerio cDNA clone
IMAGE:3715611 3' similar to SW:COPB_RAT P23514 COATOMER BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyT not found
Seq primer: T7 ET from Amersham
POLYA-No.
                                                                                                                                                                                                                                                                                              Length 25
                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                           Score 11.6; DB 9;
Pred, No. 5.5e+05;
0; Mismatches 4;
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/db_xref="taxon:7955"
/clone="IMAGE:3715611"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                           ch 61.1%;
1 Similarity 77.8%;
14; Conservative
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                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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AUTHORS
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KEYWORDS
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/Gell type="myoellum"
/clone lib="myoellum"
/clone lib="myoellum"
/clone lib="myoellum"
/clone lib="myoellum"
/clone lib="myoellum"
/clone lib="myoellum"
/note="Voctor: pBluescriptSK-; Site_l: EcoRI; Site_2:
Xhol; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on Xhol side of insert.
Nitrogen starvation library. Cells were inoculated into minimal medium and grown for two days with shaking (150 rpm) at room temperature. Culture was harvested, blended, inoculated into minimal medium as above for 24 h. Cells were harvested, washed with water and inoculated into minimal medium base lacking nitrogen source for 6 h. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."
                                                                                                                                                                                                                                                   CD029249 29 Dp mRNA linear EST 07-MAY-2003 mgns012x001f.b Magnaporthe grisea NS Uni-Zap XR Library Magnaporthe grisea cDNA clone mgns012x001 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ebbole, D. J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G.,
Bhatterai, K. and Dean, R.A.
Expressed sequence tags from the rice blast fungus, Magnaporthe
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        this sequence is available, see contact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Texas AM Univ
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/mol_type="mRNA"
/strain="Guy11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |db| xref="taxon:148305"
|clone="mgns012x001"
|sex="Mat1-2 hermaphrodite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR PRIMERS
FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgns012 row: O column: 01
Seq primer: T3.
Location/Qualifiers
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                               GGGTGACGTTCAGGGGGG 19
                                                                                          7 GGGTTAGGTGTAGGGGGG 24
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Best Local Simi
Matches 14;
                                                                                                                                                                                           RESULT 20
CD029249/c
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SOURCE
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                        sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality
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PRI0144b_D10_2 - PRI0144b.BR (28) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic
/note="Vector: pSPORT1; Site_1: Not1; Site_2: Sal1; 1st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="Mixed stage fosmid library of P. pacificus var. California"
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Nucleic Acids Res. 32 (1), D421-D422 (2004)
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This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
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Pristionchus pacificus
Eukaryota, Metazoa, Nematoda, Chromadorea, Diplogasterida,
Neodiplogasteridae, Pristionchus.
1 (bases 1 to 28)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.1%; Score 11.6; DB 1; Length 28; 77.8%; Pred. No. 5.5e+05; ive 0; Mismatches 4; Indels
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Max-Planck-Institute for Developmental Biology
Spenannstr. 37-39, Tuebingen D-72076, Germany
Tal: 00497071601371
Pax: 00497071601498
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/mol_type="genomic DNA"
/strain="California"
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Gaps

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Eukaryota; Mycecczoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 35)
Urushihara, H., Morio, T., Saito, T., Kohara, Y., Koriki, E., Ochiai, H., Amaeda, M., Williams, J.G., Takeuchi, I. and Tanaka, Y.
Analyses of cDNAs from growth and slug stages of Dictyostelium
                                                                                    BI259582 34 bp mRNA linear EST 17-JUL-2001
602968347F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5108146 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-WGC http://wgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: Libralian.gov

Plate: Libralian.gov

Plate: Libralian.gov

Plate: Libralian.gov
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/note="Organ: Cervix; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
Technologies."
                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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/db xref="taxon:9606"
/clone="InAge:5108146"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH108"
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/organism="Homo sapiens"
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Location/Qualifiers
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B1259582
B1259582.
B1259582.1 GI:14817058
EST.
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Dictyostelium discoideum
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1 (bases 1 to 34)
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Best Local Similarity 77.8
Matches 14; Conservative
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                          RESULT 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                         GSS 16-FEB-2001
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                                                            AZ783946
2M0026B08F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0026B08 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi, Muroidea, Muridae, Murinae, Mus.

1 (Dases 1 to 30)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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/clone lib="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD42nv, Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
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Pred. No. 5.6e+05;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0026 Low: B column: 08
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0026B08"
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Location/Qualifiers
                                                                                                                                                                                                                                                  Mus musculus (house mouse)
Mus musculus
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Unpublished (2000)
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Fax: 801 585 7177
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RESULT 21
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discoideum Nucleic Acids Res. 32 (5), 1647-1653 (2004) 15010511 Contact: Hideko Urushihara

PUBMED COMMENT

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1 GGGGTGACGTTCAGGGGG 18

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/clone_lib="Sugano mouse liver mlia"
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Best Local Similarity
Matches 14; Conserv
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CF291715/c
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37 bp mRNA linear EST 28-MAY-1998
uc73e01.x1 Sugano mouse liver mlia Mus musculus cDNA clone
limags:1431288 3' similar to SW:PRP2 MOUSE P05142 PROLINE-RICH
PROTEIN MP-2 PRECURSOR. ;, mRNA sequence.
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1 (bases 1 to 37)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL , contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Faz: 314 286 1810
Email: mouseest@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                           Query Match 61.1%; Score 11.6; DB 1; Length 35; Best Local Similarity 77.8%; Pred. No. 5.6e+05; Matches 14; Conservative 0; Mismatches 4; Indels
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Possible reversed clone: similarity on wrong strand
Seq primer: primer name ambiguous
High quality sequence stop: 1.
Location/Qualifiers
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.
                                                                                                                                                                    /organism="Dictyostelium discoideum"
/mol_type="mRNA"
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                            /dev_stage="vegetative"
/clone_lib="VS"
                                                                                                                                                                                                                    /strain="AX4"
/db_xref="taxon:44689"
/clone="VSD330"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:1431288"
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GGGTGACGTTCAGGGGGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGTTACTTTGGGGGGGG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA986717.1 GI:3167719
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                                                                                                                                                                                                                                                                                        /sex="mat A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 24
AA986717/c
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VERSION
KEYWORDS
SOURCE
ORGANISM
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JOURNAL
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// CACCETAINT LIVER: WELLES-FL3; Site 1: Draill (CACCATGTGTG); Site 2: Draill (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer (ACCATGTGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a Draill adaptor [TGTTGGCTACTGG], digested and cloned into distinct Draill sites of the pWELBS-FL3 vector (5' site CACTGTGTG, 3' site CACTGTGTG, 3' site CACTGTGTG, 1' site caction was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGTAAAAGCTGCG and 3' end primer CGACCTGGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (japonica cultivar-group)

ENKarycra, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

ENKarycra, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzae; Oryza;

EN (M., J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

M. Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355
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/organism="Oryza sativa (japonica cultivar-group)"
/oultivar="mRNA"
/cultivar="mackdong"
/db xref="taxon:39947"
/clone="14ROOT-02-E03"
/fissue type="root"
/dev stage="14 days after germination"
/dev stage="14 days after germination"
/done="loot" DH108"
/clone="loot" DH108"
/clone="loot" pR108"
/clone="loot" pR24-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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14-AUG-2003

14ROOT--02-E03.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--02-E03, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.1%; Score 11.6; DB 1; Length 37; ilarity 77.8%; Pred. No. 5.6e+05; Conservative 0; Mismatches 4; Indels
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Location/Qualifiers
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/d_one="IMAGE:1560394"
/tissue_type="adenocarcinoma"
/lab_host="MIDB"
/clone_lib="NCI_CGAP_CO8"
/clone_lib="NCI_CGAP_CO8"
/note="organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3
vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NGI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BX569627 Glossina morsitans morsitans adult infected gut Glossina morsitans cDNA clone Tse9f08_q1c, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glossina morsitans morsitans Glossina morsitans morsitans morsitans Glossina morsitans morsitans Glossina morsitans Glossina Mexaryota; Metaryota; Metaryota; Metaryota; Metaryota; Metaryota; Endopreryota; Diptera; Brachycera; Muscomorpha; Hippoboscoidea; Glossinidae; Glossina.

1 (bases 1 to 44)
1 (bases 1 to 44)
1 Lehane, M., Asory,S., Gibson,W., Kerhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans and expression analysis of putative immune
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                        61.1%; Score 11.6; DB 1; Length 43; 77.8%; Pred. No. 5.7e+05; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trace considered overall poor quality Insert Length: 1892 Std Error: 0.00 Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 1. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .43
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 response genes
Genome Biol. 4 (10), R63 (2003)
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/db_xref="taxon:9606"
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 14; Conserv
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                                                                                 REFERENCE
AUTHORS
TITLE
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BX569627
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="hypothalamus"
/lab_host="DH10B"
/lab_host="DH10B"
/cloo= llb="MIH_MGG_96"
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamH1; Site_2: Sall-XhoI (grcgag); Oligo-dT primed using primer
5-TTTTTTTTTTTTTTTTTTTTVTV ; size_selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHORI, National Institutes of Health). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 4)

1 (bases 1 to 4)

NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapba-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

Contact: Robert Stravyed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:

http://image.llnl.gov mcolumn: 23

High quality sequence stop: 41.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                      BI669410 41 bp mRNA linear EST 12-SEP-2001
603295295F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5314750 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
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/organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:5314750"
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     32 GGCTGACGGCGAGGGGGG 15
                                                                                                                                                                                                                                                    BI669410.1 GI:15583643
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AA948503.1 GI:3109756
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Homo sapiens
                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                                              mRNA sequence.
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Matches 14; Conserva
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AA948503/c
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                                                                                      RESULT 26
BI669410
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TITLE
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VERSION
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BI544737
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                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="country: Zimbabwe; EST from adult gut infected with
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84112, USA
          The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 18A, UK Request for clones, please contact: Mike Lehane Prof. M.J.Lehane School of Biological Sciences, University of Wales, Bangor LL57 2UW Bangor LL57 2UW All clones with suffix qlc are reverse primer reads starting at 5' end of the CDNA all plc reads are from the 3' end.
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                 /moi_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse9168 q1c"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans adult infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 45)
Dunn,D., Acyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Waiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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    .44
    /organism="Glossina morsitans"

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Insert Length: 10000 Std Brror: 0.00
Plate: 0517 row: O column: 13
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Class: plasmid ends
High quality sequence stop: 45.
Location/Qualifiers
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Pathogen Sequencing Unit
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMAP120/T2.11, a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XIIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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I (bases 1 to 47)

S NIH-WGC http://mgc.nci.nih.gov/.

I (bases 1 to 47)

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Ggapbs mail. nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

Contact Robert Strausberg, Ph.D.

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

Contact Robert Strausberg, Ph.D.

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://mage.llnl.gov

Plate: LiAM11719 row: a column: 01
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602242001F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5284488 5',
                                                                                                       /lab_host="B. Coli strain XLIO-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PMP42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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61.1%; Score 11.6; DB 9; Length 45;
Best Local Similarity 77.8%; Pred. No. 5.7e+05;
Matches 14; Conservative 0; Mismatches 4; Indels
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/tissue_type="hippocampus"
/lab_host="DH108"
/clone_lib="NIH_MGC_95"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:10090"
/clone="UUGC1M0517013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 47.
Location/Qualifiers
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/db_xref="taxon:9606"
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Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NT-CGAP clone distribution information can be
found through the I.M.A.G.E., Consortium/LIML at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="pooled germ cell tumors"
/lab host="DH108"
/clone_lib="NCI_CGAP_GC4"
/note="Vectors: pT7130-Pec (Pharmacia) with a modified
polylinker; lst strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo (dT) primer: Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT773
vector. Library is normalized. Library was constructed by
Bento Soares and M. Patima Bonaldo. "
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BE615718
              nns/2/3/6 CGAP GC4 Homo sapiens cDNA clone IMAGE:1520002 3' similar to TR:\overline{0}39614 PROLINE-RICH PROTEIN. ;, mRNA sequence. AA922976
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                  Hominidae, Homo.

1. (bases 1 to 49)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Seg primer: -40ml3 fwd. BT from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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/organism="Homo sapiens"
/nol_type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:1520002"
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                                                                                                                                       AA922976.1 GI:3070285
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Homo sapiens
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1 (bases 1 to 49)
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nes 14; Conserv
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/lab_host="XL10 Gold"
/lab_host="Lib"whole Heart Library (DOGESTS)"
/clone lib="whole Heart Library constructed using pBluescript In Sk is te_2:
/note="Gorgan: Heart, Vector: pBluescript II Sk, Site_1:
ECORI; Site_2: Mol; Library constructed using pBluescript XR kit from Stratagene. Cloned cDNA was size selected between 1-3 kb. Mark Haskins WMD, PhD, Pathology and Medical Genetics, School of Veterinary Medicine, University of Pennsylvania, 3800 Spruce Street, Philadelphia, PA 19104-6051"
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Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
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/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamH1, Site_2: Sall-XhoI (qtcgaq), Oligo-dT primed using primer S.-TTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NIGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CX013593 47 bp mRNA linear EST 06-DEC-io66b06.bl Whole Heart Library (DOGESTS) Canis familiaris cDNA,
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                                                                                                                                                                                                                                                                                                                           Score 11.6; DB 3; Length 47;
Pred. No. 5.7e+05;
0; Mismatches 4; Indels
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Location/Qualifiers
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/db_xref="taxon:9615"
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Canis familiaris
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1 Similarity 77.8%;
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RESULT 31 CX013593/c DEFINITION

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/organism="Homo sapiens"
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AUJ02320 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ADSE01801, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatcku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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I (bases 1 to 50.

Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,

Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,

Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.

Initiation revealed by fine, large-scale
mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=_Organ: pancreas; Vector: pOTB7; Site 1: XhOI; Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life
                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
http://mage.lln.gov
Plate: LLCM296 row: o column: 07.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:3622110"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_39"
                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
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Best Local Similarity 77.8
Matches 14; Conservative
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2 (Dases 1 to 35).

Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
Direct Submitssion

Bioscience and Biotechnology (KRIBB), Genome Research Institute of
Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
52, Oun-dong, Yusong-Gu, Daejeon 305-333, Korea

[E-mail:redstone@anil.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
Tel:82-42-866-7181, Fax:82-42-860-4409)

Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AG204798 35 bp DNA linear GSS 06-MAR-2004
Pan troglodytes DNA, clone: RP43-090Kl3.T7, genomic survey
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                               Gaps
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/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"
                                                         /clone="ADSE01801"
/clone lib="Sugano Homo sapiens cDNA library"
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/organism="Pan troglodytes"
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/db_xref="taxon:9598"
/clone="RP43-090K13.T7"
/mol_type="mRNA"
/db_xref="taxon:9606"
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R.Site 1 : EcoRI
R.Site 2 : EcoRI.
                                                                                                                                                                                                                                                                                                            2 GGGTGACGTTCAGGGGGG 19
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AG204798.1 GI:45236973
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/ General Documents of the plasmid UnGCIM Tl-resistant, F-" (1ab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-" (21on=11b="Mususe 10kb plasmid UUGCIM library" (21on=11b="Weator: PWMAIN; Purified genomic DNA from M. (alone="Weator: PWMAIN; Purified genomic DNA from M. (aboute DNA Resource the plasmid DNA Resource (alone DNA Resource (alone DNA Resource (alone DNA Resource)). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pubMail (31) A1194[9] AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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   Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT
84112, USA
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1 (bases 1 to 29)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Hallingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission

project, Sanger Centre, The Wellcome Trust Genome Sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, B-mail: barrell@sanger.ac.uk and
chil@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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T. brucei sheared genomic DNA clone 246h09, reverse seguence,
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                                                                                Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0072 row: G column: 21
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0072G21"
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High quality sequence stop: 22.
Location/Qualifiers
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Jniversity of Utah
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                                                                                                                                                                                                                                                                                                                                                             [ (bases I to 36) [ Randall T., Dwyer, R.A., Huitema, E., Beyer, K., Cvitanich, C., Kelkar, H., Pong, A.M., Gates, K., Roberts, S., Yatzkan, E., Gaffney, T., Law, M., Testa, A., Torto-Alalibo, A., Zhang, M., Zheng, I., Mueller, E., Windass, J., Binder, A., Birch, P.R.J., Gisi, U., Govers, F., Gow, N.A., Mauch, P., van West, P., Waugh, M.E., Yu, J., Boller, T., Kamoun, S., Lam, S.T. and Judelson, H.S.
                                         EST 25-JAN-2005
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Mus musculus
Mus musculus
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Mus musculus
Sciurognathi; Muroidea; Muridae; Murinae; Musc.
Musculus
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Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
   36 bp mRNA linear EST 25-
infestans cDNA, mRNA sequence.
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/note="Vector: pSPORT1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Plant Pathology
University of California
Webber Hall, Riverside, CA 92521,
Tel: 909 787 4199
Fax: 909 767 4294
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University of Utah Genome Center
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/strain="88069 and 618"
/db_xref="taxon:4787"
/sex="Al and A2"
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Location/Qualifiers
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (a size distribution) (a size distribution) (b size distribution) (a size distribution) (b size dis
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Mammalia, Butheria, Euarchontoglires, Glires; Rodentia,
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
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Fax: 801 585 7177
Email: ddunm@genetics.utah.edu
llatr. Length: 10000 Std Error: 0.00
Platr: 0308 row: H column: 16
Seq primer: CACACAGGAAAACAGCTAATGACC
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/mol_type="genomic DNA"
/strain="C57BL/63"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 30.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="UUGC1M0308H16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:5691"
/clone="246h09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ483233.1 GI:10647043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Greaacricaeeeae 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity #1.29
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VERSION
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SOURCE
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g 8

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Laboratory Moules DNA Resource (Attp://www.jax.orgyresources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified molar excess. The adaptored DNA was purified asize selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells
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PRI0138b_H10_2 - PRI0138b_BR (30) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic
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/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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/strain="California"
/db xref="taxon:54126"
/db xref="taxon:54126"
/clone lib="Mixed stage fosmid library of P. pacificus var. California"
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Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
AppaDB: an AcedB database for the nematode satellite organism
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Max-Planck-Institute for Developmental Biology
Speanannstr. 37-39, Tuebingen D-72076, Germany
Tel: 004970716013498
Email: ralf. sommer@tuebingen.mpg.de
Email: ralf. sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
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Eukaryota, Metazoa, Nematoda, Chromadorea, Diplogasterida,
Neodiplogasteridae, Pristionchus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.9%; Score 11.2; DB 9; Length 30; ilarity 81.2%; Pred. No. 8.7e+05; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and selected for ampicillin resistance."
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Nucleic Acids Res. 32 (1), D421-D422 (2004)
14681447
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Pred. No. 8.7e+05;
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Class: fosmid ends.
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German Genetrap Consortium (GGTC)

Email: info@genetrap.de

PlipRoSAGeoct.2 gene trap. Sequence tag generated by 5'RACE.

Additional sequence information can be found at:

'http://genetrap.gsf.de/project/web_new/database/result_clone.html?

clone id=w090F07' Es cell line harboring insertion mutation of

target gene is available at:

'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.html'

l'Inhouse Sequence Identifier: 18342
                                                                                                                          CZ294988 36 bp mRNA linear GSS 22-MAR-2005
M090F07 GGTC Gene Trap Library GV18C05 Mus musculus cDNA clone
                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciutorgathi; Murcidea; Murinae; Mus.

1 (bases 1 to 36)
Hansen, J.; Floss, T.; van Sloun, P.; Puchtbauer, E.M.; Vauti, F.;
Hansen, J.; Floss, T.; van Sloun, P.; Puchtbauer, E.M.; Vauti, F.;
Arnold, H.H.; Schuutgen, F.; Wurst, W.; Von Melchner, H. and Ruiz, P. A large-scale, gene-driven mutagenesis approach for the functional analysis of the mouse genome
Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
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tt15d10.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2240851 3'
similar to TR:Q12799 Q12799 T-COMPLEX PROTEIN 10A. ;, mRNA
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/cell_type="Bmbryonic stem cell"
/cell_line="ES cells [CS7BL/6J x 12986/SvEvTac] Fl"
/clone_lib="GGTC Gene Trap Library GV18C05"
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1 (bases 1 to 37)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 58.9%; Score 11.2; DB 10;
Best Local Similarity 68.4%; Pred. No. 8.8e+05;
Matches 13; Conservative 0; Mismatches 6;
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    .36
    /organism="Mus musculus"

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/clone="M090F07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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/strain="129 Sv"
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                                                                                                                                                                      M090F07, mRNA sequence.
CZ294988
                                                                                                                                                                                                                                  CZ294988.1 GI:61682738
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EST.
31 GGGGACCTTCTGGGGG 16
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Mammalia, Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Class: Gene Trap.
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                                                                                                                                                                                                                                                                                                                 musculus
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A1696220/c
LOCUS
DEFINITION
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ORGANISM
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PUBMED
COMMENT
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AUTHORS
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AUTHORS
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LOCUS
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/ corganism="Drosophila melanogaster"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
/strain="isogenic w- strain"
/db_xref="taxon:7227"
/clone_lib="Exclisis" pelement XP insertions"
/clone_lib="Exclisis" pelement XP (GenBank accession number AYS15149); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. For the P element XP, we selected an easily mobilized ammunition element among inserts hopped onto the Binsinscy balancer. New insertions were collected in vials from dysgenic females using the standard chromosomal source of transposase, deltaz-3. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability and used for recovery of flanking genomic sequence by inverse PCR."
                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Roydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 33)

2 Thibault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A.,

Singh, C.M., Buchholz, R., Demsky, M., Frawcett, R., Francis-Lang, H.L.,

Ryner, L., Cheung, L.M., Chong, A., Erickson, C., Fisher, W.W.,

Greer, K., Hartouni, S.R., Howie, E., Jakkula, L., Joo, D., Killpack, K.,

Iaufer, A., Mazzotta, J., Smith, R.D., Stevens, L.M., Stuber, C.,

Tan, L.R., Ventura, R., Woo, A., Zakrajsek, I., Zhao, L., Chen, F.,

Swimmer, C., Kopczynski, C., Duyk, G., Winberg, M. L. and Margolis, J.

A complementary transposon tool kit for Drosophila melanogaster
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                                                                                                                                                                                                                                                           d06009-5prime Exelixis P element XP insertions Drosophila melanogaster genomic Sequence recovered from 5' end of P element,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The P element insertion position is 26 in the 33 bases. This insertion position refers to the first base of the 8 base target recognition sequence.
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: RHoskinselbl.gov
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailbrop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
TTE: 510 486 4015
Fax: 510 486 6798
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Indels
3,
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Mismatches
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Nat. Genet. 36 (3), 283-287 (2004)
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Location/Qualifiers
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13; Conservative
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Seg primer: M13RP1
High quality sequence stop: 1.
Location/Qualifiers
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/clone="IMAGE:166322"
                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
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                                                                                                                                                                                                                            /sex="Male'
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                                                                                                                                                                                Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LiNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seg primer: -40UP from Gibco

High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /.clone_lib="NICL CGAP_GGG"
//clone_lib="VGCCCT." CGAP_GGG"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_l: Not_l; Site_2: Eco_RI; Plasmid DNA
from the normalized library NCT_GGAP_GG4 was prepared, and
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
1257096-1228631, 1469064-1470983, and 1475592-1476743).
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Bmail: info@genetrap.de

FlipROSACeoC-2 gene trap. Sequence tag generated by 5'RACE.

Additional sequence information can be found at:

'http://genetrap.gsf.de/project/web_new/database/result clone.html?

clone_id=M033F02' ES cell line harboring insertion mutaTion of

target_gene is available at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CZ294761 39 bp mRNA linear GSS 22-MAR-2005 M093F02 GGTC Gene Trap Library GV14C05 Mus musculus cDNA clone M093F02, mRNA sequence.
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Hansen,J., Floss,T., van Sloun,P., Fuchtbauer,E.M., Vauti,F.,
Arnold,H.H., Schnutgen,F., Wuret,W., von Malchner,H. and Ruiz,P.
A large-scale, gene-driven mutagenesis approach for the functional analysis of the mouse genome
Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Mus.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
                   Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                    'organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="IMAGE:2240851"
                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Email: 626 1800
Email: est@watson.wustl.edu
Insert Size: 2019
Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL, contact the IMAGE Consortium (info@image.llnl.gov)
for further information. Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 2019 Std Error: 0.00
'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm
1' Inhouse Sequence Identifier: 18341
Class: Gene Trap.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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ym91g02.rl Soares adult brain N2b4HB55Y Homo sapiens CDNA clone IMAGE:166322 5' similar to SP:S27887 S27887 NEUREXIN II-ALPHA PRECURSOR - ;, mRNA sequence.
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1 (bases 1 to 40)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hellman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                       /cell_type="Embryonic stem cell"
|cell_line="ESS cells [C57BL/6J x 129S6/SvEvTac] F1"
|clone_lib="ESC Gene Trap Library GV14C05"
|nobe="Vector: FlipROSACeOC-2"
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/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 11.2; DB 10;
Pred. No. 8.9e+05;
0; Mismatches 6;
                                                                                                                                                     /organism="Mus musculus"
/mol_type="mRNA"
fatrain="129 Sv"
/db_xref="taxon:10090"
/clone="M093F02"
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/mol_type="mRNA"
/db_xref="GDB:587017"
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linear

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mRNA sequence.
                                                                                                                                            Mus musculus
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Les 13; Conserv
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Humphray, S.J., Huckle, E. and Durham, J.L.
Direct Submission
Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 41)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bX128210 41 bp DNA linear GSS 28-JAN-Danio rerio genomic clone DKEY-279M17, genomic survey sequence.
BX128210
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Best Local Similarity 81.2%; Pred. No. 8.9e+05;
Matches 13; Conservative 0; Mismatches 3; Indels
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/note="vector pindigoBAC-536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/db_xref="taxon:7955"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="DKEY-279M17"
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Best Local Similarity
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JOURNAL
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RESULT 47 W34290/c

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BH802996 48 bp DNA linear GSS 25-APR-2002
1008098B12.2EL_y1 1008 - RescueMu Grid I Zea mays genomic, genomic
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                                                                                                                                                                                                                                                                                                    1 (bases 1 to 46)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
                                                                    .:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
W34290
mRNA linear EST 12-SEP-
ma99607.r1 Soares mouse p3NNF19-5. Mus musculus cDNA clone
IMAGE:318828 5' similar to SW:GBG3 BOVIN P29798 GUANINE
NUCLEOTIDE-BINDING PROTEIN G(I)/G($\overline{S}$)/G(0) GAMMA-3 SUBUNIT. [1]
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                           The WashU-HHMI Mouse BST Project
Unpublished (1996)
Contact: Marra M/Mouse BST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.9%; Score 11.2; DB 8; Length 46; ilarity 81.2%; Pred. No. 8.9e+05; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28Ml3 rev2 from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                     Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          survey sequence.
BH802996
BH802996.1 GI:20317698
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                                                                                                                                            W34290.1 GI:1316200
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VERSION
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Stanford University
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AUTHORS
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/tissue_tryac="mixeu background wis/Albe/B/3"
/tissue_trye="lad"
/dev stage="adult"
/lab_host="bloom="lad"
/lab_host="bloom="lad"
/clone lib="loom="lad"
/clone lib="lad"
/c
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11191516D01.1EL x1 1119 - RescueMu Grid AA Zea mays genomic, genomic
survey sequence.
CG732711
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                                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Pepermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                            Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
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Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                               Department of Biological Sciences
Stanford University
Stanford University
Stanford University
Stanford University
Stanford University
Fax: 650 723 2227
Fax: 650 725 8221
Benail: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1008098 row: 14
Class: transposon-tagged.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
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Best Local Similarity
Matches 13; Conserva
                                                                                                                                                                                                                         Walbot, V.
                                      Zea mays
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/clone lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHi; Site_2: BgJII;
RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zamdb.iastate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BgJII, and ligated to form circular plasmids. DNIOB cells were transformed and then screened on LB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 50)
Alonso,Jun, Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
                                                                                     Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1119150 row: 46
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0
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/mol type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 49;
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Contact: Joseph R. Bcker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 658 678
Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.9%; Score 11.2; DB 10;
81.2%; Pred. No. 9e+05;
iive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plates with ampicillin."
                                                                                                                                                                                                                                 Class: transposon-tagged.
Location/Qualifiers
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Best Local Similarity 81.2
Matches 13; Conservative
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Class: TDNA tagged.

Location/Qualifiers

1. .50

/ organism="Arabidopsis thaliana"

/ mol_type="genomic DNA"
/ ecotype="Col-0"

/ db xref="taxon:3702"

/ clone="SALK_115432.18.90.x"

/ clone="Ib="Arabidopsis thaliana TDNA insertion lines"

/ note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Deteails of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 58.9%; Score 11.2; DB 9; Length 50; Best Local Similarity 81.2%; Pred. No. 9e+05; Matches 13; Conservative 0; Mismatches 3; Indels
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                                                                           Bource
                                          FEATURES
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Search completed: February 15, 2006, 21:10:07 Job time : 1283.74 secs

29 GGGAGATGTTAAGGG 44

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              GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-538-073-18

US-09-538-073-18

US-08-852-001-5

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74.7%; Score 14.2; DB 3;
Best Local Similarity 84.2%; Pred. No. 7.1e+02;
Matches 16; Conservative 0; Mismatches 3;
                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/386,063
FILLING DATE:
CLASSIFICATION HOPRWATION:
NAWE: ARNOLD, BETH E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIZ-013CP
TELECOMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
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ZONDUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/386,063
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ARNOLD, BETH E.
REGISTRATION NUMBER: 35,430
REPRESENCE/DOCKET NUMBER: UIZ-OFFECOMMUNICATION INFORMATION:
TELECHONE: (617)227-7400
TELEFAX: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
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MASSACHUSETTS
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                  COUNTRY:
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Patent No. 6008200
GENERAL INFORMATION:
APPLICANT: Archur M. Krieg, M.D.
TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, SUITE 510
        US-09-050-739-162

US-09-622-745B-15

US-09-622-745B-15

US-07-911-471B-32

US-07-174-131C-32

US-08-409-442A-32

US-08-409-443-32

US-09-502-344-32-10

US-09-502-34-32-10

US-09-502-34-32-10

US-09-517-849-39

US-09-517-849-39

US-09-517-849-39

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US-09-143-270-8

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Sequence 18, Application US/09538873

Sequence 18, Application US/09538873

Patent NO. 6566500

GENERAL INPORMATION:
APPLICANT: GHETIE, VICTOR F.
APPLICANT: BALUAN, JOAN

TITLE OF INVENTION: SYNDROME (VLS)
FILE REFERENCE: UTSD:603

CURRENT APPLICATION NUMBER: US/09/538,873

CURRENT APPLICATION NUMBER: 06/126,826

BARLIER PILING DATE: 2000-03-30

CURRENT PILING DATE: 1999-03-30

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin Ver. 2.1

LENGTH: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:

APPLICANT: VITETTA, ELLEN S.

APPLICANT: VITETTA, ELLEN S.

APPLICANT: GHALUNA, JOAN F.

APPLICANT: BALUNA, JOAN G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF TITLE OF INVENTION: PROFEINACEOUS COMPOUNDS

TITLE OF INVENTION: PROFEINACEOUS COMPOUNDS

FILE REFERENCE: UTSD: 884US

CURRENT APPLICATION NUMBER: US/10/282,935

CURRENT APPLICATION NUMBER: 09/538,873

PRIOR FILING DATE: 2000-03-30

PRIOR FILING DATE: 2000-03-30

PRIOR FILING DATE: 1999-03-30

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PATENTIN VEY: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Primer
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
73.7%; Score 14; DB 3; Length 39;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                      ; OTHER INFORMATION: synthetic oligonucleotide US-09-965-101-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-282-935-18/c
; Sequence 18, Application US/10282935
; Patent No. 6960652
                                                                                                                                                                                                                                                                                                                        1 GGGGTGACGTTCAGGGGG 19
                                                                                                                                                                                                                                                                                                                                                                        2 GGGTTGACGTTTTGGGGGG 20
SEQ ID NO 63
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GGTGACGTTCAGGG 16
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US-09-538-873-18/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Davis, Heather L.
APPLICANT: Schort, Joachim
APPLICANT: Schort, Joachim
APPLICANT: Schort, Joachim
APPLICANT: Schort, Joachim
APPLICANT: Wu, Tong
TITLE OF INVENTION: Vectors and Methods for Immunization or
TITLE OF INVENTION: Therapeutic Protocols
TITLE OF INVENTION: Therapeutic Protocols
FILE REFERENCE: C1391/7009
CURRENT APPLICATION NUMBER: US/09/082,649B
CURRENT PILING DATE: 1999-05-20
PRIOR FILING DATE: 1997-05-20
PRIOR FILING DATE: 1997-05-20
NUMBER OF SEQ ID NOS: 85
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 63
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
US-09-965-101-63
is Sequence 63, Application US/09965101
is Patent No. 6821957
is GENERAL INFORMATION:
is APPLICANT: Davis, Heather L.
is APPLICANT: Krieg, Arthur M.
is APPLICANT: Krieg, Arthur M.
is APPLICANT: Wu, Tong
it TITLE OF INVENTION: Vectors and Methods for Immunization or TITLE OF INVENTION: Vectors and Methods for Immunization or TITLE OF INVENTION: Vectors and Methods for Immunization or TITLE OF INVENTION: Vectors and Methods for Immunization or TITLE OF INVENTION: Vectors and Methods for Immunization or TITLE OF INVENTION: Vectors and Methods for Immunization or TITLE OF INVENTION: WHERE: US 09/082,649
is PRIOR APPLICATION NUMBER: US 60/047,233
is PRIOR FILING DATE: 1997-05-20
is NUMBER OF SEQ ID NOS: 84
is NUMBER OF SEQ ID NOS: 84
                                                                                                                                      Score 14.2; DB 3; Length 20;
Pred. No. 7.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 74.7%; Score 14.2; DB 3; Length 20; Best Local Similarity 84.2%; Pred. No. 7.1e+02; Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: synthetic oligonucleotide US-09-082-6498-63
                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
US-09-082-649B-63
US-09-082-649B-63
Sequence 63, Application US/09082649B
Patent No. 6339068
GENERAL INFORMATION:
APPLICANT: Davis, Heather L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGGGTGACGTTCAGGGGGG 19
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ORGANISM: Artificial Sequence
                                                                                                                                      Query Match
Best Local Similarity 84.2%;
Matches 16; Conservative
        STRANDEDNESS: single
                                 ; TOPOLOGY: linear; MOLECULE TYPE: DNA US-08-386-063-1
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Gaps

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TELEFAX: (202) 672-5399
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                                                                                               OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Primer
US-10-282-935-18
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Patent No. 6197556
GENERAL INFORMATION:
APPLICANT: Ulanovsky, Levy
APPLICANT: Ulanovsky, Levy
TITLE OF INVENTION: BRANCHED PRIMERS
TITLE OF INVENTION: BRANCHED PRIMERS
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: Plaza Drive
STREET: Plaza Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 13.4; DB 3; Length 22;
Pred. No. 1.8e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                Query Match 73.7%; Score 14; DB 3; Length 39; Best Local Similarity 100.0%; Pred. No. 9.5e+02; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 60611-5599
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Parent PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,001
FILING DATE: 06-MAY-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 18..19
CTHER INFORMATION: /product= "N = inosine"
US-08-852-001-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Martin, Alice O.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 6837/7
TELEPHONE: 312-321-4200
TELEPAX: 312-321-420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer"
                                      TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 93.3%;
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chicago
: Illinois
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                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
US-08-852-001-5
SEQ ID NO 18
LENGTH: 39
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                                                                                  FEATURE:
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; Sequence 29, Application US/08666221B
; Patent No. 613544
; GENERAL INFORMATION:
; APPLICANT: Nutt, Stephen
; TITLE OF INVENTION: QLUTAMATE RECEPTOR (OR EAA RECEPTOR)
; TITLE OF INVENTION: POLYNUCLEOTIDES AND THEIR USES
; CORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 & Street, N.W., Suite 500
; CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                              69.5%; Score 13.2; DB 3; Length 50; 83.3%; Pred, No. 2.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/666,221B
APPLICATION NUMBER: US/08/666,221B
                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         016777/0308
Sequence 3663, Application US/10131827 Patent No. 6905827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 20-UN-1996
CLASSIFICATION: 435
PRIOR APPLICATION ONTA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT: INFORMATION:
NAME: Bent, Stephen A.
REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 0167'
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGGGTGACGTTCAGGGGG 18
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N: 435
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Matches 15; Conservative
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APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Elik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED NUMBER OF SEQUENCES: 94
SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                 COMPUTER: USA

ZIP: 1053
ZIP: 1053
ZIP: 1053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/951,715A
FILING DATE: 25-SEP-1992
CLASSIFICATION: 800
PRIOR APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: SPENIALI, W. Murray
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 32,943
REGISTRATION STANDARATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8615
TELEFRAX: (919) 541-8615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 12.8; DB 2;
Pred. No. 3.7e+03;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer P5(a)"
  TITLE OF INVENTION: SYNTHETIC DNA SE
TITLE OF INVENTION: INSECTICIDAL ACT
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-CELIGY Corporation
STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 43, Application US/08459448A Patent No. 5859336 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Koziel, Michael G. APPLICANT: Desai, Nalini M. APPLICANT: Lewis, Kelly S. APPLICANT: Kramer, Vance C. APPLICANT: Warren, Gregory W. APPLICANT: Evola, Stephen V. APPLICANT: Crossland, Lyle D. APPLICANT: Wright, Martha S. APPLICANT: Wellin, Ellis J. APPLICANT: Launis, Karen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 43: SEQUENCE CHARACTERISTICS: LENGTH: 32 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 67.4%;
Best Local Similarity 87.5%;
Matches 14; Conservative
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                                                                                                                                         CITY: Hawthorne
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-07-951-715A-43
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
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                                                                                                                                                                                                                                                               Length 20;
                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-396-196G-120261/C

Sequence 120261, Application US/09396196G

Sequence 120261, Application US/09396196G

Patent No. 6821724

GENERAL INFORMATION:

APPLICANT: Michael Mittmann

APPLICANT: David Lockhart

APPLICANT: David Mack

APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFREENCE: 3101.1

CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-09-15

NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FREESE for Mindows Version 4.0
                                                                                                                                                                                                                                                           Query Match 67.4%; Score 12.8; DB 3;
Best Local Similarity 87.5%; Pred. No. 3.5e+03;
                                                                                                                                                                                                                                                                                                           0; Mismatches
       TELEX: 904136

INFORMATION FOR SEQ ID NO: 29:
SEGUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: other nucleic acid
SCRLPTION: /desc = "primer"
US-08-666-221B-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 43, Application US/07951715A Patent No. 5625136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Koziel, Michael G.
APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Wola, Stephen V.
APPLICANT: Wright, Martha S.
APPLICANT: Mright, Martha S.
APPLICANT: Mright, Martha S.
APPLICANT: Rochstein, Steven J.
                                                                                                                                                                                                                                                                                                                                                           2 GGGTGACGTTCAGGGG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GGGTGACGTTCAGGGG 17
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Suttie, Janet L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dawson, John L.
Dunder, Erik M.
                                                                                                                                                                                                                                                                                                                                                                                                       16 GGGTGATGGTCAGGGG 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 87.5'
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-396-196G-120261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
US-07-951-715A-43/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 120261
LENGTH: 25
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                Matches
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Gaps

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Warren, Gregory W.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Merlin, Ellis J.
APPLICANT: Bowman, Clindy G.
APPLICANT: Bowman, Clindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dawson, John L.
APPLICANT: Dauson, John L.
APPLICANT: Dauson, John L.
APPLICANT: Suctie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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            CORRESPONDED TO THE STATE OF THE STATE OF THE STATE OF THE STREET: Patent & Trademark Dept., 520 White Plains STREET: Patent & Trademark Dept., 520 White Plains STREET: Rd., POB 2005
CITY: Tarrytown STREET: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                        OPERATION SYSTEM:

OPERATION OF PACEDOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,595A

FILING DATE: 02-JUN-1995

CLASSIFICATION: 800

PRIOR APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

PRIOR APPLICATION NUMBER: US 07/72,027

FILING DATE: 04-OCT-1991

ATFORNEY/AGENT NUMBER: US 07/72,027

FILING DATE: 04-OCT-1991

ATFORNEY/AGENT NUMBER: 40403

REGISTRATION NUMBER: 40403

REGISTRATION NUMBER: 40403

REGISTRATION NUMBER: 40403

RELEPRA: (919)541-8692

INTELEPRA: (919)541-8692

INTELEPRA: 25-BASE PAIFS

SEQUENCE CHARACTERISTICS:

LENGTH: 32-BASE PAIFS

TVPR: LENGTH: 32-BASE PAIFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 67.4%; Score 12.8; DB 3; Best Local Similarity 87.5%; Pred. No. 3.7e+03; Matches 14; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /desc = "primer P5(a)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 43, Application US/08459504B Patent No. 6075185 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 GGTGACGTTCAGGGGG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nu
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DESCRIPTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.4%; Score 12.8; DB 2; Length 32;
87.5%; Pred. No. 3.7e+03;
tive 0; Mismatches 2; Indels
                  ADDRESSEE: No. 5859336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA
                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: U$ 07/951,715

FILING DATE: 25-SEP-1992

PRIOR APPLICATION NUMBER: U$ 07/772,027

FILING DATE: 64-OCT-1991

APPLICATION NUMBER: U$ 07/772,027

FILING DATE: 64-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Pace, Gary M.

REGISTRATION NUMBER: GG 1577/CIP/DIV4

TELECOMMULICATION INFORMATION:

NAME: Pace, Gary M.

RESTERNICE/DOCKET NUMBER: GG 1577/CIP/DIV4

TELECOMMULICATION INFORMATION:

TELEBHONE: 04-18-882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer P5(a)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 43, Application US/08459595A
Patent No. 6018104
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Bllis J.
Launis, Karen L.
Rothstein, Steven J.
Bowman, Cindy G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Desai, Nalini M.
Lewis, Kelly S.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 87.5
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
US-08-459-595A-43/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-459-448A-43
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT:
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us-09-669-187a-80.szlm50.rni

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ADDRESSEE: No. 6320100artis Agribusiness Biotechnology Research, Inc. STREET: 3054 Cornwallis Road CITY: Research Triangle Park
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                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,444A
FILING DATE: 02-Jun-1995
CLASSIFICATION NUMBER: US/08/1715
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/772,027
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-007-1991
ATTORNEY/AGENT INFORMATION:
NAME: Maigs, J. Timothy
REGISTRATION NUMBER: 8-18805/P1/CGC1577/CIP/DIV6
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 100-941-8689
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 12.8; DB 3;
Pred. No. 3.7e+03;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "primer P5(a)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
STREET: 3054 Cornwallis Road CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 16
US-09-547-422-43/C
is Sequence 43, Application US/09547422
is Patent No. 6320100
is GENERAL INFORMATION:
is APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Ewwis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Merlin, Ellis J.
                                                                                                                                         MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 32 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.4%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 GGTGACGTTCAGGGGG 18
                                                                                                              COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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Best Local Similarity 87.5
Matches 14; Conservative
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COUNTRY: USA
ZIP: 27709
                                                                   USA
                                                                                             ZIP: 27709
                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-459-444-43
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ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 67.4%; Score 12.8; DB 3; Length 32; I Similarity 87.5%; Pred. No. 3.7e+03; 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                             COMPUTER : USA

CUNTER: USA

CUNTER: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,504B
FILING DATE:
CLASSIFICATION:
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-401-1992
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
RICK APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-0CT-1991
ATTORNEY/AGENT INFORMATION:
NAMME: Meigs J. TIMOCHY
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
TELECOMMUNICATION NUMBER: CGC1577/CIP/DIV
TELECOMMUNICATION NUMBER: CGC1577/CIP/DIV
TELECOMMUNICATION NUMBER: CGC1577/CIP/DIV
  INSECTICIDAL ACTIVITY IN MAIZE
                                      AUDRESSEE: No. 6075185artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             other nucleic acid
/desc = "primer P5(a)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 43, Application US/0845944AA Patent No. 6121014
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G. Desai, Nalini M. Lewis, Kelly S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Crossland, Lyle D. Wright, Martha S. Merlin, Ellis J. Launis, Karen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GGTGACGTTCAGGGGG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 32 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
  TITLE OF INVENTION: IN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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US-08-459-444-43/c
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                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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APPLICANT: Woldgemuth, Jay

APPLICANT: Woldgemuth, Jay

APPLICANT: Woldgemuth, Jay

APPLICANT: Fry, Kirk

APPLICANT: Woodward, Robert

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE

FILE REPERBUCE: 50641200120

CURRENT FILING DATE: 2002-09-06

PRIOR APPLICATION NUMBER: US 10/006,290

PRIOR APPLICATION NUMBER: US 60/296,764

PRIOR APPLICATION NUMBER: US 60/296,764

PRIOR FILING DATE: 2001-06-08

NUMBER OF SEQ ID NOS: 9090

SOFTWARE: PatentIn version 3.1

SEQ ID NO 4733

LENGTH: 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 50;
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                      APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-No. 6720488-2001
CLASSIPICATION: -Unknown>
PRIOR APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APP-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-UNN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/72,027
FILING DATE: 04-OCT-1991
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer P5(a)"
                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REPERENCE/DOCKET NUMBER: 3-188051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8689
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; SEQUENCE DESCRIPTION: SEQ ID NO: 43: US-09-988-462-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 4733, Application US/10131827; Patent No. 6905827; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 32 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 GGTGACGTTCAGGGGG 18
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US-10-131-827-4733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-131-827-4733/c
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                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,422
FILING DATE: 11-Apr-2000
CLASSIFICATION NUMBER: US/09/595
FILING DATE: 02-UN-1995
APPLICATION NUMBER: US 08/459,595
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/72,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: MAGEN MAGEN: 38,241
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: $-18805H
TELECOMMUNICATION NOMBER: $-18805H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 67.4%; Score 12.8; DB 3; Length 32; Best Local Similarity 87.5%; Pred. No. 3.7e+03; Matches 14; Conservative 0; Mismatches 2; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFFATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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ADDRESSER: Syngenta Biotechnology, Inc.
STREET: 3054 COrnwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DESCRIPTION: /desc = "primer P5(a)" HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; SEQUENCE DESCRIPTION: SEQ ID NO: 43: US-09-547-422-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 43. Application US/09988462; Sequence 43. Application US/0998462; Patent No. 6720488; GENERAL INFORMATION:
APPLICANT: Koziel, Michael G. Lewis, Kelly S. Kramer, Vance C. Warren, Gregory W. Evola, Stephen V. Crossland, Lyle D. Wright, Martha S. Marin, Blis J. Launis, Karen L.
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 32 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GGTGACGTTCAGGGGG 18
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US-09-988-462-43/c
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GENERAL INFORMATION:

APPLICANT: Krieg, Arthur M.

APPLICANT: Schwartz, David M.

TITLE OF INVENTION: UNMETHYLATED CDG DINUCLEOTIDE IN THE TREATMENT OF TITLE OF INVENTION: UNMETHYLATED DISORDERS

TITLE OF INVENTION: LES-ASSOCIATED DISORDERS

TITLE OF INVENTION: LES-ASSOCIATED DISORDERS

FILE REFERENCE: C1039/7011

CURRENT FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 06/039,405

PRIOR APPLICATION NUMBER: 66/039,405

PRIOR APPLIAGO ATE: 1999-02-26

NUMBER OF SEQ ID NOS: 65

SOUTHARE: PASISEQ for Windows Version 3.0

SEQ ID NO 63

LENGTH: 20
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APPLICANT: Krieg et al.,
TITLE OF SEQUENCE: INMUNOSTIMULATORY NUCLEIC ACID MOLECULES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
                                                                                                                         Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
TURING DATE: 30-October-1997
CLASSIFCATION: 514
PRICR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 20;
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                                                                                                                                                                                           4; Indels
                                                                                                                     Query Match
66.3%; Score 12.6; DB 3;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 12.6; DB 3;
Pred. No. 4.4e+03;
0; Mismatches 4;
             ; OTHER INFORMATION: Synthetic oligonucleotide US-08-738-652-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: synthetic oligonucleotide US-09-030-701-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-030-701-63
; Sequence 63, Application US/09030701B
; Patent No. 6214806
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Patent No. 6239116
                                                                                                                                                                                                                                                             1 GGGGTGACGTTCAGGGGGG 19
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 78.9
Matches 15; Conservative
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USA
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US-08-960-774-90
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FEATURE:
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Sequence 12, Application US/08738652B

Sequence 12, Application US/08738652B

Sequence 12, Application US/08738652B

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                                                                                                                                                                                                                                                  APPLICANT: Hartmann, Gunther
APPLICANT: Hartmann, Gunther
APPLICANT: Eratzler, Robert L.
APPLICANT: Krieg, Arthur
TITLE OF INVENTION: Methods Related to Immunostimulatory
TITLE OF INVENTION: Mucleic Acid-Induced Interferon
FILE REPRENCE: C1039/7044
CURRENT FILING DATE: 1200-09-27
PRIOR APPLICATION NUMBER: 60/156,147
PRIOR APPLICATION NUMBER: 60/156,147
PRIOR APPLICATION NUMBER: 60/156,147
NUMBER OF SEQ ID NOS: 169
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (1)...(2)
OTHER INFORMATION: Backbone has phosphorothioate linkages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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NAME/KEY: misc_feature
LOCATION: (14)...(18)
OTHER INFORMATION: Backbone has phosphorothioate linkages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (3)...(13)
OTHER INFORMATION: Backbone has phosphodiester linkages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . LOCATION: (19)...(19)
; OTHER INFORMATION: Backbone has phosphodiester linkages.
US-09-672-126B-27
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66.3%; Score 12.6; DB 3;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Synthetic Oligonucleotide
                                                                                                                                                            Sequence 27, Application US/09672126B Patent No. 6949520 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GGGGTGACGTTCAGGGGGG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
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      21 GTGACGTTCTGGGAGG
                                                                                                                                   US-09-672-126B-27
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US-08-738-652-12
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LENGTH: 19
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic oligonucleotide
NAME/KSY: misc feature
LOCATION: (0)...(0)
OTHER INFORMATION: Has SOS-ODN backbone with two S-linkages at the 5'
OTHER INFORMATION: end, five S-linkages at the 3' end, and O-linkages
US-09-082-649B-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                          APPLICANT: Schorr, Joachim
APPLICANT: Wu, Tong
TITLE OF INVENTION: Vectors and Methods for Immunization or
TITLE OF INVENTION: Therapeutic Protocols
FILE REFERENCE: C1039/7009
CURRENT APPLICATION NUMBER: US/09/082,649B
CURRENT FILING DATE: 1998-05-20
PRIOR APPLICATION NUMBER: US 60/047,233
PRIOR APPLICATION NUMBER: US 60/047,209
PRIOR FILING DATE: 1997-05-20
NUMBER OF SEQ ID NOS: 85
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Krieg, Arthur M.
APPLICANT: Krieg, Arthur M.
APPLICANT: Hartmann, Gunther
TITLE OF INVENTION: Tor Activating Dendritic Cells
TITLE OF INVENTION: For Activating Dendritic Cells
FILE REFERENCE: C1039/7017
CURRENT APPLICATION NUMBER: US 08/960,774
EARLIER FILING DATE: 1998-11-13
EARLIER APPLICATION NUMBER: US 08/738,652
EARLIER APPLICATION NUMBER: US 08/738,652
EARLIER APPLICATION NUMBER: US 08/738,653
EARLIER APPLICATION NUMBER: US 08/26,063
EARLIER FILING DATE: 1995-02-07
EARLIER FILING DATE: 1994-07-15
NUMBER OF SEQ ID NOS: 99
SOFTWARE: RateSEQ for Windows Version 3.0
LENGTH: 20
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66.3%; Score 12.6; DB 3; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels
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Patent No. 6429199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GGGGTGACGTTCAGGGGGG 19
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          Krieg, Arthur M.
Schorr, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 78.9
Matches 15, Conservative
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US-09-191-170-47
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APPLICANT: Edvis, Arthur M.
APPLICANT: Schort, Joachim
APPLICANT: Schort, Joachim
APPLICANT: Genor, Joachim
TITLE OF INVENTION: Vectors and Methods for Immunization or TITLE OF INVENTION: Therapeutic Protocols
FILE REFERENCE: Classification NUMBER: US/09/082,649B
CURRENT APPLICATION NUMBER: US 60/047,233
FRIOR FILING DATE: 1999-05-20
FRIOR FILING DATE: 1997-05-20
FRIOR FILING DATE: 1997-05-20
NUMBER OF SEQ ID NOS: 85
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 66.3%; Score 12.6; DB 3; Length 20; Best Local Similarity 78.9%; Pred. No. 4.4e+03; Matches 15; Conservative 0; Mismatches 4; Indels
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NAME/KEY: misc_feature
; LOCATION: (0) ...(0)
; OTHER INFORMATION: Has a phosphorothioate backbone.
US-09-082-649B-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 66.3%; Score 12.6; DB 3; Best Local Similarity 78.9%; Pred. No. 4.4e+03; Matches 15; Conservative 0; Mismatches 4;
FILING DATE: October 30, 1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REGISTRATION NUMBER: 38,347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5090
INFORMATION FOR SEQ ID NO: 90: SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 52, Application US/09082649B
Patent No. 6319068
GENERAL INFORMATION:
APPLICANT: Davis, Heather L.
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US-09-082-649B-59
Sequence 59, Application US/09082649B
Patent No. 6339068
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
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MOLECULE TYPE: CDNA
US-08-960-774-90
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US-09-672-126B-1; Sequence 1, Application US/09672126B; Patent No. 6949520
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Patent No. 6821957
1 GGGGTGACGTTCAGGGGGG 19
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Best Local Similarity 78.9
Matches 15, Conservative
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US-09-965-101-52
; Sequence 52, Application US/09965101
; Patent No. 6821957
; GENERAL INFORMATION:
APPLICANT: Davis, Heather I.
APPLICANT: Schorr, Joachim
APPLICANT: Schorr, Joachim
APPLICANT: Schorr, Joachim
APPLICANT: Wu, Tong
TITLE OF INVENTION: Therapeutic Protocols
TITLE OF INVENTION: Therapeutic Protocols
TITLE OF INVENTION: Therapeutic Protocols
FILE REFERENCE: C1039/7057 (HCL/MAT)
CURRENT APPLICATION NUMBER: US 09/082,649
PRIOR FILING DATE: 1997-05-20
PRIOR APPLICATION NUMBER: US 60/047,233
PRIOR APPLICATION NUMBER: US 60/047,233
PRIOR APPLICATION NUMBER: US 60/047,209
PRIOR APPLICATION NUMBER: US 60/047,209
PRIOR PILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 52
LENGTH: 20
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                                             GENERAL INFORMATION:
APPLICANT: Krieg Arthur M.
APPLICANT: Krieg Arthur M.
TITLE OF INVENTION: Methods of Treating Cancer Using
TITLE OF INVENTION: Methods of Treating Cancer Using
TITLE OF INVENTION: Methods of Treating Cancer Using
FILE REFERENCE: C1039/7021/HGL
CURRENT TAILNG DATE: 1990-06-21
CURRENT FILING DATE: 1990-06-21
EARLIER APPLICATION NUMBER: US 08/366, 774
EARLIER FILING DATE: 1997-10-30
EARLIER FILING DATE: 1996-10-30
EARLIER PELLORY ON WUMBER: US 08/386, 063
EARLIER RELING DATE: 1996-10-30
EARLIER RELING DATE: 1996-10-37
EARLIER REPLING DATE: 1994-07-15
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FatESEQ for Windows Version 3.0
EARLIER PELLORY
SEQ ID NO 12
EARLIER PELLORY
EARLIER APPLICATION NUMBER: US 08/276, 358
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66.3%; Score 12.6; DB 3;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4;
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   Sequence 12, Application US/09337619
Patent No. 6653292
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US-09-965-101-59
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JAPPLICANT: Krieg, Arthur M.
JAPPLICANT: Krieg, Arthur M.
JAPPLICANT: Schort, Joachim
JAPPLICANT: Schort, Joachim
JAPPLICANT: Schort, Joachim
JAPPLICANT: Schort, Joachim
JAPPLICANT: With Tong
JIILE OF INVENTION: Vectors and Methods for Immunization or
JIILE OF INVENTION: Therapeut. Protocols
JIILE OF INVENTION: Therapeut. Protocols
JIILE REFERENCE: C1039/7057 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/965,101
CURRENT PILING DATE: 1998-05-20
PRIOR PILING DATE: 1998-05-20
PRIOR PILING DATE: 1997-06-20
PRIOR PILING DATE: 1997-06-20
PRIOR FILING DATE: 1997-05-20
NUMBER: FEASTER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 20
Query Match 66.3%; Score 12.6; DB 3; Length 20; Best Local Similarity 78.9%; Pred. No. 4.4e+03; Matches 15; Conservative 0; Mismatches 4; Indels
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| GENERAL INFORMATION: |
| APPLICANT: Hartmann, Gunther |
| APPLICANT: Brazzler, Robert L. |
| TITLE OF INVENTION: Methods Related to Immunostimulatory |
| TITLE OF INVENTION: Mucleic Acid-Induced Interferon |
| FILE REPRENCE: C1039/7044 |
| CURRENT APPLICATION NUMBER: US/09/672,126B |
| CURRENT APPLICATION NUMBER: US/09-27 |
| PRIOR PILING DATE: 1999-09-29 |
| NUMBER OF SEQ ID NOS: 169 |
| SOFFWARE: FastSEQ for Windows Version 3.0 |
| SEQ ID NO 1 |
| LENGTH: 20 |
| TYPE: DNA
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Score 12.6; DB 3; Length 20; Pred. No. 4.4e+03;
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; Battent No. 6949520
; GENERAL INFORMATION:
    APPLICANT: Hartmann, Gunther
; APPLICANT: Brateler, Robert L.
; APPLICANT: Brateler, Robert L.
; APPLICANT: Brateler, Robert L.
; TITLE OF INVENTION: Methods Related to Immunostimulatory; TITLE OF INVENTION: Mucleic Acid-Induced Interferon; FILE REFERENCE: 10139/7044
; CURRENT APPLICATION NUMBER: US/09/672,126B
; CURRENT PAPLICATION NUMBER: 60/156,147
; PRIOR PILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 169
; SCOTWARE: FESTESEQ for Windows Version 3.0
; SEQ ID NO 136
LENTH: 20
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            APPLICANT: Bratzler, Robert L.
APPLICANT: Krieg, Arthur
TITLE OF INVENTION: Methods Related to Immunostimulatory
TITLE OF INVENTION: Mucleic Acid-Induced Interferon
FILE REFERENCE: C1039/7044
CURRENT APPLICATION NUMBER: US/09/672,126B
CURRENT FILING DATE: 2000-09-27
PRIOR FILING DATE: 1999-09-29
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Patent No. 6949520
REDERAL INFORMATION:
APPLICANT: Bratchann, Gunther
APPLICANT: Bratcher, Robert L.
APPLICANT: Krieg, Arthur
TITLE OF INVENTION: Methods Related to Immunostimulatory
TITLE OF INVENTION: Nucleic Acid-Induced Interferon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , OTHER INFORMATION: Synthetic Oligonucleotide US-09-672-126B-136
                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Synthetic Oligonucleotide
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 135
LENGTH: 20
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Best Local Similarity 78.9%;
Matches 15; Conservative
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APPLICANT: Hartmann, Gunther
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 78.9
Matches 15, Conservative
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US-09-672-126B-136
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APPLICANT: Krieg, Arthur
TITLE OF INVENTION: Methods Related to Immunostimulatory
TITLE OF INVENTION: Mucleic Acid-Induced Interferon
TITLE OF INVENTION: Nucleic Acid-Induced Interferon
FILE REFERENCE: C1039/7044
CURRENT APPLICATION NUMBER: US/09/672,126B
CURRENT FILING DATE: 2000-09-27
PRIOR PILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 169
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 20
                                                                                          NAME/KEY: misc_feature
COCATION: (1)...(2)
COTHER INFORMATION: Backbone has phosphorothioate linkages.
FEATURE:
MAME/KEY: misc_feature
LOCATION: (3)...(14)
OTHER INFORMATION: Backbone has phosphodiester linkages.
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NAME/KEY: misc_feature
LOCATION: (15)...(19)
OTHER INFORMATION: Backbone has phosphorothioate linkages.
PEATURE:
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; OTHER INFORMATION: Backbone has phosphorothioate linkages. US-09-672-1268-5
                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (20) ...(20)
OTHER INFORMATION: Backbone has phosphodiester linkages.
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Pred. No. 4.4e+03;
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OTHER INFORMATION: Synthetic Oligonucleotide
                                               OTHER INFORMATION: Synthetic Oligonucleotide
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US-09-672-126B-135
Sequence 135, Application US/09672126B
Patent No. 6949520
GENERAL INFORMATION:
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Patent No. 0549520
GENERAL INFORMATION:
APPLICANT: Hartmann, Gunther
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78.9%;
ORGANISM: Artificial Seguence
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ORGANISM: Artificial Sequence
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Best Local Similarity 78.9
Matches 15; Conservative
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US-09-672-126B-5
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; OTHER INFORMATION: Synthetic Oligonucleotide US-09-672-126B-165
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Best Local Similarity 78.9%; Pred. No. 4.6e
Matches 15; Conservative 0; Mismatches
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.; Sequence 225, Application US/09907794A
.; Patent No. 6655468
.; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Godowski, Paul J.
Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
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Gerber, Hanspeter
Gerritsen, Mary E.
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Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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      US-09-672-126B-165
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                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (1)...(2)
OTHER INFORMATION: Backbone has phosphorothioate linkages.
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LOCATION: (16) ... (20)
OTHER INFORMATION: Backbone has phosphorothioate linkages.
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OTHER INFORMATION: Backbone has phosphodiester linkages
                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (3).7.(15)
OTHER INFORMATION: Backbone has phosphodiester linkages
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US-09-396-196G-78259/C

Sequence 78259 Application US/09396196G

Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Lockhart
CURRENT PAPLICANTON NUMBER: US/09/396,196G
CURRENT APPLICANTON NUMBER: 60/100,678
PRIOR APPLICANTON NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
FILE REFERENCE: C1039/7044

CURRENT APPLICATION NUMBER: US/09/672,126B

CURRENT FILING DATE: 2000-09-27

FRIOR APPLICATION NUMBER: 60/156,147

PRIOR FILING DATE: 1999-09-29

NUMBER OF SEQ ID NOS: 169

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 21
                                                                                                                                                                                                                                                                         OTHER INFORMATION: Synthetic Oligonucleotide
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                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
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NAME/KEY: misc_feature
LOCATION: (3)...(15)
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Best Local Similarity
Matches 15; Conserv
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RESULT 35

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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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Sequence 165, Application US/09672126B
; Sequence 165, Application US/09672126B
; Patent No. 6949520
; GENERAL INFORMATION:
    APPLICANT: Hartmann, Gunther
; APPLICANT: Brateler, Robert L.
; APPLICANT: Brateler, Robert L.
; APPLICANT: Krieg, Arthur
; TITLE OF INVENTION: Methods Related to Immunostimulatory;
TITLE OF INVENTION: Nucleic Acid-Induced Interferon
; TILE REFERENCE: 10139/7044
; CURRENT APPLICATION NUMBER: 0/09-07-7
; PRIOR PLIING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: FESTSEQ for Windows Version 3.0
; SEQ ID NO 165
; LENGTH: 30
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Pred. No. 4.6e+03;
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CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR PLING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PLING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Walliams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: 10466-14
CURRENT FILING DATE: 2001-07-12
PRIOR PLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-09-06
PRIOR FILING DATE: 1999-09-06
PRIOR FILING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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PRIOR PELICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-30
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; Sequence 225, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
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                          Roy, Margaret Ann
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botsein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-20
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2-09-905-125A-225/c
; Sequence 225, Application US/09905125A
; Patent No. 6664376
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Grimaldi, Christopher J.
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Hillan, Kenneth, J
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Filvaroff, Ellen
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Gerritsen, Mary E.
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Mather, Jennie P.
Pan, James
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botsein, David
APPLICANT: Baton, Darid
APPLICANT: Baton, Dan L.
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Best Local Similarity 78.9
Matches 15, Conservative
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Gao, Wei-Qiang
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APPLICANT: Williams, P. Mickey
APPLICANT: William, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: 10466-1040-18
FILE REPERSOR: 10466-1040-18
FILE APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 1999-07-07-08
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-03
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/2054
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21309
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/2814
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-12-26
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FILING DATE: 1999-12-20
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Sequence 225, Application US/09906700
Patent No. 6723535
GENERAL INFORMATION:
APPLICANT: Genenech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Betkenazi, Avi
APPLICANT: Betkenazi, Avi
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                 19 GGAGCGTCGCTCAGGGGGG
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Filvaroff, Ellen
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Goddard, A.
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Gao, Wei-Qiang
Gerber, Hanspeter
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Eaton, Dan L.
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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   Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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ORGANISM: Artificial Seguence
                                                                                                                     Gerber, Hanspeter
Gerritsen, Mary E
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APPLICATION NUMBER: PCT/US99/28214
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APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: William, P. Mickey
APPLICANT: William, P. Mickey
APPLICANT: William, P. Mickey
APPLICANT: William, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: GNE. 161892.02
CURRENT APPLICATION NUMBER: US/09/903,603A
CURRENT FILING DATE: 2000-02-22
RIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/146,22
PRIOR PLING DATE: 1999-07-08
PRIOR PLING DATE: 1999-07-08
PRIOR PLING DATE: 1999-07-08
PRIOR PLING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: PCT/US99/2094
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: POST/US99/23089
PRIOR PLING DATE: POST/US99/23089
PRIOR PLING DATE: POST/US99/23089
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VS-09-903-603A-225/c
Sequence 225, Application US/09903603A
Patent No. 6767995
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jannie P.
Pan, James
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Filvaroff, Ellen
                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 225
LENGTH: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
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APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: William, P. Mickey
APPLICANT: William, I.
APPLICANT: Wood, William, I.
APPLICANT: Wood, William, I.
APPLICANT: Mode William, I.
APPLICANT: Mode Borotted and Transmembrane Polypeptides and Nucleic
IITLE OF INVENTION: Acids Encoding the Same
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PRIOR FILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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CURRENT APPLICATION NUMBER: US/09/904,920A
CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
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; Sequence 225, Application US/09904920A
; Patent No. 6806352
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Godowski, Paul J.
Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ferrara, Napoleone
Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goddard, A.
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APPLICANT: Williams, bantel, APPLICANT: Williams, bantel, APPLICANT: Williams, bantel, APPLICANT: Williams, bantel, APPLICANT: Williams, b. Mickey, APPLICANT: Wood, William, I.
ITILE OF INVENTION: Acids Encoding the Same
PILE REPRENEUE: 10466-1.
ITILE REPRENEUE: 10466-1.
ITILE APPLICATION NUMBER: 107/050/0414
PRIOR APPLICATION NUMBER: US/09/909,064
CURRENT FILING DATE: 2001-07-18
PRIOR PILLING DATE: 1999-07-26
PRIOR PILLING DATE: 1999-09-18
PRIOR PELLING DATE: 1999-10-05
PRIOR PELLING DATE: 1999-10-05
PRIOR PELLING DATE: 1999-10-05
PRIOR PELLING DATE: 1999-11-29
PRIOR PELLING DATE: 1999-11-29
PRIOR PELLING DATE: 1999-11-20
PRIOR PELLING DATE: 1999-11-20
PRIOR PELLING DATE: 1999-11-20
PRIOR PELLING DATE: 1999-12-06
PRIOR PELLING DATE: 1999-12-07
PRIOR PELLING DATE: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: oligonucleotide probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.3%; Score 12.6; DB 3; 78.9%; Pred. No. 4.8e+03; tive 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-905-381A-225/C
US-09-905-381A-225/C
US-09-905-381A-225/C
PATENT NO. 6818746
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGGGTGACGTTCAGGGGGG 19
                                                                           Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 deadcercecrcadeded
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ORGANISM: Artificial Sequence
FEATURE:
                                           Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 78.9
Matches 15; Conservative
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PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
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PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
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PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
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PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-06
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Patent No. 6818449
GENERAL INFORMATION:
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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ORGANISM: Artificial Sequence
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Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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US-09-909-064-225/c
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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0; Gaps

Indels

4 ;

0; Mismatches

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15; Conservative
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Matches
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PPLICANT: Mather, James
PPLICANT: Pand, Micholas F.
PPLICANT: Milliam, P. Micholas F.
PPLICANTON NOBER: US/09/965,381A
CUDREMENT APPLICANTON NOBER: US/09/965,381A
CUDREMENT APLICATION NOBER: US/01/45,698
PRIOR PLILING DATE: 1999-07-28
PRIOR PLILING DATE: 1999-07-28
PRIOR PLILING DATE: 1999-09-08
PRIOR PLILING DATE: 1999-09-09
PRIOR PLILING DATE: 1999-09-09
PRIOR PLILING DATE: 1999-09-09
PRIOR PLILING DATE: 1999-09-12
PRIOR PLILICATION NUMBER: PCT/US99/2030
PRIOR PLILING DATE: 1999-09-12
PRIOR PLILICATION NUMBER: PCT/US99/2030
PRIOR PLILING DATE: 1999-10-20
PRIOR PLILING DATE: 1999-10-20
PRIOR PLILING DATE: 1999-10-20
PRIOR PLILICATION NUMBER: PCT/US99/20314
PRIOR PRIOR DATE: 1999-11-20
PRIOR PRIOR PLILICATION NUMBER: PCT/US99/20313
PRIOR PLILICA
                                                                                                                                                                                                                                                         Godowski, Paul J.
Grimaldi, Christopher J.
                                                                                                                                                                                                                                                                                                                      Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
                                                                                                                Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
                           Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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66.3%; Score 12.6; DB 3; Length 44; 78.9%; Pred. No. 4.8e+03;

Query Match Best Local Similarity

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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,618
CURRENT FILING DATE: 2001-07-16
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PRIOR PILLING DATE: 2000-02-27
PRIOR FILLING DATE: 2000-02-27
PRIOR PILLING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILLING DATE: 1999-07-07
PRIOR PILLING DATE: 1999-07-26
PRIOR PILLING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILLING DATE: 1999-07-28
PRIOR PILLING DATE: 1999-09-08
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APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
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APPLICATION NUMBER: PCT/US99/28313
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FILING DATE: 1999-12-20
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                                                                                                                                                    US-09-906-618-225/c
; Sequence 225, Application US/09906618
; Patent No. 6828146
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
1 GGGGTGACGTTCAGGGGGG 19
                                              19 GGAGCGTCGCTCAGGGGGG 1
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Gao, Wei-Qiang
Gerber, Hanspeter
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Mather, Jennie P.
Pan, James
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                                                                                                                                                                                                                                                         APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L
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HITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IIILE OF INVENTION: Acids Encoding the Same
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                      PRIOR MILING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
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PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-26
PRIOR PLING DATE: 1999-12-26
PRIOR PLING DATE: 1999-12-26
PRIOR PLING DATE: 1999-12-26
PRIOR PLING DATE: 1999-12-36
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CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: 09/665,350
     APPLICATION NUMBER: PCI/US99/23089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 225, Application US/09904462
Patent No. 6878807
GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description
OTHER INFORMATION: oligonuclec
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Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hillan, Kenneth, J
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Gerber, Hanspeter
Gerritsen, Mary E.
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Mather, Jennie P.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 46
US-09-904-462-225/c
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APPLICANT:
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APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart. Timothy A.
APPLICANT: Tumes, Daniel
APPLICANT: Tumes, Daniel
APPLICANT: Tumes, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
CURRENT FILING DATE: 2000-01-22
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
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PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 225
LENGTH: 44
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Patent No. 6852848
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Filvaroff, Ellen
                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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Best Local Similarity 78.94
These 15; Conservative
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US-09-906-646-225/c
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APPLICANT:
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: William, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,736A
CURRENT FILING DATE: 2001-07-10
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PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR PILING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-30
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423

LENGTH: 44
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PRIOR PLILING DATE: 2001-07-10
PRIOR PLILING DATE: 2000-02-22
PRIOR PLILING DATE: 1000-02-22
PRIOR PLILING DATE: 1999-07-07
PRIOR PLLING DATE: 1999-07-07
PRIOR PLLING DATE: 1999-07-28
PRIOR PLLING DATE: 1999-09-08
PRIOR PLLING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21647
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US-09-906-722A-225/c
Sequence 225, Application US/09906722A
; Patent No. 6946262
; GENERAL INFORMATION:
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                 Hillan, Kenneth, J
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                                                                                                                                                Paoni, Nicholas F.
                                                    Kljavin, Ivar J.
Mather, Jennie P.
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Best Local Similarity 78.9
Matches 15; Conservative
                                                                                                                Pan, James
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PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR PILING DATE: 2000-02-22
PRIOR PILING DATE: 1990-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-08
PRIOR PLING DATE: 1999-07-08
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-0-28
PRIOR PLING DATE: 1999-09-18
PRIOR PLING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-20
PRIOR PLING DATE: 1999-11-20
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
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PRIOR PLING DATE: 1999-12-06
PRIOR PRIOR DATE: 1999-12-07
PRIOR PRIOR DATE: 1999-12-07
PRIOR PRIOR DATE: 1999-12-06
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US-09-902-736A-225/c
Sequence 225, Application US/09902736A
Patent No. 689414B
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Gerritsen, Mary E.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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LENGTH: 44
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APPLICANT:
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APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, 11ya
APPLICANT: Chumakov, 11ya
APPLICANT: Cohen, Annick
APPLICANT: Cohen, Annick
APPLICANT: Cohen, Annick
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILLE REPRENDE: GENEST: 051CP1
CURRENT APPLICATION NUMBER: US 09/502,330
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR PILING DATE: 2000-02-11
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1999-01-23
PRIOR PILING DATE: 1999-02-12
PRIOR PILING DATE: 1999-01-23
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Sequence 1255, Application US/10170097

Sequence 1255, Application US/10170097

GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Bouqueleret, Lydie
APPLICANT: Cohen, Annick
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: GEN-T114XC2D1
CURRENT FILING DATE: 2002-06-10
CURRENT FILING DATE: 2002-06-10
PRIOR PILING DATE: 2000-08-16
PRIOR FILING DATE: 2000-08-16
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR PLING DATE: 2000-02-11
PRIOR PLING DATE: 2000-02-11
PRIOR PLING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
                   66.3%; Score 12.6; DB 3; Length 44; 78.9%; Pred. No. 4.8e+03; ive 0; Mismatches 4; Indels
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NAME/KEY: allele

LOCATION: 24

OTHER INFORMATION: 10-387-371 : polymorphic base C or T
US-09-641-638-1255
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                                                                                                                                                                                                                                                                                                                                                                                     US-09-641-638-1255/c; Sequence 1255, Application US/09641638; Patent No. 6432648
                                                                                                                                                                         1 GGGGTGACGTTCAGGGGGG 19
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APPLICANT: Blumenfeld, Marta
                       Query Match
Best Local Similarity 78.9°
Matches 15; Conservative
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ORGANISM: Homo Sapiens
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Best Local S
Matches 15
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acide Encoding the Same FILE REPERBARE: GNR. 161892661
CURRENT APPLICATION NUMBER: US/09/906,722A
CURRENT APPLICATION NUMBER: US/01-07-16
PRIOR PLING DATE: 2001-07-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PLING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PLING DATE: 1999-07-08
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-08
PRIOR PRIOR MAREN: US 60/146,222
PRIOR PRIOR DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-05
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-01-15
PRIOR PLING DATE: 1999-10-29
PRIOR PLING DATE: 1999-10-29
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
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CRGANISM: Artificial Sequence
FATURE:
COTHER INFORMATION: Description of Artificial Sequence: Synthetic
COTHER INFORMATION: oligonucleotide probe
US-09-906-722A-225
                                                                                                                                                                                                                                                                                                                                                                                                                                   Godowski, Paul J.
Grimaldi, Christopher J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Williams, P. Mickey
Wood, William, I.
                                                                                                                                                                                                                                                  Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                         Ferrara, Napoleone
Filvaroff, Ellen
                              Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 423
SEQ ID NO 225
LENGTH: 44
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APPLICANT:
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sequence 1, Appli
sequence 224, Appli
sequence 1, Appli
sequence 32, Appli
sequence 1, Appli
sequence 29133,
sequence 29133,
sequence 21, Appl
sequence 22, Appl
sequence 521, Appl
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Sequence 133352,
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414070,
651111,
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                   Sequence
US-10-314-578-224
US-10-631-676-1
US-10-630-495-1
US-10-789-95-1
US-10-888-885-1
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US-10-818-659-63
US-10-818-659-63
US-10-818-659-63
US-11-067-516-1
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US-10-036-317-982239
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US-09-911-904-180
US-10-719-900-460201
US-10-956-157-223860
US-10-194-882-1
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US-10-719-900-651111
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Sequence 74, Appl
Sequence 80, Appl
Sequence 80, Appl
Sequence 44, Appl
Sequence 82, Appl
Sequence 82, Appl
Sequence 82, Appl
Sequence 82, Appl
Sequence 81, Appl
Sequence 81, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 224, Appl
                                                                                                             February 16, 2006, 01:43:22; Search time 275.736 Seconds (without alignments) 569.815 Million cell updates/sec
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/ cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/USIO8_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/USIO8_PUBCOMB.seq:*
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                     GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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US-09-776-479-80
US-09-776-479-80
US-10-112-653-74
US-10-017-995-80
US-10-314-578-80
US-10-314-578-80
US-09-888-326-448
US-09-776-479-82
US-09-776-479-82
US-10-112-653-76
US-10-113-453-78
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US-09-888-326-449
US-09-91-583-1
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US-10-112-653-216
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                                                                                 OM nucleic - nucleic search, using sw model
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Sequence 319, Appl Sequence 519, Appl Sequence 767, Appl Sequence 968, Appl Sequence 969, Appl Sequence 14, Appl Sequence 4, Appli	Sequence 12, Appl Sequence 52, Appl Sequence 59, Appl Sequence 12, Appl	Sequence 12, Appl Sequence 30, Appl Sequence 30, Appl	Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl	Sequence 12, Appl Sequence 12, Appl	Sequence 12, Appl Sequence 60, Appl	Sequence 30, Appl Sequence 12, Appl	Sequence 12, Appl Sequence 12, Appl	Sequence 1, Appli Sequence 5, Appli	Sequence 135, App	Sequence 12, Appl	Sequence 1004, Ap	Sequence 957, App Sequence 1004, Ap	Sequence 57, Appl Sequence 1004, Ap	Sequence 1004, Ap Sequence 156, App	Sequence 510, App Sequence 518, App Sequence 495, App	Sequence 518, App	Sequence 518, App	Sequence 8, Appli Sequence 78259, A	Sequence 175123,	Sequence 233148,	Sequence 244153, Sequence 244353,	Sequence 360572, Sequence 265364,	Sequence 301924,	Sequence 109, App	equenc	equenc	equenc	equenc equenc	equenc	equenc equenc	00
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Sequence 120261, Sequence 186456, Sequence 265641, Sequence 278238, Sequence 280869, Sequence 42252, A Sequence 503752.	703160, 894738, 954962, 219170,	. 13, Appl 1698, Ap 43, Appl	822, App 4733, Ap 976, App	1046, Ap 1046, Ap 976, App	1046, Ap 930, App	976, App 1046. Ap	976, App	1046, App	1040, Ap : 27, Appl 436, App	edneuce	equence	Sequence 757, App Sequence 909, App	equence equence	equence	equence	equence	equence	equence 496, App	equence 0.0, App equence 923, App	equence 1040, Ap equence 519, App	equence 767, App equence 909, App	equence 968, App	edneuc	equence 89, Applequence 35, Appl	Seguence 12, Appl	equence	equence /6/, App equence 909, App	equence 968, App	equence 3, Appli	equence 12, Appl	ance 12, Appl c
US-10-809-189-120261 Sequence US-10-956-157-186456 Sequence US-10-956-157-265641 Sequence US-10-956-157-280869 Sequence US-10-956-157-280869 Sequence US-11-036-137-280870 Sequence US-11-036-137-252 Sequence US-11-036-137-503752 Sequence US-11-036	US-11-036-317-703160 Sequence 703160, US-11-036-317-894738 Sequence 894738, US-11-036-317-954962 Sequence 954962, US-11-060-756-219170 Sequence 219170,	US-11-027-767A-13 Sequence 13, Appl US-09-801-274-1698 Sequence 1698, Ap US-09-988-462-43 Sequence 43, Appl	US-10-035-893A-822 Sequence 822, App US-10-131-827-4733 Sequence 4733, Ap US-10-176-479-976 Sequence 976, Ann	US-09-776-479-1046 Sequence 976, App US-09-776-479-1046 Sequence 1046, App US-09-776-479-976 Sequence 976, App	US-09-776-479-1046 Sequence 1046, Ap 11S-10-112-653-930 Sequence 930. App	US-10-117-995-976 Sequence 7976, App 118-10-017-995-1046 Sequence 976, App	US-10-11-253-10-10-10-10-10-10-10-10-10-10-10-10-10-	US-10-314-376-1046 Sequence 1049, Ap US-10-31-778-976 Sequence 976, App US-10-33-378-1046 Sequence 976 bn	US-11-051-705-1040 Sequence 1040, Ap. 105-463-27 Sequence 27. Appl 106-106-106-106-106-106-106-106-106-106-	US-09-888-326-437 Sequence	US-09-888-326-443 Sequence US-09-818-918-12 Sequence US-09-818-918-12 Sequence	US-09-776-479-767 Sequence US-09-776-479-909 Sequence	US-09-776-479-968 Sequence US-09-776-479-969 Sequence	US-09-967-464-3 Sequence US-09-776-479-519 Sequence	US-09-776-479-767 Sequence	US-09-776-479-969 Sequence US-09-776-479-969 Sequence	US-09-965-101-52 Sequence US-09-965-101-59 Sequence	US-10-112-653-496 Sequence 496, App US-10-112-653-740 Sequence 740, App	US-10-112-653-923 Sequence 923, App	US-10-112-653-1040 Sequence 1040, Ap US-10-017-995-519 Sequence 519, App	US-10-017-995-767 Sequence 767, App US-10-017-995-909 Sequence 909, App	US-10-017-995-968 Sequence 968, App	US-10-161-229-47 Sequence	US-10-194-035-89 Sequence 89, Appl US-10-224-523-35 Sequence 35, Appl	US-10-187-264A-12 Sequence	US-10-314-578-519 Sequence	US-10-314-5/8-76/ Sequence /6/, App US-10-314-578-909 Sequence 909, App	US-10-314-578-968 Sequence 968, App US-10-314-578-969 Sequence 969, App	US-10-455-247-3 Sequence 3, Appli	US-10-(27-331-12 Sequence 12, Appl	US-10-73-022-12 Sequence 12, Appl C US-10-769-282-12 Sequence 12, Appl C C
US-10-809-189-120261 Sequence US-10-956-157-186456 Sequence US-10-956-157-265641 Sequence US-10-956-157-280869 Sequence US-10-956-157-280869 Sequence US-10-956-157-280869 Sequence US-11-34-317-503752 Sequence US-11-34-34-34-34-34-34-34-34-34-34-34-34-34-	10 US-11-036-317-703160 Sequence 703160, 10 US-11-036-317-894738 Sequence 894738, 10 US-11-036-317-954962 Sequence 954962, 10 US-11-060-756-219170 Sequence 219170,	10 US-11-027-767A-13 Sequence 13, Appl 3 US-09-801-274-1698 Sequence 1698, Ap 3 US-09-988-462-43 Sequence 43, Appl	7 US-10-035-833A-822 Sequence 822, App 6 US-10-131-827-4733 Sequence 4733, Ap 3 IS-08-776-479-976 Sequence 978, App	3 US-09-776-479-976 Sequence 7.0, App. 3 US-09-776-479-1046 Sequence 1046, Ap 3 US-09-776-479-976 Sequence 976, App.	3 US-09-776-479-1046 Sequence 1046, Ap. 5 US-10-112-653-930 Sequence 930, App.	5 US-10-117-995-976 Sequence 976, App 5 US-10-017-995-976 Sequence 976, App	5 US-10-314-578-976 Sequence 976 App 6 US-10-314-578-376 Sequence 976 App	6 US-10-214-370-1046 Sequence 1049, Ap. 8 US-10-831-778-976 Sequence 976, App. 9 US-10-831-778-1046 Sequence 1046 br	10 US-11-051-//0-1046 Sequence 1049, Appl 10 US-11-056-463-27 Sequence 27, Appl 10 To no	3 US-09-888-326-437 Sequence	3 US-09-888-326-443 Sequence 3 US-09-889-12 Sequence 3 US-09-818-918-12 Sequence	3 US-09-776-479-767 Sequence 3 US-09-776-479-909 Sequence	3 US-09-776-479-968 Sequence 3 US-09-776-479-969 Sequence	3 US-09-967-464-3 Sequence 3 US-09-776-479-519 Sequence	3 US-09-776-479-767 Sequence 3 US-09-776-479-909 Sequence	3 US-09-776-479-968 Sequence 3 US-09-776-479-969 Sequence	3 US-09-965-101-52 Sequence 3 US-09-965-101-59 Sequence	5 US-10-112-653-496 Sequence 496, App Sequence 70, App Sequence 70, App	5 US-10-112-653-878 Sequence 0.0, App. 5 US-10-112-653-923 Sequence 923, App.	5 US-10-112-653-1040 Sequence 1040, Ap 5 US-10-017-995-519 Sequence 519, App	5 US-10-017-995-767 Sequence 767, App 5 US-10-017-995-909 Sequence 909, App	5 US-10-017-995-968 Sequence 968, App 5 HS-10-017-995-969 Sequence 969, App	5 US-10-161-229-47 Sequence	6 US-10-194-035-89 Sequence 89, Appl 6 US-10-224-523-35 Sequence 35, Appl	6 US-10-187-264A-12 Sequence 6 US-10-306-522-12 Sequence	6 US-10-314-578-519 Sequence	6 US-10-314-5/8-76/ Sequence 767, App 6 US-10-314-578-909 Sequence 909, App	6 US-10-314-578-968 Sequence 968, App 6 HS-10-314-578-969 Sequence 969, App	6 US-10-455-247-3 Sequence 3, Appli	7 US-10-(27-33)-12 Sequence 12, Appl 7 US-10-(27-33)-12 Sequence 12, Appl	7 US-10-679-710-12 Sequence 12, Appl c 7 US-10-769-712 Sequence 12, Appl c 7 US-10-769-282-12 Sequence 12, Appl c
25 9 US-10-809-189-120261 Sequence 25 9 US-10-956-157-186456 Sequence 25 9 US-10-956-157-265641 Sequence 25 9 US-10-956-157-280869 Sequence 25 9 US-10-956-157-280870 Sequence 25 9 US-10-956-157-280870 Sequence 25 10 US-11-036-317-42252 Sequence 25 10 US-11-036-317-42252 Sequence	25 10 US-11-036-317-303152 Sequence 703160, 1 25 10 US-11-036-317-894738 Sequence 894738, 1 25 10 US-11-036-317-954962 Sequence 954962, 25 10 US-11-060-756-219170 Sequence 219170,	1 26 10 US-11-027-767A-13 Sequence 13, Appl 1 31 3 US-09-801-274-1698 Sequence 1698, Ap 1 32 3 US-09-988-462-43 Sequence 43, Appl	1 41 7 US-10-035-833A-822 Sequence 822, App 1 50 6 US-10-131-827-4733 Sequence 4733, Ap 1 10 3 US-10-476-476 Seminore 976, Ann	3 US-03-776-479-1976 Sequence 776, App. 19 3 US-09-776-479-1046 Sequence 1046, App. 19 3 US-09-776-479-976 Sequence 976, App.	3 19 3 US-09-776-479-1046 Sequence 1046, App. 19 5 US-10-112-653-930 Sequence 930, App.	19 5 US-10-117-955-976 Sequence 975, App 10 5 US-10-055-976 Sequence 976, App	3 19 6 US-10-314-578-976 Sequence 978, App	19 6 US-10-314-5/6-1046 Sequence 1046, App. 19 8 US-10-31-778-776 Sequence 976, App. 10 110-10-10-10-10-10-10-10-10-10-10-10-10-	19 10 US-11-056-463-27 Sequence 1049, Appl 3 19 10 US-11-056-463-27 Sequence 27, Appl	20 3 US-09-888-326-437 Sequence	3 20 3 US-09-888-326-443 Sequence 3 20 3 US-09-818-918-12 Sequence	3 20 3 US-09-776-479-767 Sequence 3 20 3 US-09-776-479-767 Sequence	3 20 3 US-09-776-479-968 Sequence 3 20 3 US-09-776-479-969 Sequence	3 20 3 US-09-967-464-3 Sequence 3 20 3 US-09-776-479-519 Sequence	3 20 3 US-09-776-479-767 Sequence 3 20 3 US-09-776-479-909 Sequence	3 20 3 US-09-776-479-968 Sequence 3 20 3 US-09-776-479-969 Sequence	3 20 3 US-09-965-101-52 Sequence 3 20 3 US-09-965-101-59 Sequence	3 20 5 US-10-112-653-496 Sequence 496, App	3 20 5 US-10-112-653-923 Sequence 923, App	3 20 5 US-10-112-653-1040 Sequence 1040, Ap 3 20 5 US-10-017-995-519 Sequence 519, App	3 20 5 US-10-017-995-767 Sequence 767, App 3 20 5 US-10-017-995-909 Sequence 909, App	3 20 5 US-10-017-995-968 Sequence 968, App	20 5 US-10-161-229-47 Sequence	3 20 6 US-10-194-035-89 Sequence 89, Appl 3 20 6 US-10-224-523-35 Sequence 35, Appl	3 20 6 US-10-187-264A-12 Seguence	3 20 6 US-10-314-578-519 Sequence	3 20 6 US-10-314-5/8-76/ Sequence /6/, App 3 20 6 US-10-314-578-909 Sequence 909, App	3 20 6 US-10-314-578-968 Sequence 968, App 3 20 6 US-10-314-578-969 Sequence 969, App	20 6 US-10-455-247-3 Sequence 3, Appli	3 20 7 US-10-71331-12 Sequence 12, Appl	3 20 7 US-10-679-710-12 Sequence 12, Appl C 3 20 7 US-10-79-282-12 Sequence 12, Appl C C
25 9 US-10-809-189-120261 Sequence 25 9 US-10-956-157-186456 Sequence 25 9 US-10-956-157-26541 Sequence 25 9 US-10-956-157-278238 Sequence 25 9 US-10-956-157-280869 Sequence 25 9 US-10-956-157-280870 Sequence 25 10 US-11-036-317-42252 Sequence 25 10 US-11-036-317-42252 Sequence 25 10 US-11-036-317-42252 Sequence	2.8 67.4 25 10 US-11-036-317-303722 Sequence 703160, 2.8 67.4 25 10 US-11-036-317-894738 Sequence 894738, 2.8 67.4 25 10 US-11-036-317-954962 Sequence 954962, 2.8 67.4 25 10 US-11-060-756-219170 Sequence 219170,	.8 67.4 26 10 US-11-027-767A-13 Sequence 13, Appl .8 67.4 31 3 US-09-801-274-1698 Sequence 1698, Ap .8 67.4 32 3 US-09-988-462-43 Sequence 43, Appl	2.8 67.4 41 7 US-10-035-833A-822 Sequence 822, App 2.8 67.4 50 6 US-10-131-827-4733 Sequence 4733, Ap 2.8 66.3 19 3 TG-09-776-4743 Sequence 473, App	2.6 66.3 19 3 US-09-776-479-1046 Sequence 1046, App 2.6 66.3 19 3 US-09-776-479-1046 Sequence 1046, App 2.6 66.3 19 3 US-09-776-479-976 Sequence 976, App	2.6 66.3 19 3 US-09-776-479-1046 Sequence 1046 Ap 2.6 66.3 19 5 US-10-112-653-930 Sequence 930, App	2.6 66.3 19 5 US-10-112-033-530 Geguence 300, App. 2.6 66.3 19 5 US-10-017-995-976 Sequence 976, App. 2.6 66.3 19 5 US-10-017-996-1046 Sequence 1046, App.	2.6 66.3 19 6 US-10-314-578-976 Sequence 976, App	2.6 66.3 19 8 US-10-214-3/6-1046 Sequence 1046, App. 2.6 66.3 19 8 US-10-831-778-976 Sequence 976, App.	.6 66.3 19 0 US-11-056-463-27 Sequence 1040, Ap. 10 US-11-056-463-27 Sequence 27, Appl	2.6 66.3 20 3 US-09-888-326-437 Sequence	2.6 66.3 20 3 US-09-888-326-443 Sequence 2.6 66.3 20 3 US-09-818-918-12 Sequence 2.7 66.3 20 3 US-09-818-918-12 Sequence	. 6 66.3 20 3 US-09-776-479-717 Sequence 6 66.3 20 3 US-09-776-479-909 Sequence	2.6 66.3 20 3 US-09-776-479-968 Sequence 2.6 66.3 20 3 US-09-776-479-969 Sequence	2.6 66.3 20 3 US-09-967-464-3 Sequence 2.6 66.3 20 3 US-09-776-479-519 Sequence	2.6 66.3 20 3 US-09-776-479-767 Sequence	2.6 66.3 20 3 US-09-776-479-968 Sequence 2.6 66.3 20 3 US-09-776-479-969 Sequence	.6 66.3 20 3 US-09-965-101-52 Sequence .6 66.3 20 3 US-09-965-101-59 Sequence	.6 66.3 20 5 US-10-112-653-496 Sequence 496, App	.6 66.3 20 5 US-10-112-653-978 Sequence 979, App .6 66.3 20 5 US-10-112-653-923 Sequence 923, App	.6 66.3 20 5 US-10-112-653-1040 Sequence 1040, Ap .6 66.3 20 5 US-10-017-995-519 Sequence 519, App	.6 66.3 20 5 US-10-017-995-767 Sequence 767, App .6 66.3 20 5 US-10-017-995-909 Sequence 909, App	.6 66.3 20 5 US-10-017-995-968 Sequence 968, App	.6 66.3 20 5 US-10-161-229-47 Sequence	.6 66.3 20 6 US-10-194-035-89 Sequence 89, Appl .6 66.3 20 6 US-10-224-523-35 Sequence 35, Appl	.6 66.3 20 6 US-10-187-264A-12 Sequence	.6 66.3 20 6 US-10-314-578-519 Sequence	.6 66.3 20 6 US-IU-314-5/8-767 Sequence /6/, App .6 66.3 20 6 US-IU-314-578-909 Sequence 909, App	.6 66.3 20 6 US-10-314-578-968 Sequence 968, App	.6 66.3 20 6 US-10-455-247-3 Sequence 3, Appli	.6 66.3 20 7 US-10-713-733-12 Sequence 12, Appl	.e 66.3 20 7 US-10-679-716-72 Sequence 12, Appl C .e 66.3 20 7 US-10-679-716-12 Sequence 12, Appl C .e 66.3 20 7 US-10-769-282-12 Sequence 12, Appl C

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; OTHER INFORMATION: chimeric phosphorothioate/phosphodiester backbone; OTHER INFORMATION: with phosphorothioate at 5' and 3' ends US-09-888-326-447
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APPLICANT: Petersen, Deanna M.
APPLICANT: Petersen, Deanna M.
APPLICANT: Petersen, Deanna M.
TITLE ON TOWENTION: Treatment of Asthma and Allergy
TITLE OF INVENTION: Treatment of Asthma and Allergy
FILE REPERINCE: C1037/7013 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/776,479
CURRENT APPLICATION NUMBER: US 60/176,991
PRIOR PELLING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 19
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100.0%; Score 19; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 0; Indels
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Publication No. US20040067902A9
GENERAL INFORMATION:
APPLICANT: Bratzler, Robert L.
APPLICANT: Petersen, Deanna M.
TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Treatment of Asthma and Allergy
FILE REPERENCE: C1027/7013 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/776,479
                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
 CURRENT APPLICATION NUMBER: US/09/888,326
CURRENT FILING DATE: 2001-06-22
PRIOR PILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 848
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 447
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Synthetic Sequence
                                                                                                                                                                                                                                                                                                                               ; Sequence 80, Application US/09776479; Publication No. US20030087848A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                   1 GGGGTGACGTTCAGGGGGG 19
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US-09-776-479-80
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; Sequence 447, Application US/0988326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
US-09-906-742-225
US-09-906-838-225
US-09-907-613-225
US-09-907-613-225
US-09-904-805-225
US-09-904-805-225
US-09-904-805-225
US-09-904-805-225
US-09-904-805-225
US-09-904-905-225
US-09-903-749A-225
US-09-903-749-225
US-09-903-749-225
US-09-903-904-485-225
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US-09-905-768-225
US-09-905-777-225
US-09-906-815A-225
US-09-906-815A-225
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US-09-906-815A-225
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US-09-904-525-225
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US-09-906-618-225
US-09-907-728-225
US-09-904-805-225
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FEATURE:
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; Sequence 74, Application US/10112653
; Publication No. US20030050268A1
; Publication No. US20030050268A1
; GENERAL INFORMATION:
   APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
   TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; CURRENT PAPLICATION NUMBER: US 60/210/112,653
; CURRENT PILING DATE: 2002-03-29
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 74
: INDICATED TO THE PROPERTY OF THE PARTY 
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US-10-017-995-80
US-10-017-995-80

US-10-017-995-80

Sequence 80, Application US/10017995

Publication No. US20030055014A1

GENERAL INFORMATION:

APPLICANT: BRAITAICN:

TILE REFERENCE: C1037/7025 (HCL/MAT)

CURRENT APPLICATION NUMBER: US/10/017,995

CURRENT FILING DATE: 2001-12-18

PRIOR APPLICATION NUMBER: US 60/255,534

PRIOR PILING DATE: 2001-12-14

NUMBER OF SEQ ID NOS: 1093

SOFTWARE: FastSEQ for Windows Version 3.0
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100.0%; Score 19; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 0; Indels
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100.0%; Score 19; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 0; Indels
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        CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: US 60/179,991
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: PASISEQ for Windows Version 3.0
SEQ ID NO 80
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                   ), OTHER INFORMATION: Synthetic Sequence US-09-776-479-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGGGTGACGTTCAGGGGGG 19
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-10-112-653-74
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LENGTH: 19
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; Sequence 80, Application US/10831778
; Publication No. US20040235774A1
; Publication No. US20040235774A1
; APPLICANT: Brataler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Petersen, Deanna M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Teatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; LENGTH: 19
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US-10-314-578-80

JOSQUEACE 80, APDLication US/10314578

SEQUENCE 80, APDLication US/10314578

PUBLICATION NO. US20030212026A1

JENDICATE Krieg, Arthur M.

APPLICANT: Krieg, Arthur M.

APPLICANT: Vollmer, Jorg

TILE OF INVENTION: Immunostimulatory Nucleic Acids

FILE REFERENCE: C1039/7035 (HCL/MAT)

CURRENT FILING DATE: 2002-12-09

PRIOR PILING DATE: 1999-09-25

PRIOR PILING DATE: 1999-09-25

PRIOR APPLICATION NUMBER: US 60/156,113

PRIOR PILING DATE: 1999-09-27

PRIOR PILING DATE: 1999-09-27

PRIOR PILING DATE: 1999-09-27

PRIOR PILING DATE: 1999-09-27

PRIOR FILING DATE: 1999-09-27

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PRIOR DATE: 1999-09-27

PRIOR DATE: 1999-09-27

PRIOR DATE: 1999-09-27

PRIOR DATE: 1999-09-27
                                                                                                                              Query Match 100.0%; Score 19; DB 5; Best Local Similarity 100.0%; Pred. No. 21; Matches 19; Conservative 0; Mismatches 0
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FEATURE:
OTHER INFORMATION: Synthetic Sequence
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; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-80
) OTHER INFORMATION: Synthetic Sequence US-10-017-995-80
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 19; Conservative
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US-10-831-778-80
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Sequence 76, Application US/10112653
; Publication No. US2003005026841
; GENERAL INFORMATION:
    APPLICANT: Raieg, Arthur M.
    APPLICANT: Berg, Daniel J.
    TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
    TITLE OF INVENTION: TRAFFINENCE: CO1039/700604Mws)
; FILE REPERBICE: CO1039/700604Mws)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT APPLICATION NUMBER: US 60/279,642
; PRIOR PILING DATE: 2001-03-29
; NUMBER OF SEC ID NOS: 1040
; SOFTWARE: EastSEC for Windows Version 3.0
; BENGTH: 19
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### Sequence 
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Query Match 91.6%; Score 17.4; DB 3; Length 19; Best Local Similarity 94.7%; Pred. No. 1.3e+02; Matches 18; Conservative 0; Mismatches 1; Indels
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91.6%; Score 17.4; DB 5;
Best Local Similarity 94.7%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 1;
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Matches 18; Conservative
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US-10-112-653-76
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NAME/KEY: misc_feature
| IOCATION: (0) ...(0) |
| OTHER INFORMATION: chimeric phosphorothioate/phosphodiester backbone |
| OTHER INFORMATION: with phosphorothioate at 5' and 3' ends |
| US-09-888-326-448
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; Sequence 82, Application US/0976479
; Publication No. US20030087848A1
; GRNERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Imminostimulatory Nucleic Acids for the TITLE OF INVENTION: Imminostimulatory Nucleic Acids for the TITLE OF INVENTION: UNMERR: US/09/776.479
; CURRENT APPLICATION NUMBER: US/09/776.479
; CURRENT PILING DATE: 2000-02-02
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: PastSEQ for Windows Version 3.0
; LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 448, Application US/0988326

Publication No. US20030026801A1

GENERAL INFORMATION:

APPLICANT: Weiner, George

APPLICANT: Weiner, George

TITLE OF INVENTION: Methods for Enhancing Antibody-Induced

TITLE OF INVENTION: Cell Lyais and Treating Cancer:

FILE REFERENCE: C1039/7052 (Aws)

CURRENT APPLICATION NUMBER: US/09/888,326

CURRENT FILIAG DATE: 2001-06-22

PRIOR PILIAG DATE: 2000-06-22

NUMBER OF SEQ ID NOS: 848

SOFTWARE: PRESENCE for Windows Version 3.0

SEQ ID NO 448

LENGTH: 19
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                                                                   100.0%; Score 19; DB 8; Length 19; 100.0%; Pred. No. 21;
                                                                                                                                       0; Indels
                                                                                                   ; Pred. No. 21;
0; Mismatches
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                                                                                                                                                                                                                                              1 GGGGTGACGTTCAGGGGGG 19
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ORGANISM: Artificial Sequence
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                                                                Query Match
Best Local Similarity 100.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-888-326-448
   US-10-831-778-80
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WS-11-036-317-815104/c
Sequence 815104, Application US/11036317
Sequence 815104, Application US/11036317
Sequence 815104, Application US/1036317
Sequence 815104, Application US/020050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Williams, Alan
TILLE OF INVENTION Method of Analysis of Alternative Splicing in Mouse
FILE REPERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT PILING DATE: 2005-01-13
PRIOR FILING DATE: 2004-01-13
          publication No. US20040235774A1
| Publication No. US20040235774A1
| GENERAL INPORMATION:
| APPLICANT: Bratzler, Robert L.
| APPLICANT: Petersen, Deanna M.
| APPLICANT: Fouron, Yees
| TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the CURRENT PRIME REFERENCE: C103777013 (HCL/MAT)
| CURRENT APPLICATION NUMBER: US/10/831,778
| PRIOR FILING DATE: 20004-04-23 |
| PRIOR FILING DATE: 2000-02-03 |
| NUMBER OF SEQ ID NOS: 1093 |
| SEQ ID NO 82 |
| LENGTH: 19 |
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SOFTWARE: Micrarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 815104
LENGTH: 25
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Publication No. US2003002678241
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Klinman, Dennis
APPLICANT: Steinberg, Alfred D.
TITLE OF INVENTION: INMUNOMODULATORY OLIGONUCLECTIDES
FILE REPERENCE: C1039/7029
CURRENT APPLICATION NUMBER: US/09/415,142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 81.1%; Score 15.4; DB 10; Best Local Similarity 94.1%; Pred. No. 1.2e+03; Matches 16; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 17.4; DB 8;
Pred. No. 1.3e+02;
0; Mismatches 1;
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Application US/10831778
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Best Local Similarity 94.7%;
Matches 18; Conservative
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CORGANISM: Mus musculus
US-11-036-317-815104
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US-09-415-142-1
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                                                                                                                     Sequence 82, Application US/10017995
; Sequence 82, Application Ws/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
    APPLICANT: BETAILEF, Robert L.
; TILLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT APPLICATION NUMBER: US 60/255,534
; PRIOR PILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SEQ ID NO 82
LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 91.6%; Score 17.4; DB 5; Length 19; Best Local Similarity 94.7%; Pred. No. 1.3e+02; Matches 18; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-10-314-578-82
Sequence 82, Application US/10314578
Publication No. US20030212026A1
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Vollmer, Jorg
TITLE OF INVENTION: Immunostimulatory Nucleic Acids
FILE REFERENCE: C1039/7035 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/10/314,578
CURRENT PILING DATE: 1999-09-25
PRIOR FILING DATE: 1999-09-27
NUMBER OF SEQ ID NOS: 1145
SOFTWARE: FASELSEQ for Windows Version 3.0
SEQ ID NO 82
LENGTH: 19
TVENT NAMER: PASELSEQ for Windows Version 3.0
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, OTHER INFORMATION: Synthetic Sequence US-10-314-578-82
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          1 GGGGTGTCGTTCAGGGGGG 19
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-10-831-778-82
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FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Synthetic Oligonucleotide
PRIOR APPLICATION NUMBER: US 09/415,142
PRIOR FILING DATE: 1999-10-09
NUMBER OF SEQ ID NOS: 75
SOGTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 84.2
Matches 16; Conservative
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APPLICANT: Krieg, Arthur
APPLICANT: Klinman, Dennis
APPLICANT: Steinberg, Alfred
TITLE OF INVENTION: Methods and Products for Treating HIV Infection
FILE REFERENCE: C1039/7053(HCL)
CURRENT APPLICATION NUMBER: US/09/931, 583
CURRENT FILING DATE: 2001-08-16
PRIOR PAPPLICATION NUMBER: US 08/276,358
PRIOR FILING DATE: 1994-07-15
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APPLICANT: Hartmann, Gunther
TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
TITLE OF INVENTION: Cell Lysis and Treating Cancer
FILE REPERENCE: C1039/7052 (AMS)
CURRENT APPLICATION NUMBER: US/09/888,326
CURRENT PILING DATE: 2001-06-22
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 848
SOFTWARE FASTESQ for Windows Version 3.0
SEQ ID NO 449
LENGTH: 20
                                                                                                                                                                                                                                                                                                         Score 14.2; DB 3; Length 20; Pred. No. 4.6e+03; 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                       ; OTHER INFORMATION: Synthetic oligonucleotide
US-09-415-142-1
    CURRENT FILING DATE: 1999-10-09
PRIOR APPLICATION NUMBER: US 08/386,063
PRIOR FILING DATE: 1995-02-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                           1 GGGGTGACGTTCAGGGGGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTCAACGTTCAGGGGGG 20
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84.28;
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Best Local Similarity 84.2<sup>3</sup>
Matches 16; Conservative
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Matches 16; Conservative
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US-09-888-326-449
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US-09-931-583-1
                                                                                                                                                                        TYPE: DNA
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US-09-776-479-224

i Sequence 224, Application US/09776479

j Sequence 224, Application US/09776479

j Publication No. US20030087848A1

j GENERAL INFORMATION:
    APPLICANT: Bratzler, Robert L.
    APPLICANT: Petersen, Deanna M.
    APPLICANT: Petersen, Deanna M.
    TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Treatment of Asthma and Allergy FILE REFERENCE: C1037/7013 (HCL/MAT); CURRENT APPLICATION NUMBER: US/09/776,479

CURRENT PLING DATE: 2001-02-02

PRIOR FILING DATE: 2001-02-03

SOFTWARE: PASCESQ for Windows Version 3.0

SEQ ID NO 224

LENGTH: 20
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Bublication No. US20040067902A9

FUBLICANT: Bratzler. Robert L.

APPLICANT: Petersen, Deanna M.

APPLICANT: Fetersen, Deanna M.

TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Treatment of Asthma and Allergy TITLE OF INVENTION: UNWBER: US/09/776,479

CURRENT APPLICATION NUMBER: US 60/176,479

CURRENT FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: US 60/179,991

PRIOR SEQ ID NOS: 1093

NUMBER OF SEQ ID NOS: 1093

SOFTWARE: FastSEQ for Windows Version 3.0
         Length 20;
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Query Match
74.7%; Score 14.2; DB 3;
Best Local Similarity 84.2%; Pred. No. 4.6e+03;
Matches 16; Conservative 0; Mismatches 3;
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84.2%; Pred. No. 4.6e+03;
ive 0; Mismatches 3;
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
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; OTHER INFORMATION: Synthetic Sequence US-10-017-995-224
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                      TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 84.2%;
Matches 16; Conservative
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ORGANISM: Artificial Sequence
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Best Local Similarity 84.2%;
Matches 16; Conservative
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US-10-314-578-224
  LENGTH:
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APPLICANT: Krieg, Arthur M.
APPLICANT: Berg, Daniel J.
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
FILE REPERENCE: C01039/70060(AWS)
CURRENT APPLICATION NUMBER: US/10/112,653
CURRENT FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: US 60/279,642
PRIOR FILING DATE: 2001-03-29
                                                                                                                                                                                                                                                                                                                                     RESULT 21
US-09-965-101-63
US-09-965-101-63

Sequence 63, Application US/09965101

Publication No. US20040186067A1

GENERAL INFORMATION:

APPLICANT: Davis, Heather I.

APPLICANT: Schort, Joachim

APPLICANT: Schort, Joachim

TITLE OF INVENTION: Therapeutic Protocols

TITLE OF INVENTION: Therapeutic Protocols

TITLE OF INVENTION: Therapeutic Protocols

FILE REFRENCE: C1039/7057 (HCL/MAT)

CURRENT APPLICATION NUMBER: US/09/965,101

CURRENT APPLICATION NUMBER: US 60/047,233

PRIOR FILING DATE: 1998-05-20

PRIOR FILING DATE: 1999-05-20

PRIOR PLICATION NUMBER: US 60/047,233

PRIOR FILING DATE: 1997-05-20

PRIOR APPLICATION NUMBER: US 60/047,209

PRIOR PLING DATE: 1997-05-20

NUMBER OF SEQ 1D NOS: 84

SOFTWARE: FRESESE FOR Windows Version 3.0

LENGTH: 20
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Pred. No. 4.6e+03;
0; Mismatches 3; Indels
                                                                                                                                                                         Score 14.2; DB 3; Length 20;
Pred. No. 4.6e+03;
                                                                                                                                                                                                                    3; Indels
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                                                                                                                                                                                                                  0; Mismatches
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                                                                                    FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-224
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                                                                                                                                                                                                                                                              1 GGGGTGACGTTCAGGGGGG 19
                                                                                                                                                                                                                                                                                                2 GGGTTGACGTTTTGGGGGG 20
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Best Local Similarity 84.2%;
Matches 16; Conservative C
SEQ ID NO 224
LENGTH: 20
TYBE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                         74.78;
84.28;
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Best Local Similarity 84.28
Matches 16; Conservative
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US-10-112-653-216
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US-011. 6.2
US-010.017-995-224

Sequence 224, Application US/10017995

Publication No. US20030055014A1

GENERAL INFORMATION:

TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids

TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids

TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids

CURRENT APPLICATION NUMBER: US/10/017,995

CURRENT FILING DATE: 2001-12-18

PRIOR FILING DATE: 2000-12-14

NUMBER OF SEQ ID NOS: 1093

SOGTWARE: FastSEQ for Windows Version 3.0

LENGTH: 20
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Publication No. US20030212026A1

GENERAL INFORMATION:
APPLICANT: Schetter, Christian
APPLICANT: Schetter, Christian
APPLICANT: Vollmer, Jorg
TITLE OF INVENTION: Immunostimulatory Nucleic Acids
FILE REFERENCE: C1039/7035 (HCL/MAT)
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US 60/156,113
PRIOR APPLICATION NUMBER: US 60/156,113
PRIOR FILING DATE: 1999-09-25
PRIOR FILING DATE: 1999-09-27
PRIOR FILING DATE: 1999-09-27
PRIOR FILING DATE: 1909-09-27
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 1145
SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 20
                                                                                            Score 14.2; DB 5;
Pred. No. 4.6e+03;
0; Mismatches 3;
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Pred. No. 4.6e+03;
FEATURE:
COTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-216
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74.7%; Score 14.2; DB 7; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                APPLICANT: Krieg, Arthur M.
APPLICANT: Klieg, Arthur M.
APPLICANT: Steinberg, Alfred D.
APPLICANT: Steinberg, Alfred D.
TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
FILE REFERENCE: CLO39/7029
CURRENT APPLICATION NUMBER: US/10/690,495
CURRENT APPLICATION NUMBER: US/10/690,495
PRIOR APPLICATION NUMBER: US 08/386,063
PRIOR FILING DATE: 1995-02-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 20
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APPLICANT: Klinman, Dennis
APPLICANT: Klinman, Dennis
APPLICANT: Steinberg, Alfred D.
TITLE OF INVENTION: INVUNNED DENIS
FILE REFERENCE: C1039/7029
CURRENT APPLICATION NUMBER: US/10/788,191
CURRENT FILING DATE: 2004-02-26
PRIOR APPLICATION NUMBER: US 08/386,063
PRIOR PILING DATE: 1995-02-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 20
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US-10-690-495-1
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                                                                                               US-10-690-495-1; Sequence 1. Application US/10690495; Publication No. US20040143112A1; GENERAL INFORMATION:
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Publication No. US20040152656A1
GENERAL INFORMATION:
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; Sequence 1, Application US/10789536
1 GGGGTGACGTTCAGGGGGG 19
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Matches
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                                       Length 20;
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Pred. No. 4.6e+03;
0; Mismatches 3; Indels
                                                                              3; Indels
                                                                                                                                                                                                                                                                                                             APPLICANT: KILLMan, Dennie
APPLICANT: KILLMan, Dennie
APPLICANT: Steinberg, Alfred D.
TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
FILE REFERENCE: C1039/7029
CURRENT APPLICATION NUMBER: US/10/789,051
CURRENT FILING DATE: 2004-02-26
PRIOR APPLICATION NUMBER: US 08/386,063
PRIOR PILLING DATE: 1995-02-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 3.0
                                       Score 14.2; DB 6;
Pred. No. 4.6e+03;
                        74.7%; Scor.
84.2%; Pred. No. 4...
... 0; Mismatches
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                                                                                                                                                                                                                                                     Sequence 1, Application US/10631676
Publication No. US20040087534A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 1, Application US/10789051; Publication No. US20040142469A1; GENERAL INFORMATION:
                                                                                                                  1 GGGGTGACGTTCAGGGGGG 19
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 84.2%;
Matches 16; Conservative
                                     Query Match
Best Local Similarity 84.2
Matches 16; Conservative
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Matches 16; Conserv
US-10-314-578-224
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US-10-789-051-1
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LENGTH: 20
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Pred. No. 4.6e+03;
0; Mismatches 3; Indels
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Publication No. US20040181045A1
| GENERAL INFORMATION:
| APPLICANT: Krieg, Arthur M. |
| APPLICANT: Klinman, Dennis |
| APPLICANT: Steinberg, Alfred D. |
| TILLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES |
| FILE REFERENCE: C1039/7029 |
| CURRENT PILING DATE: 2004-02-26 |
| PRIOR APPLICATION NUMBER: US 08/386,063 |
| PRIOR APPLICATION NUMBER: US 08/386,063 |
| NUMBER OF SEQ ID NOS: 27 |
| SOFTWARE: FASTEED for Windows Version 3.0 |
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Sequence 1, Application US/10787737

Sequence 1, Application US/1078737

GENERAL INFORMATION:

APPLICANT: Krieg, Arthur M.

APPLICANT: Krieg, Arthur M.

APPLICANT: Steinberg, Alfred D.

TITLE OF INVENTION: IMMINOMOUULATORY OLIGONUCLEOTIDES

FILE REFERENCE: C1039/7029

CURRENT APPLICATION NUMBER: US/10/787,737

CURRENT PILING DATE: 2004-02-26

PRIOR APPLICATION NUMBER: US 08/386,063

PRIOR FILING DATE: 1995-02-07

NUMBER OF SEQ ID NOS: 27

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 20
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Pred. No. 4.6e+03;
0; Mismatches 3;
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                                                                                                                                                                                                                                                          j OTHER INFORMATION: Synthetic oligonucleotide
US-10-789-353-1
CURRENT APPLICATION NUMBER: US/10/789,353
CURRENT FILING DATE: 2004-02-26
PRIOR PILLING DATE: 1995-02-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PASLSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 20
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Best Local Similarity 84.2%;
Matches 16; Conservative
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Best Local Similarity 84.2%;
Matches 16; Conservative
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Pred. No. 4.6e+03;
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Publication No. US20040162258A1

GENERAL INFORMATION

APPLICANT: Klinman, Dennis

APPLICANT: Klinman, Dennis

APPLICANT: Steinberg, Alfred D.

TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES

FILE REFERENCE: C1039/7029

CURRENT APPLICATION NUMBER: US/10/769,626

CURRENT FILING DATE: 1995-02-07

PRIOR FILING DATE: 1995-02-07
                       GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Klinen, Dennis
APPLICANT: Klinen, Dennis
APPLICANT: Stinnen, Dennis
APPLICANT: Stinnen, Dennis
TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
FILE REFERENCE: C1039/709 US/10/789,536
CURRENT APPLICATION NUMBER: US/20/789,536
CURRENT FILING DATE: 2004-02-26
FRIOR PELLING DATE: 1995-02-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FABELSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 20
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APPLICANT: Klinman, Dennis
APPLICANT: Steinberg, Alfred D.
TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
FILE REFERENCE: C1039/7029
                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GGGGTGACGTTCAGGGGGG 19
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Best Local Similarity 84.2%;
Matches 16; Conservative C
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ORGANISM: Artificial Sequence
           Publication No. US20040152657A1
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Best Local Similarity 84.2
Matches 16; Conservative
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US-10-789-353-1
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OTHER INFORMATION: synthetic oligonucleotide
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PRIOR PILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 09/082,649
PRIOR FILING DATE: 1998-05-20
PRIOR FILING DATE: 1997-05-20
PRIOR FILING DATE: 1997-05-20
PRIOR FILING DATE: 1997-05-20
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 3.0
SSOFTWARE: 7805-05-20
LENGTH: 20
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Publication No. US20050032734A1
                                                                                                                                                                                                                                                                         Sequence 1, Application US/1088888
Publication No. US20050009774A1
GENERAL INFORMATION:
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               Query Match
Best Local Similarity 84.2%;
Matches 16; Conservative
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Matches 16; Conservative
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; Sequence 224, Application US/10831778
; Publication No. US20040235774A1
; GRNERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; TILLE OF INVENTION: Immunostimulatory Nucleic Acids for the TILLE OF INVENTION: Immunostimulatory Nucleic Acids for the TILLE OF INVENTION: Immunostimulatory Nucleic Acids for the TILLE OF INVENTION NUMBER: US/10/831,778
; CURRENT FILLING DATE: 2004-04-23
; PRIOR PILLING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 14.2; DB 8; Length 20;
Pred. No. 4.6e+03;
0; Mismatches 3; Indels
                                                                                                                                                             Length 20;
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APPLICANT: Klinman, Dennis
APPLICANT: Steinberg, Alfred D.
TITLE OF INVENTION: IMMUNOMOULATORY OLIGONUCLEOTIDES
FILE REPERENCE: C1039/7029
CURRENT APPLICATION NUMBER: US/10/847,650
CURRENT APPLICATION NUMBER: US/08497,650
FRIOR APPLICATION NUMBER: US 08/386,063
PRIOR FILING DATE: 1995-02-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 20
                                                                                                                                                             Score 14.2; DB 8;
Pred. No. 4.6e+03;
0; Mismatches 3;
                                                                                       ; OTHER INFORMATION: Synthetic oligonucleotide
US-10-788-199-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Synthetic Sequence US-10-831-778-224
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                                                                                                                                                                                                                                                            1 GGGGTGACGTTCAGGGGGG 19
                                                                                                                                                                                                                                                                                                          GGGTCAACGTTCAGGGGGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGGGTGACGTTCAGGGGGG 19
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                    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                             Query Match
Best Local Similarity 84.2%;
Matches 16; Conservative (
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84.28;
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ORGANISM: Artíficial Sequence
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Best Local Similarity 84.2
Matches 16; Conservative
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US-10-831-778-224
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LENGTH: 20
LENGTH: 20
                                                                      FEATURE:
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     Length 20;
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APPLICANT: Davis, Heather L.
APPLICANT: Schorr, Joachim
APPLICANT: Schorr, Joachim
APPLICANT: Wu, Tong
TITLE OF INVENTION: Vectors and Methods for Immunization or
TITLE OF INVENTION: Therapeutic Protocols
FILE REPERENCE: C1039.70057US01
CURRENT APPLICATION UNMBER: US/10/838,659
PRIOR APPLICATION NUMBER: US/10/838,659
                                                      Indels
                                                                                                                                                                                                                                                                                                                                              APPLICANT: Klinman, Dennis
APPLICANT: Klinman, Dennis
APPLICANT: Steinberg, Alfred D.
APPLICANT: Steinberg, Alfred D.
TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
FILE REFERENCE: CLO39/7029
CURRENT APPLICATION NUMBER: US/10/888,885
CURRENT APPLICATION NUMBER: US/80,063
PRIOR APPLICATION NUMBER: US 08/386,063
PRIOR FILING DATE: 1995-02-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 20
Score 14.2; DB 8;
Pred. No. 4.6e+03;
0; Mismatches 3;
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USS-117-185300

| Sequence 185300, Application US/11036317
| Sequence 185300, Application US/11036317
| Publication No. US20050214823A1
| GENERAL INFORMATION:
| APPLICANT: Williams, Alan
| APPLICANT: Blume, John
| TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
| FILE REFERENCE: 3654.1
| CURRENT FILING DATE: 2005-01-13
| PRIOR APPLICATION NUMBER: US/11/036,317
| PRIOR PILING DATE: 2004-01-13
| NUMBER OF SEQ ID NOS: 991174
| SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
| SENGIH: 25
                                                                                         Gaps
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                                      74.7%; Score 14.2; DB 8; Length 20; 84.2%; Pred. No. 4.6e+03; ive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                             Sequence 1, Application US/11067516;
Publication No. US20050239736A1
| GENERAL INFORMATION:
| APPLICANT: Krieg, Arthur M. APPLICANT: Krieg, Arthur M. APPLICANT: Krieg, Arthur M. APPLICANT: Steinberg, Alfred D. TILLE OF INVENTION: IMMUNMODULATORY OLIGONUCLEOTIDES;
| FILE REPERENCE: C1039/7029
| CURRENT APPLICATION NUMBER: US/11/067,516
| CURRENT PILING DATE: 2003-10-21
| PRIOR FILING DATE: 2003-10-21
| PRIOR APPLICATION NUMBER: US 08/386,063
| PRIOR FILING DATE: 1995-02-07
| NUMBER OF SEQ ID NOS: 27
| SOFTWARE: PASESEQ for Windows Version 3.0
| SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 74.7%; Score 14.2; DB 10; Best Local Similarity 84.2%; Pred. No. 4.6e+03; Matches 16; Conservative 0; Mismatches 3;
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                                                                                                                                         1 GGGGTGACGTTCAGGGGGG 19
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                                                                                           16; Conservative
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US-11-036-317-185300
                                             Query Match
Best Local Similarity
Matches 16; Conserve
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US-11-067-516-1
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US-10-649-584-1
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APPLICANT: Steinberg, Alfred
TITLE OF INVENTION: Methods and Products for Treating HIV Infection
FILE REFERENCE: C1039.700840800
CURRENT APPLICATION NUMBER: US/10/649,584
CURRENT APPLICATION NUMBER: US 09/931,583
PRIOR PRILICATION NUMBER: US 09/931,583
PRIOR APPLICATION NUMBER: US 09/931,583
PRIOR APPLICATION NUMBER: US 09/415,142
PRIOR FILING DATE: 1994-07-15
PRIOR PILING DATE: 1994-07-15
PRIOR FILING DATE: 1999-10-09
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Version 3.0
                                                                                                   Gaps
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                                             Score 14.2; DB 8; Length 20;
Pred. No. 4.6e+03;
0; Mismatches 3; Indels
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APPLICANT: Klinman, Dennis
APPLICANT: Klinman, Dennis
APPLICANT: Steinberg, Alfred D.
TITLE OF INVENTION: INMUNOMOULATORY OLIGONUCLEOTIDES
FILE REFERENCE: C1039/7029
CURRENT APPLICATION NUMBER: US/10/888,089
CURRENT FILING DATE: 2004-709
FRIOR APPLICATION NUMBER: US/10/690,495
FRIOR APPLICATION NUMBER: US 08/386,063
FRIOR APPLICATION NUMBER: US 08/386,063
FRIOR APPLICATION NUMBER: US 08/386,063
FRIOR FILING DATE: 1995-02-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FABELSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 20
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NAME/KEY: misc_feature
OTHER INFORMATION: Synthetic Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Synthetic oligonucleotide US-10-888-089-1
                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/10888089; Publication No. US20050037403A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 1, Application US/10649584; Publication No. US20050037985A1; GENERAL INFORMATION:
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                                                Query Match
Best Local Similarity 84.2%;
Matches 16; Conservative
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ORGANISM: Artificial Sequence
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     US-10-838-659-63
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US-10-888-089-1
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CURRENT FILING DATE:
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US-10-282-935-18/C
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                                                                                                                                                                    APPLICANT: Williams, Alan
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REPERRNCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR PILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SSOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 222532
LENGTH: 25
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TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse FILE REPERENCE: 365-01
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT PILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SEQ ID NOS: 991174
SEQ ID NO 382608
LENGTH: 25
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; Publication No. US20050214823A1
; GENERAL INFORMATION:
APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
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Pred. No. 4.4e+03; 
0; Mismatches 3; Indels
                                                                                                       ; Sequence 282532, Application US/11036317; Publication No. US20050214823A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 382608, Application US/11036317; Publication No. US20050214823A1; GENERAL INFORMATION:
APPLICANT: Williams, Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGGGTGACGTTCAGGGGGG 19
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7 GGGGAGACGTTCATGGGCG
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84.28;
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Best Local Similarity 84.2
Matches 16; Conservative
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Matches 16; Conservative
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; ORGANISM: Mus musculus
US-11-036-317-382608
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; ORGANISM: Mus musculus
US-11-036-317-282532
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US-11-036-317-382608
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| Separation | Sep
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TILE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.11
CURRENT PILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SEQ ID NO 398410
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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            PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SEQ ID NO 395403
LENGTH: 25
TYPE: DNA
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-395403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 14.2; DB 10;
Pred. No. 4.4e+03;
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84.2%; Pred. No. 4.4e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 398410, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGGGTGACGTTCAGGGGGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 GGGGAGACGTTCATGGGCG 22
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2005-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 84.2%;
Matches 16; Conservative
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Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Williams, Alan APPLICANT: Blume, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
CORGANISM: Mus musculus
US-11-036-317-398410
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Sequence 18, Application US/10440796

| Sequence 18, Application No. US20040009148A1
| GENERAL INFORMATION:
| APPLICANT: VICTOR F. |
| APPLICANT: SMALLSHAW, JOAN |
| APPLICANT: BALLING COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK |
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK |
| TITLE OF INVENTION: SYNDROME (VLS) |
| TITLE OF INVENTION: SYNDROME (VLS) |
| TITLE OF INVENTION: SYNDROME (VLS) |
| FILE REFERENCE: USD:603 |
| CURRENT FILING DATE: 2003-05-19 |
| PRIOR APPLICATION NUMBER: US/09/538,873 |
| PRIOR APPLICATION NUMBER: US/09/538,873 |
| PRIOR FILING DATE: 1999-03-30 |
| PRIOR FILING DATE: 1999-03-30 |
| NUMBER OF SEQ ID NOS: 19 |
| SEQ ID NO 18 |
| LENGTH DATE: 1999-03-30 |
| LENGTH DATE: 1999-03-3
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; Sequence 292133, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVERTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2004-01-13
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; LEMOTH: 25
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) ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Primer

US-10-282-935-18
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                                                                                                                                                                                                                                                             Ouery Match 73.7%; Score 14; DB 6; Length 39; Best Local Similarity 100.0%; Pred. No. 5.3e+03; Matches 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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ORGANISM: Artificial Sequence
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US-11-036-317-292133
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US-10-440-796-18/c
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gequence 815105, Application US/11036317

publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

APPLICANT: Blume, John

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT APPLICATION NUMBER: US 60/536,639

PRIOR APPLICATION UNMBER: US 60/536,639

PRIOR PILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25

LENGTH: 25
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Length 25;
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72.6%; Score 13.8; DB 10;
88.2%; Pred. No. 7e+03;
tive 0; Mismatches 2;
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88.2%; Pred. No. 7e+03;
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                                                              1 GGGGTGACGTTCAGGGG 17
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                                                                                             8 GGGGAGACGTTCATGGG 24
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Best Local Similarity 88.2
Matches 15; Conservative
 Query Match 72.6°
Best Local Similarity 88.2°
Matches 15; Conservative
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Best Local Similarity 88.2
Matches 15; Conservative
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CORGANISM: Mus musculus
US-11-036-317-815105
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ORGANISM: Mus musculus
US-11-036-317-822290
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US-11-036-317-815105/c
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Sequence 836953,
Sequence 836494,
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Sequence 16126, A
Sequence 97, Appl
Sequence 14533,
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Sequence 321322,
Sequence 1319423,
Sequence 1319423,
Sequence 132628,
Sequence 22043, A
Sequence 22043, A
Sequence 181131,
Sequence 181131,
Sequence 1198991,
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Sequence 62, Appl
                      Sequence 518042
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Sequence 9
Sequence 1
   Sequence
US-10-310-914A-114797
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US-10-310-914A-13122628
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US-10-939-294A-17580
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Sequence 1, Appli
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Sequence 1202061,
Sequence 524757,
Sequence 853757,
Sequence 1185102,
Sequence 1185102,
Sequence 1185206,
Sequence 118547,
Sequence 1188547,
Sequence 1188547,
Sequence 673587,
Sequence 673587,
Sequence 673587,
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Sequence 501, App
Sequence 872061,
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                                                                               February 16, 2006, 02:03:53 ; Search time 177.124 Seconds (without alignments) 98.157 Million cell updates/sec
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12: /cgn2_6/prodata/2/pubpna/USOB_NEW_PUB.seq:*
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              GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-127-797-1
US-11-127-803-1
US-11-128-127-1
US-11-127-654-216
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US-11-127-654-501
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                                                                                                                                                                                                                    6247088 segs, 457523669 residues
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Maximum Match 100%
Listing first 300 summaries
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Result ò

Sequence 338521, Sequence 477171, Sequence 550477, Sequence 33, Appl Sequence 34, Appl Sequence 34, Appl Sequence 5629, Ap Sequence 5629, Ap Sequence 5629, Ap Sequence 5639, Ap Sequence 20837, Sequence 12889, A Sequence 132817, Sequence 551178, Sequence 132817, Sequence 132817, Sequence 132817, Sequence 114520, Sequence 114520, Sequence 1229178, Sequence 1229178, Sequence 1229178, Sequence 132817, Sequence 132817, Sequence 132817, Sequence 13287, Sequence 13287, Sequence 13287, Sequence 13287, Sequence 13287, Sequence 145320, Sequence 168356, Sequence 168356, Sequence 168356, Sequence 168359, Sequence 240891, Sequence 240891, Sequence 240891, Sequence 240891, Sequence 168359, Sequence 168359, Sequence 168359, Sequence 168359, Sequence 240891, Sequence 240891, Sequence 1883713, Sequence 188359, Sequence 188359, Sequence 188359, Sequence 188359, Sequence 1883713, Sequence 188359, Sequence 1883713, Sequence 240891, Sequence 240891, Sequence 1883713,	ouenbes
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32 7 US-10-939-294A-19419 Sequence 50 11 US-11-101-244-665663 Sequence 19 9 US-11-101-244-665663 Sequence 19 9 US-11-101-244-665663 Sequence 19 9 US-11-101-244-665663 Sequence 19 10 US-11-103-784-665663 Sequence 19 10 US-11-103-784-665663 Sequence 19 10 US-11-103-784-665663 Sequence 19 10 US-11-103-654-827 Sequence 10 US-11-103-654-827 Sequence 10 US-11-103-644-823 Sequence 10 US-11-103-644-83 Sequence 10 US-10-310-3144-134 Septence	2 2 7 US-10-310-914A-1950340 Sequence 2 2 7 US-10-310-914A-793125 Sequence 2 2 7 US-10-310-914A-793125 Sequence 2 3 7 US-10-310-914A-773124 Sequence 2 3 7 US-10-310-914A-477182 Sequence 2 3 7 US-10-310-914A-137191 Sequence 2 2 7 US-10-310-914A-8052 Sequence 2 2 7 US-10-310-914A-8052 Sequence 2 2 1 US-11-121-849-20799 Sequence 2 2 1 US-11-131-849-20796 Sequence 2 2 1 US-11-131-849-20796 Sequence 2 2 1 US-11-136-527-30636 Sequence 2 2 1 US-11-136-527-308360 Sequence 2 2 1 US-11-136-527-308360 Sequence 2 2 1 US-11-136-527-338502 Sequence 2 2 2 1 US-11-136-527-338502 Sequence 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
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66.3 32 7 US-10-939-294A-19419 Sequence 66.3 50 11 US-11-175-859-18833 Sequence 65.3 19 9 US-11-101-244-665663 Sequence 65.3 19 9 US-11-101-244-665663 Sequence 65.3 19 10 US-11-103-744-1238420 Sequence 65.3 2 19 10 US-11-103-654-503 Sequence 65.3 2 20 11 US-11-121-654-503 Sequence 65.3 2 20 11 US-11-121-649-2242 Sequence 65.3 2 21 US-10-121-649-2242 Sequence 65.3 2 21 US-10-121-849-2242 Sequence 65.3 2 21 US-11-121-849-2242 Sequence 65.3 2 21 US-11-121-849-2243 Sequence 65.3 2 21 US-11-121-849-231305 Sequence 65.3 2 21 US-11-121-849-231305 Sequence 65.3 2 21 US-11-121-849-531305 Sequence 65.3 2 21 US-11-121-849-531305 Sequence 65.3 2 21 US-11-121-849-531305 Sequence 65.3 2 2 11 US-11-121-849-531305 Sequence 64.2 2 10 US-11-121-849-531305 Sequence 64.2 11 US-11-121-849-531305 Sequence 64.2 11 US-11-121-849-531305 Sequence 64.2 11 US-11-131-849-531305 Sequence 64.2 11 US-11-131-9144-121205 Sequence 64.2 11 US-11-131-9144-121205 Sequence 64.2 11 US-11-131-9144-121205 Sequence 64.2 11 US-11-131-9144-121205 Sequence 64.2 11 US-11-131-9144-121305 Sequence 64.2 11 US-11-131-9144-1313149 Sequenc	12.2 64.2 22 7 US-10-310-914A-377036 Sequence 12.2 64.2 22 7 US-10-110-914A-377036 Sequence 12.2 64.2 22 7 US-10-110-914A-77034 Sequence 12.2 64.2 22 7 US-10-310-914A-77224 Sequence 12.2 64.2 23 7 US-10-310-914A-57225 Sequence 12.2 64.2 23 7 US-10-310-914A-477182 Sequence 12.2 64.2 23 7 US-10-310-914A-477182 Sequence 12.2 64.2 23 7 US-10-310-914A-477182 Sequence 12.2 64.2 23 7 US-10-310-914A-135774 Sequence 12.2 64.2 23 7 US-10-310-914A-135774 Sequence 12.2 64.2 23 7 US-10-310-914A-131919 Sequence 12.2 64.2 23 7 US-10-310-914A-131919 Sequence 12.2 64.2 25 7 US-10-310-914A-86553 Sequence 12.2 64.2 25 7 US-10-310-914A-86553 Sequence 12.2 64.2 25 1 US-10-310-914A-86553 Sequence 12.2 64.2 25 1 US-11-121-849-20796 Sequence 12.2 64.2 25 11 US-11-121-849-56055 Sequence 12.2 64.2 25 11 US-11-136-527-30636 Sequence 12.3 64.2 25

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APPLICANT: Krieg, Arthur M.
APPLICANT: Krieg, Arthur M.
APPLICANT: Berg, Daniel J.
TITLE OF INVENTION: IMMONSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC TITLE OF INVENTION: IMPLAMMATORY DISEASES
FILE REFERENCE: C1039.70060US01
CURRENT APPLICATION NUMBER: US/11/12,654
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: US 60/279,642
PRIOR APPLICATION NUMBER: US 60/279,642
PRIOR PILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 1040
SEQ ID NO 76
LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Synthetic oligonucleotide US-11-127-654-76
                                                                                                                                                                                                                             , OTHER INFORMATION: Synthetic oligonucleotide US-11-127-654-74
          FILE REFERENCE: C1039.70060US01;
CURRENT APPLICATION NUMBER: US/11/127,654
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: US 10/112,653
PRIOR FILING DATE: 2002-03-29
PRIOR PILING DATE: 2001-03-29
PRIOR PILING DATE: 2001-03-29
PRIOR PILING DATE: 2010-03-29
SOFTWARE: PATENTIN VERSION 3.2
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 74
TYPE: DNA
ORGANISM: Artificial sequence
TITLE OF INVENTION: INFLAMMATORY DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 76, Application US/11127654; Publication No. US20050250726A1; GENERAL INFORMATION:
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Sequence 1358363,
Sequence 1358363,
Sequence 3104, A
Sequence 31060,
Sequence 795738,
Sequence 97322,
Sequence 91222,
Sequence 911, App,
Sequence 63127, A
Sequence 63127, A
Sequence 63127, A
                                                            Sequence 13925, A Sequence 13933, A Sequence 13933, A Sequence 13936, A Sequence 13942, A Sequence 13942, A Sequence 13942, A Sequence 94751, A Sequence 255965, Sequence 255965, Sequence 25601, Sequence 296024, Sequence 296024, Sequence 296034, Sequence 296034,
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Sequence 1122826,
Sequence 1181622,
Sequence 1211520,
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Sequence 543421,
Sequence 673169,
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Sequence 39373, A
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Sequence 369887,
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Sequence 961314,
Sequence 1021596
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US-10-310-914A-147289
US-10-310-914A-369060
US-10-310-914A-795738
US-10-310-914A-873292
US-10-310-914A-873292
US-10-310-914A-1049795
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US-10-310-914A-673169
US-10-310-914A-91314
US-10-310-914A-961314
US-10-310-914A-1021596
US-10-310-914A-1349901
US-10-310-914A-1349901
US-10-310-914A-135469
US-10-310-914A-35298
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US-10-310-914A-53127
US-10-310-914A-142175
US-10-310-914A-142175
US-10-310-914A-154172
US-10-310-914A-36812
US-10-310-914A-36887
US-10-310-914A-36887
US-10-310-914A-543421
                                                          US-11-136-527-13925
US-11-136-527-13933
US-11-136-527-13934
US-11-136-527-13936
US-11-136-527-13938
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US-11-136-527-94751
US-11-136-527-96001
US-11-136-527-265981
US-11-136-527-265981
US-11-136-527-266001
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APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A

Sequence 74, Application US/11127654
Publication No. US20050250726A1
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Berg, Daniel J.
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC

RESULT 1 US-11-127-654-74

; Sequence 1228446, Application US/10310914A; Publication No. US20060003322A1; GENERAL INFORMATION:

US-10-310-914A-1228446

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TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
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Publication No. US2005024547741
GENERAL INFORMATION:
APPLICANT: Klinman, Dennis
APPLICANT: Klinman, Dennis
APPLICANT: Steinberg, Alfred D.
TILLE REFERENCE: C1039/7029
CURRENT APPLICATION: IMMUNOMODULATORY OLIGONUCLEOTIDES
FILE REFERENCE: C1039/7029
CURRENT APPLICATION NUMBER: US/11/127,797
CURRENT APPLICATION NUMBER: US/05-05-11
PRIOR PILING DATE: 2003-06-05-11
PRIOR PILING DATE: 1995-02-07
PRIOR FILING DATE: 1995-02-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FRALESQ for Windows Version 3.0
SEQ ID NO 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | APPLICANT: Krieg, Arthur M. |
| APPLICANT: Krieg, Arthur M. |
| APPLICANT: Krieg, Arthur M. |
| APPLICANT: Steinberg, Affred D. |
| TITLE OF INVENTION: INMUNOMOBULATORY OLIGONUCLEOTIDES |
| TITLE REFERENCE: C1039/7029 |
| CURRENT APPLICATION NUMBER: US/11/127,803 |
| CURRENT FILING DATE: 2005-05-11 |
| PRIOR APPLICATION NUMBER: US/0690,495 |
| PRIOR APPLICATION NUMBER: US/08/386,063 |
| PRIOR FILING DATE: 1995-02-07 |
| NUMBER OF SEQ ID NOS: 27 |
| SOFTWARE: FastSEQ for Windows Version 3.0 |
| SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
74.7%; Score 14.2; DB 9;
Best Local Similarity 84.2%; Pred. No. 8.1e+02;
Matches 16; Conservative 0; Mismatches 3;
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Publication No. US20050244379A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                         1 GGGAUGACCUUGAGGGGGG 19
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CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1228446
LENGTH: 19
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                                                                                                                                                                                                                       Best Local Similarity 68.4
Matches 13; Conservative
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                                                                                                                                     ORGANISM: Human
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US-11-127-803-1
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US-11-127-797-1
                                                                                                                  TYPE: RNA
                                                                                                                                                                                                         Query Match
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WESULT 7

US-11-127-654-216

US-11-127-654-216

Sequence 216, Application US/11127654

Publication No. US20050250726A1

GENERAL INFORMATION:

APPLICANT: Krieg, Arthur M.

APPLICANT: Ext. Sequence 1 NPLAMMATORY DISEASES

TITLE OF INVENTION: INFLAMMATORY DISEASES

FILE REFERENCE: C1039,70060US01

CURRENT APPLICATION NUMBER: US/11/127,654

CURRENT FILING DATE: 2005-03-12

PRIOR PILING DATE: 2005-03-29

PRIOR PILING DATE: 2001-03-29

PRIOR PILING DATE: 2001-03-29

NUMBER OF SEQ ID NOS: 1040

SOFTWARE PATENTIN VERSION 3.2

SOFTWARE PETENTIN VERSION 3.2

SEQ ID NO 216

LENGTH: 20
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Sequence 1, Application US/11128127
Sequence 1, Application NO: US20050244380A1
GENERAL INCRMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Klinman, Dennis
APPLICANT: Steinberg, Alfred D.
TITLE OF INVENTION: IMMUNOMOBULATORY OLIGONUCLEOTIDES
FILE REFERENCE: C1039/7029
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74.7%; Score 14.2; DB 9;
Best Local Similarity 84.2%; Pred. No. 8.1e+02;
Matches 16; Conservative 0; Mismatches 3;
                                                                                                                                            Query Match
74.7%; Score 14.2; DB 9;
Best Local Similarity 84.2%; Pred. No. 8.1e+02;
Matches 16; Conservative 0; Mismatches 3;
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-803-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-128-127-1
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CURRENT FILING DATE: 2005-05-11
PRIOR APPLICATION NUMBER: US/10/690,495
PRIOR FILING DATE: 2003-10-21
PRIOR PILING DATE: 1995-02-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 20
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ORGANISM: Artificial Sequence
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Sequence 895439, Application US/10310914A
Publication No. US/20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bantwich, Kvuzat
TITLE OF INVENTION:
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
TITLE REFERENCE: 06097.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 895439
                     GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses 1,000,000
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses 1,000,000
TITLE OF INVENTION: uses thereof
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Publication No. US2060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Besinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
TITLE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION VMDER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1185102
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Pred. No. 1.3e+03;
0; Mismatches 2; Indels
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Pred. No. 1.3e+03;
3; Mismatches 2;
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88.2%;
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Best Local Similarity 70.6%;
Matches 12; Conservative
Publication No. US20060003322A1
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Best Local Similarity 88.2'
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US-10-310-914A-1185102
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US-10-310-914A-1185102
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                    TYPE: RNA
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| Publication No. US20060003322A1
| GENERAL INPORTATION:
| APPLICANT: Bentwich, Isaac
| APPLICANT: Shiler, Kvuzat
| APPLICANT: Shiler, Kvuzat
| APPLICANT: Shiler, Kvuzat
| TITLE OF INVENTION: Uses thereof
| TITLE OF INVENTION: Uses thereof
| TITLE OF INVENTION: Uses thereof
| FILE REFERENCE: 06097.0200.CPUS01
| CURRENT APPLICATION NUMBER: US/10/310,914A
| CURRENT FILING DATE: 2002-12-06
| NUMBER OF SEQ ID NOS: 1388402
| SEQ ID NO 1202061
| LENGTH: 28
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Publication No. US20060003322A1
GENERAL INFORMATION:
GENERAL SHILE, Kvuzat
FITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FITLE OF INVENTION: uses thereof
FITLE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PATENTIN version 3.3
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                                                                            Score 14.2; DB 11; Length 20;
Pred. No. 8.1e+02;
0; Mismatches 3; Indels
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Pred. No. 1e+03;
0; Mismatches 0; Indels
OTHER INFORMATION: Synthetic oligonucleotide
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Best Local Similarity 84.2%;
Matches 16; Conservative
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Matches 14; Conservative
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US-10-310-914A-1202061/c
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US-10-310-914A-895375/c
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US-10-310-914A-524757
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US-10-310-914A-524757
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LENGTH: 20
            ; UTHER INFORMA
US-11-127-654-216
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US-11-083-784-1188547/C

Sequence 1188547, Application US/11083784

Publication No. USCO050245475A1

GENERAL INFORMATION:

APPLICAMT: Baracon, Inc.

APPLICAMT: Reynolds, Angela

APPLICAMT: Berei, Devin

APPLICAMT: Marshall, William

APPLICAMT: Marshall, William

APPLICAMT: Marshall, William

APPLICAMT: Marshall, William

APPLICAMT: Scaringe, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/083,784

CURRENT FILING DATE: 2003-19-10

PRIOR FILING DATE: 2003-19-10

PRIOR FILING DATE: 2003-19-10

PRIOR FILING DATE: 2003-19-10

PRIOR FILING DATE: 2002-11-14

NUMBER: Proprietary

SOFTWARE: Proprietary

SOFTWARE: Proprietary

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LEMSTH: NUMBER: Proprietary

LEMSTH: NUMBER: Proprietary

LEMSTH: NUMBER: Proprietary
                                   APPLICANT: KNOOTOVA, ANGELASIA
APPLICANT: KNOOTOVA, ANGELASIA
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marchall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PLING DATE: 2003-09-10
PRIOR PELING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: PEPPIFELATY
LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 13.4; DB 9;
Pred. No. 1.9e+03;
0; Mismatches 1;
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Best Local Similarity 93.3
Matches 14; Conservative
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Matches 14; Conservative
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US-11-101-244-1188547
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US-10-310-914A-673587/c
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US-10-310-914A-530908/C
US-10-310-914A-530908/C
Sequence 530908, Application US/10310914A
Publication No. US20060003322A1
Publication No. US20060003322A1
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kuuzat
TITLE OF INVENITON: uses thereof
FILE REPREBNCE: 06087,0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SSEQ ID NO 530908
LENGTH: 23
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1185206, Application US/10310914A

Fublication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Benewich, Isaac

APPLICANT: Bene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.6%; Score 13.8; DB 7; Length 22; 70.6%; Pred. No. 1.3e+03;
                                                    Query Match 72.6%; Score 13.8; DB 7; Length 21; Best Local Similarity 88.2%; Pred. No. 1.3e+03; Matches 15; Conservative 0; Mismatches 2; Indels
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Best Local Similarity 88.2
Matches 15, Conservative
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Best Local Similarity 70.6
Matches 12, Conservative
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US-11-101-244-1188547/c
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US-10-310-914A-1185206
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US-10-310-914A-1185206
US-10-310-914A-895439
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Sequence 872061, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Bentwich, Isaac

APPLICANT: Bentwich, Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Uses thereof

TITLE OF INVENTION: Uses thereof

TITLE OF INVENTION: Uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: Patentin version 3.3

SEQ ID NO 872061

LENGTH: 21
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APPLICANT: Krieg, Arthur M.
APPLICANT: Krieg, Arthur M.
APPLICANT: Krieg, Arthur M.
APPLICANT: Berg Daniel J.
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC TITLE OF INVENTION: IMMUNOSTIMULATORY DISEASES
FILE REFERENCE: C1039.70060US01
CURRENT PEPLICATION NUMBER: US/11/12,653
PRIOR APPLICATION NUMBER: US 10/112,653
PRIOR FILING DATE: 2002-03-29
PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 1040
SOFTWARE: Astentin version 3.2
SEQ ID NO 501
LENGTH: 20
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                                                                                                                                                                                                                                                                                        Score 13.2; DB 11;
Pred. No. 2.4e+03;
0; Mismatches 3;
                                                                      TYPE: DNA
CRGANISM: Artificial sequence
FEATURE:
JOTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-498
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Publication No. US20050250726A1
GENERAL INFORMATION:
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Best Local Similarity 83.3%;
Matches 15; Conservative
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ORGANISM: Human
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   SEQ ID NO 498
LENGTH: 20
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                                                      APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUSO1
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 673587
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Publication No. US20060003322A1
Publication No. US2006000332A1
GENERAL INFORMATION:
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION UNDERE: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 308426
LENGTH: 18
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APPLICANT: Krieg, Arthur M.
APPLICANT: Berg, Daniel J.
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
TITLE OF INVENTION: INFLAMMATORY DISEASES
FILE REFERENCE: C1039.70060US01
CURRENT APPLICATION NUMBER: US/11/127,654
CURRENT APPLICATION NUMBER: US 10/112,653
PRIOR APPLICATION NUMBER: US 10/112,653
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Pred. No. 1.9e+03;
0; Mismatches 1; Indels
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Publication No. US20060003322A1
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Best Local Similarity 93...
Best Local 4; Conservative
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Best Local Similarity 83.3
Matches 15; Conservative
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US-10-310-914A-308426/c
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ORGANISM: Human
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RESULT 26

US-10-310-914A-896494/C

Sequence 896494, Application US/10310914A

Sequence 896494, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Bhiler, Kvuzat

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Uses thereof

FILE REFERENCE: 06087.0200.CFUS01

CURRENT APPLICATION WHMER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SEQ ID NO 896494

LENGTH: 23
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof FILE REFERENCE: 06087.0200.CURNENT PRILIS APPLICATION NUMBER: US/10/310,914A CURRENT FILING DATE: 2002-12-06 NUMBER OF SEQ ID NOS: 1388402 SOFTWARE: Patentin version 3.3 SEQ ID NO 518042
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Publication No. US20060003322A1

GENERAL INFORMATION.

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TITLE OF INVENTION: Uses thereof

TITLE OF INVENTION: Uses the Uses the Uses the Uses the Uses the Uses the Uses th
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Pred. No. 2.4e+03;
0; Mismatches 3;
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Pred. No. 2.4e+03;
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Best Local Similarity 83.3
Matches 15; Conservative
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Best Local Similarity
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Matches 12; Conserv
                                                                                                                                                                                                                                        ; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-518042
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US-10-310-914A-836953
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US-10-310-914A-896494
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Pred. No. 2.4e+03;
0; Mismatches 3; Indels
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                  Pred. No. 2.4e+03;
3; Mismatches 3; Indels
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US-10-310-914A-518042/c
; Sequence 518042, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
                                                                                          2 GGGTGACGTTCAGGGGGG 19
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Best Local Similarity 83.3%;
Matches 15; Conservative
                  L Similarity 72.2%;
13; Conservative
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Best Local Similarity 83.33
Matches 15; Conservative
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; APPLICANT: Shiler, Kvuzat
                                                                                                                                                                                                                 RESULT 22
US-10-310-914A-114797/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-310-914A-114797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: RNA
ORGANISM: Human
                  Best Local
Matches 1
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TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF FILE REPERRORS: 017733-198
CURRENT APPLICATION NUMBER: 105/11/012,353
CURRENT FILING DATE: 2004-12-16
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                       CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 16126
LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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PRIOR FILING DATE: 2003-12-16
PRIOR FILING DATE: 2003-12-16
PRIOR FILING DATE: 2003-01-11
PRIOR FILING DATE: 2003-01-20
PRIOR PILING DATE: 2003-01-20
PRIOR APPLICATION NUMBER: FR 020653
PRIOR APPLICATION NUMBER: FR 020653
PRIOR FILING DATE: 2002-05-07
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: PATENTIN VET: 3.3
LENGTH: 32
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PRIOR APPLICATION NUMBER: 10/735,916
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Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: GOETSCH, LILLIANE
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APPLICANT: DUFLOS, ALAIN
BAPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: LEGER, OLIVIER
APPLICANT: BECK, ALAIN
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-16126
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Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof
FILE REFERENCE: 066097.0200.CPUSOI;
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-112-06
NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: Patentin version 3.3
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APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-112-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
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; Publication No. US20050272080A1
; GENERAL INFORMATION:
APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; TITLE OF INVENTION: Microarrays
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83.3%; Pred. No. 2.4e+03;
ive 0; Mismatches 3; Indels
Indels
3;
0; Mismatches
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US-10-310-914A-509542/C
US-10-310-914A-509542, Application US/10310914A
; Sequence 509542, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
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                                                                      GGGTGACGTTCAGGGGG 19
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Best Local Similarity 66.79
Matches 12, Conservative
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Best Local Similarity 83.3*
Matches 15; Conservative
15; Conservative
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; ORGANISM: Human
US-10-310-914A-837004
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US-11-121-849-16126
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ORGANISM: Human
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Matches
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Sequence 966777

Sequence 966777
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Publication No. US20060003322A1
GERREAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: uses thereof
TITLE REPERENCE: 06097.0200.CPUS01
TITLE OF INVENTION: uses thereof
TITLE APPLICATION NUMBER: US/10/310,914A
TITLE OF INVENTION: uses thereof
TITLE APPLICATION NUMBER: 03.13
TITLE OF INVENTION: uses thereof
TITLE REPERENCE: 06097.0200.CPUS01
TITLE REPERENCE: 06097.0200.CPUS01
TITLE REPERENCE: 06097.0200.CPUS01
TITLE REPERENCE: 06097.0200.CPUS01
TITLE OF INVENTION: uses thereof
TITLE REPERENCE: 06097.0200.CPUS01
TITLE OF INVENTION: uses thereof
TITLE REPERENCE: 06097.0200.CPUS01
TITLE OF INVENTION: 1309402
TITLE REPERENCE: 06097.0200.CPUS01
TITLE REPERE
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67.4%; Score 12.8; DB 7;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2;
                                                                                                                                                       TYPE: DNA
ROGANISM: Homo sapiens
REATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(23)
CTHER INFORMATION: CD90 antisense primer
US-10-522-362-49
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-310-914A-746353/c
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US-10-310-914A-966777/c
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                                                    SEQ ID NO 49
LENGTH: 20
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                                        GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Yuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
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**PRILICANT: Bentwich, Isaac

**TITLE OF INVENTION: uses thereof

**TITLE USE OF I
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Pred. No. 3.7e+03;
2; Mismatches 2; Indels
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Publication No. US20050281788A1

GENERAL INFORMATION:

APPLICANT: De Bari, Cosimo

APPLICANT: De Bari, Cosimo

APPLICANT: Luyten, Francesco

TITLE OF INVENTION: Progenitor Cells and Uses Thereof

TITLE OF INVENTION: Progenitor Cells and Uses Thereof

FILE REFERENCE: 50304/030001

CURRENT FILING DATE: 2005-01-26

PRIOR PRLICATION NUMBER: PCT/EP03/009008

PRIOR PLLING DATE: 2003-07-30

PRIOR PLLING DATE: 2003-07-30

PRIOR FILING DATE: 2003-07-30

PRIOR FILING DATE: 2003-07-30

NUMBER OF SEQ ID NOS: 49
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75.08;
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     Publication No. US20060003322A1
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Best Local Similarity 87.2.
المالية المال
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Best Local Similarity 75.0
Matches 12; Conservative
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ORGANISM: Human
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US-10-522-362-49
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Sequence 15921, Application US/1121849
Fublication No. US20050272080A1
Fublication No. US20050272080A1
Fublication No. US20050272080A1
Fublication No. US20050272080A1
Fublication No. US200502720B1
FILE REPERENCE: 3684.1
FILE REFERENCE: 3684.1
FULL REPERENCE: 3684.1
FULL REPE
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US-11-121-849-22103/c
US-11-121-849-22103, Application US/11121849
; Sequence 22103, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S:
TITLE OF INVENTION: Microarrays
; TITLE OF INVENTION: Wicroarrays
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR PILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SEQ ID NO 22103
; LENGTH: 25
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Pred. No. 3.7e+03;
0; Mismatches 2;
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Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                            Score 12.8; DB 7;
Pred. No. 3.7e+03;
2; Mismatches 2;
CURRENT APPLICATION NUMBER: US/10/310,914A CURRENT FILING DATE: 2002-12-06 NUMBER OF SEQ ID NOS: 1388402 SOFFWARE: Patentin version 3.3 SEQ ID NO 1145337
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Best Local Similarity 87.5%;
Matches 14; Conservative
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Best Local Similarity 75.0
Matches 12; Conservative
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ORGANISM: Homo sapien
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US-11-121-849-15921/C
                                                                                                                                                                                                   TYPE: RNA
ORGANISM: Human
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                                                                                                                                                                                                          Sequence 240915, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06097.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO SEQ ID NOS: 1388402
SEQ ID NOS: 1388402
SEQ ID NOS: 1388402
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Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
APPLICANTON: Back thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION WUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ INFORMATE: Patentin version 3.3
SEQ INFORMATE: 24
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Sequence 1145337, Application US/10310914A
Sequence 1145337, Application No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Baniler, Kouzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
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Pred. No. 3.7e+03;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: uses thereof FILE REFERENCE: 06087.0200.CPUS01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.4%;
81.2%;
   1 GGGGTGACGTTCAGGG 16
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                                                             GGGGAGACGCTCAGGG 2
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Matches 13; Conservative
                                                                                                                                                                    RESULT 36
US-10-310-914A-240915/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-411534
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US-10-310-914A-411534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: RNA
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Sequence 476398, Application US/11121849

Sequence 476398, Application US/11121849

Fublication No. US20050272080A1

GENERAL INFORMATION:

APPLICANT: John Palma

TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded Settle OF INVENTION: Microarrays

TITLE OF INVENTION: Microarrays

TITLE OF INVENTION: Microarrays

CURRENT PILING DATE: 2005-05-03

CURRENT FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SEQ ID NO 476398

LENGTH: 25
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Sequence 568167, Application US/11121849

Publication No. US20050272080A1

GENERAL INFORMATION:

TITLE OF INVENTION: Microarrays

TITLE OF INVENTION: Microarrays

FILE REFERENCE: 3684.1

CURRENT APPLICATION NUMBER: US/11/121,849

CURRENT APPLICATION NUMBER: US/11/121,849

PRIOR FILING DATE: 2005-05-03

PRIOR FILING DATE: 2004-05-03
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TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR PILING DATE: 2004-05-03
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 115643
LENGTH: 25
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SOFWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 568167
LENGTH: 25
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Pred. No. 3.7e+03;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                             Score 12.8; DB 11;
Pred. No. 3.7e+03;
0; Mismatches 2;
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87.5%;
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Best Local Similarity 87.5%;
Matches 14; Conservative
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Best Local Similarity 87.5
Matches 14; Conservative
                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-115643
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US-11-121-849-476398
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; ORGANISM: Homo sapien
US-11-121-849-568167
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**Bublication No. US20050272080A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: John Palma

TITLE OF INVENTION: Microarrays

FILE REFERENCE: 3684.1

CURRENT APPLICATION NUMBER: US/11/121,849

CURRENT PILING DATE: 2005-05-03

PRIOR APPLICATION NUMBER: 60/567,949

PRIOR APPLICATION NUMBER: 60/567,949

RIOR PILING DATE: 2004-06-03

NUMBER OF SEQ ID NOS: 673904

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 107577
                                                                                                                                                               US-11-121-849-24138/c

Sequence 24138, Application US/11121849

Fublication No. US20050272080A1

GENERAL INFORMATION:

APPLICANT: John Palma

TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded STITLE OF INVENTION: Microarrays

TITLE OF INVENTION: Microarrays

TITLE OF INVENTION: Microarrays

FILE REPRENCE: 3684.1

CURRENT APPLICATION NUMBER: US/11/121,849

FRIOR FILING DATE: 2004-05-03

PRIOR FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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, TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.4%; Score 12.8; DB 11; Length 25; 87.5%; Pred. No. 3.7e+03; ive 0; Mismatches 2; Indels
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                               3 GGTGACGTTCAGGGGG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 GGTGACGTTCAGGGGG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGGGTGACGTTCAGGG 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 GGTGATGTTCTGGGGG 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 67.4
Best Local Similarity 87.5
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-107577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapien
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US-11-121-849-115643/c
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US-11-121-849-107577
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APPLICANT: Pingle, Maneesh
APPLICANT: Pingle, Hanna
TITLE OF INVENTION: McLhods for identifying target nucleic acid molecules
FILE REFERENCE: 19603/4121 (CRF D-2995-02)
CURRENT PEPLICATION NUMBER: US/10/939,294A
CURRENT FILING DATE: 2004-09-10
PRIOR FILING DATE: 2003-09-12
NUMBER OF SEQ ID NOS: 38895
SOFTWARE: Patentin version 3.3
SEQ ID NO 19843
LENGTH: 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.4%; Score 12.8; DB 6;
87.5%; Pred. No. 3.7e+03;
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87.5%; Pred. No. 3.7e+03;
cive 0; Mismatches 2;
                                                      PILING DATE: 20-NOV-2001
APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APP-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/712,027
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/712,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timochy
REGISTRATION NUMBER: 38,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLBCULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer P5(a)"
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/988,462
                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: 43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Oligonucleotide probe US-10-939-294A-19843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19843, Application US/10939294A Publication No. US20050266417A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (919)541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 32 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GGTGACGTTCAGGGGG 18
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Best Local Similarity 87.5
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Barany, Francis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-10-939-294A-19843
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US-11-121-849-570964
is Sequence 570964, Application US/11121849
is Publication No. US2050272080A1
is GENERAL INFORMATION:
is TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded STITLE OF INVENTION: Microarrays
if TITLE INVENTION: Microarrays
if TITLE Microarrays
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| Sequence 43, Application US/10755092
| Publication No US20060021095A1
| GENERAL INFORMATION:
| APPLICANT: Koziel, Michael G. Lewis, Kelly S. Kener, Vance C. Kramer, Vance C. Warren, Gregory W. Evola, Stephen V. Crossland, Lyle D. Wright, Martha S. Marin, Blis J. Launis, Karen L. Launis, Karen L. Launis, Karen L. INSCTICIDAL ACTIVITY IN MAIZE
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         Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRING APPLICATION DATA:
FILING DATE: 08-Jan-2004
                                                                      Indels
      67.4%; Score 12.8; DB 11; ilarity 87.5%; Pred. No. 3.7e+03; Conservative 0; Mismatches 2;
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ADDRESSER: Syngenta Biotechnology, Inc. STREET: 3054 Cornwallis Road CITY: Research Triangle Park
                                                                                                                                   1 GGGGTGACGTTCAGGG 16
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                                                                 Sequence 51905, Application US/11175859
; bublication No. US20060024715A1
; GRNERAL INFORMATION:
    APPLICANT: Affymetrix, Inc.
; APPLICANT: Affymetrix, Inc.
; TILE OF INVENTION: Method of Analysis of Human Polymorphism
; TILE OF INVENTION: Method of Analysis of Human Polymorphism
; CURRENT APPLICATION UNDHER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR APPLICATION NUMBER: US 60/585,352
; NUMBER OF SEQ ID NOS: 116251
; SEQ ID NO 51905
; LENGTH: 50
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, ORGANISM: homo sapien
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RESULT 1 AX103889 LOCUS DEFINITION ACCESSION	

synthetic construct synthetic construct other sequences; artificial sequences.

AX546942.1 GI:25812086

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE

PAT 30-APR-2001

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24 bp WO0122972.

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ALIGNMENTS

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PAT 06-FEB-2002
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                                                    Krieg,A.M., Schetter,C. and Vollmer,J.C.
Immunostimulatory nucleic acids
Patent: WO 0122972-A 81 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical GmbH (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                  1. .24
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phosphorothioate at 5' and 3' ends"
                                                                                                                                                                                                                                                                                                                                                           Weiner, G. and Hartmann, G. Methods for enhancing and treating
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Patent: WO 0197843-A 440 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
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/organism='Artificial Sequence'
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     /note="Single strand DNA oligonucleotide"
                                                 Length 30;
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1 (bases 1 to 33)
Horlick, R. A. and Chelsky, D.
Method for maintenance and selection of episomes
Patent: US 6417002-A 11 09-UUL-2002;
Pharmacopeia, Inc.; Cranbury, NJ
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Local Similarity 100.0%; Pred. No. 5.9e+04;
Nes 16; Conservative 0; Mismatches 0;
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Patent: JP 2002238769-A 5 19-NOV-2002;
UNIVERSITY OF NEBRASKA LINCOLN
OS Artificial Sequence
PN JP 2002538769-A/5
PD 19-NOV-2002
PF 29-OCT-1999 JP 2000579763
PR 30-OCT-1999 US 60/106321,09-JUN-1MARTIN B DICKMAN
PC A01HS/00,C12N5/10,C12N15/09,C12Q1/66
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1 (bases 1 to 33)
Dickman, M.B.
                                                 Query Match 66.7%; Score 16; DB Best Local Similarity 100.0%; Pred. No. 6e+Matches 16; Conservative 0; Mismatches
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Sequence 11 from patent US 6417002.
AR217874
AR217874.1 GI:23317768
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                                                                                                                                                                                                                                   Gaps
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Jevnikar, A.M., Ma, S. and Stiller, C.R.
Methods and products for controlling the immune response of a mammal to glutamic acid decarboxylase
Patent: US 6338850-A 1 15-JAN-2002;
Location/Qualifiers
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85.7%; Pred. No. 5.2e+04;
ive 0; Mismatches 3; Indels
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Best Local Similarity 100.0%; Pred. No. 33;
Matches 24; Conservative 0; Mismatches 0; Indels
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Bratzler, R. L.
Inhibition of angiogenesis by nucleic acids
Patent: WO 02053141-A 81 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
Location/Qualifiers
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/note="Synthetic Sequence"

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/mol_type="unassigned DNA"
    /db_xref="taxon:32630"

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Sequence 2 from Patent WO2004072225.
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CQ859706.1 GI:51981619
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muniostimulatory nucleic acids
Patent: WO 0122972-A 90 05-ARR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
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/mol_type="unassigned DNA"
/db xref="taxon:32630"
/noTe="synthetic oligonucleotide
chimeric phosphorothioate/phosphodiester backbone with
phosphorothioate at 5' and 3' ends"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weiner, G. and Hartmann, G. Methods for enhancing antibody-induced cell lysis and treating
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100.0%; Pred. No. 1.7e+05;
ive 0; Mismatches 0; Indels
85.0%; Pred. No. 1.3e+05;
tive 0; Mismatches 3; Indels
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UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
Location/Qualifiers
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Sequence 533 from Patent W00197843.
AX355505
AX355505.1 GI:18620173
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AX103898
AX103898.1 GI:13920095
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                                                     2 GGGTCCAGCGTGCGCCATGG 21
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Best Local Similarity
Matches 17; Conserv
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Kim,J. P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
Sheppard,L.T., Kim,M.Y. and Bruice,T.W.
Promoters for regulated gene expression
Patent: US 6838556-A 69 04-JAN-2005;
Genelabs Technologies, Inc.; Redwood City, CA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F., Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A., Sheppard,L.T., Lim,M.Y. and Bruice,T.W. Promoters for regulated gene expression parent: WO 0194600-A 69 13-DEC-2001; GENELABS TECHNOLOGIES, INC. (US)
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                                                                                                        66.7%; Score 16; DB 6; Length 33; 100.0%; Pred. No. 5.9e+04; rive 0; Mismatches 0; Indels
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Pred. No. 1.3e+05;
0; Mismatches 3;
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other sequences; artificial sequences.
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Sequence 69 from patent US 6838556.
AR630015.1 GI:59762210
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                                                                                                                                           16; Conservative
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AX754696/c
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1 (bases 1 to 27)
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Reed,J.C. and Sato,T.
Reed,J.C. and Sato,T.
Nucleic acids encoding Fas associated proteins and screening assays using same
Lecation/Qualifiers
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                                                                                                                                                          Bratzler, R.L.
Inhibition of angiogenesis by nucleic acids
Patent: WO 02053141-A 90 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
Location/Qualifiers
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Sequence 13 from patent US 5632994.
143661.1 GI:2468759
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Sequence 13 from patent US 5747245.
AR004426
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Sequence 90 from Patent WO02053141.
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synthetic construct
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Best Local Similarity 100.
Matches 15; Conservative
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143661/c
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Regulation of gene transcription by the variable number of tandem repeats (vntr) domain of the dopamine transporter gene patent: WO 03038099-A 1 08-MAY-2003;
Tcs Cellworks Ltd (GB)
Tcs Cellworks Ltd (GB)
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Reed, J.C. and Sato, T.
Interaction of proteins involved in a cell death pathway
Patent: US 5702897-A 8 30-DEC-1997;
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Sequence 1 from Patent W003038099.
AX754696.1 GI:32167230
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Sequence 8 from patent US 5702897.
186720
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1 (bases 1 to 27)
Reed.J.C. and Saco.T.
Fas associated proteins
Patent: US 5632994.A 13 27-MA
Location/Qualifiers
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Homo sapiens
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PAT 20-DEC-2002

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1 (bases 1 to 47)
Larocca,D., Kassner,P. and Baird,A.
METHODS USING GENETIC PACKAGE DISPLAY FOR DETECTING AND IDENTIFYING
METHODS USING GENETIC PACKAGE DISPLAY FOR DETECTING AND INTERACTIONS THAT FACILITATE INTERNALIZATION AND
TRANSGENE EXPRESSION AND CELLS OR TISSUES COMPETENT FOR THE SAME
AND METHODS FOR WOUVING GENE DELIVERY VECTORS
PATENT: US 6723512-A 5 20-APR-2004;
Selective Genetics Inc.; San Diego, CA
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Larocca,D., Baird,A. and Kassner,P.
Methods using genetic package display for selecting internalizing ligands for gene delivery
Patent: US 6451527-A 5 17-SEP-2002;
Selective Genetics, Inc.; San Diego, CA
Location/Qualifiers
Biopharm, Vyzkummy ustav biofarmacie a veterinarnich leciv a.s.
(C2)
                                                                   1. .20
/organism="synthetic construct"
/or Lype="unassigned DNA"
/mol type="taxon:32630"
/db xref="taxon:32630"
/note="Translational consensus WAP-EPO with NotI modification"
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                                                                                                                                                                                                                     61.7%; Score 14.8; DB 6
ilarity 88.9%; Pred. No. 2e+05;
Conservative 0; Mismatches
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/mol_type="genomic DNA"
                                              Location/Qualifiers
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Matches 16; Conserv
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                                              FEATURES
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The genomic organization of the human transcription factor 3 (TFB3)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Submitted (21-FEB-1995) A. Villa, ITBA- CNR, Via Ampere 56, 20131
                                                                 Gaps
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                              Length 40;
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1.5e+05;
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                          / Match 62.5%; Score 15; DB Local Similarity 78.3%; Pred. No. 1.5c Nes 18; Conservative 0; Mismatches
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/gene="tfe3"
/gene="tfe3"
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Sequence 12 from Patent EP1217072.
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/organism="Homo sapiens"
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transcription factor 3.
Homo sapiens (human)
Homo sapiens
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AX463650.1 GI:21886409
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Villa, A.
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PAT 08-OCT-2004

DEFINITION

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1 (bases 1 to 29)
Aujame, L., Bouchardon, A., Renauld-Mongenie, G., Rokbi, B., Nassif, X.,
Tinsley, C. and Perrin, A.
Nucleic acids and polypeptides specific of the neisseria genus
                                                                                                            PAT 14-FEB-2005
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Patent: US 6835384-A 127 28-DEC-2004;
Aventis Pateur and Institut National de la Sante et de
Recherche Medicale (INSERM); Lyons;
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Patent: FR 2785293-A 127 05-MAY-2000;
PASTEUR MERIEUX SERUMS VACC (FR)
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/mol_type="unassigned DNA"
/mol_type="taxon:32630"
/note="amorce de"
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synthetic construct
other sequences; artificial sequences.
                                                                                                        Sequence 127 from patent US 6835384.
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    /organism="unknown"
    /mol_type="genomic DNA"

               GGGATCCAACCTGCTTCATGGGTG 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAT 16-NOV-2004
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Aventis Pasteur (FR); INSTITUT NATIONAL DE LA SANTE ET RECHERCHE MEDICALE (INSERM) (FR)
Location/Qualifiers
                             60.8%; Score 14.6; DB 6; Length 47;
81.0%; Pred. No. 2.1e+05;
iive 0; Mismatches 4; Indels
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    organism="synthetic construct"

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Bacl-2 splicing variants
Patent: WO 2005012357-A I 10-FEB-2005;
Milmer, Jo (GB)
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Sequence 1 from Patent W02005012357.
CS019648.1 GI:60220655

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Sequence 129 from Patent EP1475441.
CQ902189.1 GI:55784068
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Matches 18; Conservative
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unclassified.
                                                Best Local Similarity
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                                 Query Match
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CS019648/c
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1 (bases 1 to 19)
Rao,M.S., Proschel,M.M. and Kalyani,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OS Rattus norvegicus (rat)
PN JP 2002515071-A/14
PD 21-MAY-2002
PD 21-MAY-2002
PF 03-UUJ-1998 UP 1999507430
PR 04-UUJ-1997 US 08/909435,02-JUL-1998 US 09/109858 PI
MAHENDRA S RAO, MARGOT MAYER PROSCHEL, ANJALI J KALYANI PC
A61K48/00,A61K35/30,C12N5/00,C12N5/08 CC
Lineage-restricted neuronal precursors
FH Key
         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                       Shimkets, R.A. and Leach, M. Nucleic acids containing single nucleotide polymorphisms and methods of use thereof batent: WO 0147944-A 7160 05-JUL-2001; Curagen Corporation (US)
                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25. 7.26
/note="Nucleotide deleted between bases 25 and 26
Accession number cg40388639"
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           Indels
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Patent: JP 2002515071-A 14 21-MAY-2002;
UNIVERSITY OF UTAH RESEARCH FOUNDATION
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BD194701
                                                                                                                                                                           DNA
                                                                                                                                                                       CQ008520 Sequence 7160 from Patent WO0147944.
           0; Mismatches
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Rattus norvegicus
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                                             1 GGGGTCCAGCGTGCGCCATGGGGG 24
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                                                                                 26 GGCGGCTCGCGTGCGCCAGGCGGG
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CQ008520.1 GI:41015226
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JP 2002515071-A/14.
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           18; Conservative
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BD194701
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Location/Qualifiers
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/organism='Artificial Sequence'
Location/Qualifiers
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DAIICHI PHARMACEUTICAL CO LTD
DAIICHI PHARMACEUTICAL CO LTD
OS Artificial Sequence
DN JP 2000232889-A/4
PD 29-AUG-2000
PF 30-JUL-1999 JP 1999216640
PR PI MASASHI AONUMA
PC C12N15/09, C12N19/10, C12N11/14, C12Q1/48, C12N15/PF Key
FT SOURCE LOCATION/Qualifiers
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35 bp DNA line A method for determining DNA methyltransferase.
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Patent: JP 2000232889-A 2 29-AUG-2000;
DAIICHT PHARMACEUTICAL CO LTD
OS Artificial Sequence
N JP 2000232889-A/2
PD 29-AUG-2000

    .35
        /organism="synthetic construct" mol_type="genomic DNA"
        /db_xref="taxon:32630"

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other sequences; artificial sequences.
1 (bases 1 to 35)
Aonuma,M.
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synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 35)

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    /organism="synthetic co
/mol_type="genomic DNA"
/db_xref="taxon:32630"

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BD002995.1 GI:18630956
JP 2000232889-A/4.
                                                              BD002993.1 GI:18630954
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PAT 29-SEP-1999
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Antisense oligonucleotides inhibiting human bcl-2 gene expression Patent: US 5734033-A 9 31-MAR-1998;
Location/Qualifiers
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/mol_type="unassigned DNA"
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Sequence 17 from patent US 5831066.
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Sequence 10 from patent US 5734033.
196091
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/wol_type="unassigned DNA"
                                                                                                                                                           Sequence 9 from patent US 5734033.
196090
                             37 GTTCAGCGGCGCCAGGGG 19
22
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AR052619.1 GI:5975983
GTCCAGCGTGCGCCATGGG
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1 (bases 1 to 17)
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Rao,M.S., Mayer-Proschel,M. and Kalyani,A.J.
Lineage-restricted neuronal precursors and methods of isolation
Patent: US 6787353-A 14 07-8EP-2004;
University of Utah Research Foundation; Salt Lake City, UT
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Best Local Similarity 84.2%; Pred. No. 3.6e+05;
Matches 16; Conservative 0; Mismatches 3; Indels
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/organism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"
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1. .19
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
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other sequences; artificial sequences.
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Sequence 14 from patent US 6787353.
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    19 /organism="unknown"
/mol_type="genomic DNA"

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Krieg, A.M., Kline, J., Klinman, D. and Steinberg, A.D.
Immunostimulatory nucleic acid molecules
Patent: US 6207646-A 55 27-MAR-2001;
Location/Qualifiers
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Sequence 104 from patent US 6218371.
AR146392
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/organism="unknown"
/mol_type="unassigned DNA"
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/mol_type="unassigned DNA"
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Brown,L.R. and Xu,C.
Fluorescent dibenzazole derivatives and methods related thereto
Patent: US 6140051-A 1 31-OCT-2000;
Location/Qualifiers
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100.0%; Pred. No. ...
0; Mismatches
Reed, J.C.
Regulation of bcl-2 gene expression
Patent: US 5831066-A 24 03-NOV-1998;

    .18
    /organism="unknown"
    /mol_type="unassigned DNA"

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/organism="unknown"
/mol_type="unassigned DNA"
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AR052624
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AR052624
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AR116926
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Matches

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ORIGIN

REPERENCE

REFERENCE AUTHORS

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Gaps

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PAT 08-AUG-2001

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Gaps

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PAT 08-AUG-2001

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other sequences; artificial sequences.

I (bases 1 to 18)
S Schwartz,D.A. and Krieg,A.M.
S Schwartz,D.A. and Krieg,A.M.
Use of nucleic acids containing unmethylated CPG dinucleotide in the treatment of LPS-associated disorders

L Patent: JP 2001513776-A 27 04-SEP-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION
OS Artificial Sequence
PN D 2001513776-A/27
PN 04-SEP-2001
PP 25-FEB-1999 UP 1998537810
PR 25-FEB-1997 US 60/039405
PR 28-FEB-1997 US 60/039405
PR 28-FEB-1997 US 60/039405
PR AGINGAP/OO, COTHZI/O4, A01N43/04
CC Synthetic oligonucleotide
PH Key Location/Qualifiers
FT Source Location/Qualifiers
FT FT Source Location/Qualificial Sequence'.
                                                                                                                                                PAT 27-AUG-2002
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                                                                                                                                           BD069938 1sh p DNA linear PAT 27-AUG-20
Use of nucleic acids containing unmethylated CPG dinucleotide in
the treatment of LPS-associated disorders.
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PF 28-SEP-1998 JP 2000515030
PR 20-COT-1997 US 60/060673,18-AUG-1998 US 09/136
TIMOTHY A RIBEY,BOB D BROWN, LYLE J ARNOLD
PC C12Q1/68,C07H21/04,C12N15/09,C12P19/34,C12N15/00 CC
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other sequences; artificial sequences.
1 (bases 1 to 18)
Riley, T.A., Brown, B.D. and Arnold, L.J.
Combined antisense library
Patent: JP 2001519170-A 45 23-OCT-2001;
OASIS BIOSCIENCES INC

    .18
    ^organism="synthetic construct"
|mol_type="genomic DNA"
|db_xref="taxon:32630"

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Best Local Similarity 100.0%; Pred. No. 4.4
Matches 14; Conservative 0; Mismatches
   Mismatches
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JP 2001519170-A/45
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JP 2001513776-A/27.
synthetic construct
synthetic construct
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BD076451.1 GI:22622054
JP 2001519170-A/45.
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                                   CCAGCGTGCGCCAT 19
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 14; Conservative
                                                                  CCAGCGTGCGCCAT
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BD069938
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Semple, S.C., Klimuk, S.K., Harasym, T., Hope, M.J., Ansell, S.M., Cullis, P., Scherrer, P. and Debeyer, D.
Charged therapeutic agents encapsulated in lipid particles containing four lipid components
Patent: US 6287591-A 14 11-SEP-2001;
Location/Qualifiers
1 (bases 1 to 18)

Krieg.A.M. and Weiner.G.

Methods and products for stimulating the immune system using immunotherspeutic oligonucleotides and cytokines Patent: US 6218371-A 104 17-APR-2001;

Location/Qualifiers
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Pred. No. 4.4e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunostimulatory nucleic acid molecules
Patent: US 6239116-A 45 29-MAY-2001;
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100.0%; Pred. No.
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Seguence 45 from patent US 6239116.
AR154716
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    .18
    /organism="unknown"
    /mol_type="unassigned DNA"

                                                                                                                  /organism="unknown"
/wol_type="unassigned DNA"
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/organism="unknown"
/mol_type="unassigned DNA"
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Krieg, A.M. and Kline, J.N.
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Best Local Similarity 100.
Matches 14; Conservative
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Unclassified.
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Best Local S:
Matches 14
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AR167448
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lipid vesicles
Patent: JP 2002501511-A 14 15-JAN-2002;
INEX PHARMACEUTICALS CORP
PD 15-JAN-2002
PF 14-MAY-1998 UP 1998548646
PI SEAN C SEMPLE, SANDRA K KLIMUK, TROY HARASYM, MICHAEL J HOPE, PI
STEVEN M ANSELL,
PI PIETER CULLIS, PETER SCHERRER, DAN SUITE DEBEYER PC A61K9/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description of Artificial Sequence: Designed DNA based on bcl-
1 (bases 1 to 18)
Semple.S.C., Klimuk,S.K., Harasym,T., Hope,M.J., Ansel,S.M.,
Cullis,P., Scherrer,P. and Debeyer,D.S.
High efficiency encapsulation of charged therapeutic agents in
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/organism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"
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Patent: JP 2003026609-A 17 29-JAN-2003;
John C REED
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synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 18)
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    .18
    /organism="Chlamydia sp./mol_type="genomic DNA" /db_xref="taxon:35827"

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JP 2003026609-A/17
29-JAN-2003
19-JUN-2002 JP 2002178753
20-SEP-1993 US 08/124256
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High efficiency encapsulation of charged therapeutic agents in lipid vesicles.

101016497
BD106497.1 GI:23201315
JP 2002201511-A/14.
Chlamydia sp.
Chlamydia sp.
Bacteria; Chlamydiale; Chlamydiales; Chlamydia.
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Ribonucleoside-derivative and method for preparing the same.
BD080525
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No. 18-2001515087-A/4

PN JP 2001515087-A/4

PF 17-AUG-1998 JP 2000509723

PR 18-AUG-19997 CH 1931/97

PR 18-AUG-19997 CH 1931/6, C07H23/00 CC

COTH19/16, C07H29/16, C07H29/16, C07H23/00 CC

Description of Artificial Sequence: synthetic polynucleotide FH

Location/Qualifiers

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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JP 2001515087-A/4.
synthetic construct
synthetic synthetic
1 (bases 1 to 18)
pitsch, S., Waiss, P.A and Jenny, L.
pitsch, S., Waiss, P.A and Jenny, L.
STEFAN PITSCH, PATRICK A WEISS, LUZI JENNY
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    18
    /organism='Artificial Sequence'

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100.0%; Pred. No. 4.4e+05;
tive 0; Mismatches 0;
               Location/Qualifiers

    .18
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BD2055614.1 GI:33015384

DD 2002514397-A/104.

Synthetic construct

NISM experies, artificial sequences.

Other sequences, artificial sequences.

NES Wagner, H. and Lipford, G.

Method of controlling hematopoiesis by using CpG oligonucleotide and Lipford, G.

AL CORY PHARMACEUTICALS GMBH, CORY PHARMACEUTICALS GROUP INC

OS Artificial Sequence

NY D 2002514397-A/104

PD 21-MAY-2002

PR 14-MAY-1999 IP 200051439
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Method of controlling hematopoiesis by using CpG oligonucleotide.
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Method of controlling hematopoiesis by using CpG oligonucleotide.
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JP 2002514397-A/59.
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Synthetic construct

other sequences; artificial sequences.

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L patent: JP 2002510319-A 34 02-APR-2002;

ISIS PHARMACEUTICALS INC

OS Artificial Sequence

PP 02-APR-2002

PP 01-JUL-1999 US 08/886829

PP 01-JUL-1997 US 08/886829

PP 01-JUL-1997 US 08/886829

PP C12Q1/68,AG1K9/127,AG1K48/00,C07H21/04

CC Description of Artificial Sequence: Novel Sequence FH Key

Location/Qualifiers.
  BD190420 17-JUL-2003 Microemulaions with Adsorbed Macromoelecules and Microparticles. BD190420
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JP 2002510319-A/34.
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PF 09-FEB-2000
PR 29-UUI-1999
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BD222609 18 bp DNA linear PAT 17-JUL-2003 Compositions of CPG and saponin adjuvants and uses thereof. BD222609
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PN JP 2002522510-A/1
PD 23-JUL-2002
PF 06-AUG-1999 JP 2000564661
PR 10-AUG-1999 US 60/128608 PI
CHARLOTTE A KENSIL
PC A61K39/39,A61K39/00,C12N15/09,C12N15/00
CC Compositions of CPG and saponin adjuvants and uses thereof FH
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JP 200222510-A/1.
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Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
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    .18
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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleratic nucleic search, using sw model February 15, 2006, 17:25:23; Search time 884.241 Million	US-09-669 24 1 ggggtcc IDENTITY_Gapop 10. 4996997 s hits sati ength: 0 ength: 50	Maximum Match 100% Listing first 300 summaries N Geneseq 21:* 1: geneseq11980s:* 3: geneseqn200s:* 4: geneseqn200s:* 5: geneseqn200s:* 6: geneseqn2002s:* 7: geneseqn2002as:* 7: geneseqn2002as:* 9: geneseqn2003bs:* 10: geneseqn2003bs:* 11: geneseqn2004ss:* 11: geneseqn2004ss:* 11: geneseqn2004ss:* 11: geneseqn2004ss:*	No. is the number of results predicted by chance to have greater than or equal to the score of the result being predicted by analysis of the total score distribution. SUMMARIES Auch Length DB ID Auch 24 AAF98956 Auch 24 AAF98965 Auch 24 II AAF98965 Auch 25 Auch 26 Auch 2769 Auch 26 Auch 2769 Auch 27 II AAF98965 Auch 28 Auch 2920 Auch 29 Auch 2920 Auch
OM nucleic - nucl Run on:	Perfect score: 2 Sequence: 3 Scoring table: 1 Searched: 4 Total number of P Minimum DB seq le Maximum DB seq le Post-processing:	Database:	Result Score great and is derivative great

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12-JUN-2001 (first entry)

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Aav11591 Liposomal
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The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immuno response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidate rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumnour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or or thomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Th2 to a Th1 immune response and to activate immune cells. Note: the
                                                                        Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic; immunostimulatory; tumour; viral infection; bacterial infection; tungal infection; parasitic infection; cancer; asthma; infection; datasitic infection; cancer; asthma; and infections disease; allergy; immune deficiency; phosphorothioate; ss.
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                                    Immunostimulatory nucleic acid #72.
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27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
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AAF98956 standard; DNA; 24 BP.

AAF98956

AAF98956 ID AAF9 XX AC AAF9 XX

RESULT 1

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The present invention relates to methods for treating or preventing developing administering to a subject having or at risk of developing cancer immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies. The methods are useful for treating or preventing cancer such as basal cell carcinoma, bladder ancer, bone cancer, barin and central nervous system (CNS) cancer, breast cancer, cervical cancer, colon and rectum cancer, connective tissue cancer, oesophageal cancer, eye cancer, Hodgkin's lymphoma, non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, larynx cancer, pancreatic cancer, prostate cancer, rhaddomyosarcoma, skin cancer, prostate cancer, rhaddomyosarcoma, skin cancer, stonach cancer, testicular cancer, and uterine cancer. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of the invention
                                                                                                                                                                         Treating or preventing cancer, such as basal cell carcinoma, comprises administering immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies to a subject having or at risk of
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22-JUN-2000; 2000US-0213346P.
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                                            FOUND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   administering at least one antianglogenic nucleic acid molecule. Also nichluded is a kit comprising a first container housing the antianglogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted anglogenesis. The method is useful for inhibiting anglogenesis associated with solid tumour growth, tumour metaetasis, precencerous lession, theumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler webber Syndrome, myocardial anglogenesis, plaque neovascularisation, telanglectasia, haemophiliac joints, anglofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypertrophic scars. The present sequence is an antianglogenic nucleic acid of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comprising
rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
plaque neovascularisation; telangiectasia; haemophiliac joint;
angiofibroma; wound gramulation; intestinal adhesion; atherosclerosis;
scleroderma; hypertrophic scar.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 24; DB 6; Length 24; 100.0%; Pred. No. 0.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGGTCCAGCGTGCGCCATGGGGG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 21; 276pp; English
                                                                                                                                                                                                                                                                                                                                       (COLE-) COLEY PHARM GROUP INC
                                                                                                                                                                                                                                                   14-DEC-2001; 2001WO-US048458.
                                                                                                                                                                                                                                                                                             14-DEC-2000; 2000US-025534P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JUN-2001; 2001WO-US020154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL39036 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-566690/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                           WO200253141-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200197843-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24;
                                                                                                                                                                                                                                                                                                                                                                                     Bratzler RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-DEC-2001.
                                                                                                                                                                                                       11-JUL-2002
                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL39036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Matches

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Gaps

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Gaps

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Indels

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Mismatches

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Conservative

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(FOUR/) I
                                                                                                                                                                                                                                                                                                                                                                                                                              (BRAT/)
 Matches
                                                                                                   ADU89397
                                                                                       RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method of treating or preventing allergy or asthma which comprises administering to a subject a poly-G nucleic acid in an aerosol formulation. The methods and compositions of the present invention are useful for diagnosling and/or treating asthma and allergy especially in a hypo-responsive subject. The present sequence represents an immunostimulatory nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.
                                                                        The invention describes a method of treating non-allergic inflammatory disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases, such as psoriasis, eczema, allergic contact dermatitis, latex dermatitis or inflammatory bowel disease e.g., ulocrative collits or Crohn's disease. This sequence represents an immunostimulatory nucleic acid
Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
                                                                                                                                                                                                                                                 Gaps
            allergic contact dermatitis, latex dermatitis or inflammatory bowel disease by administering an immunostimulatory nucleic acid.
                                                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ds; allergy; asthma; poly-G nucleic acid; aerosol formulation; hypo-responsive subject; immunostimulatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 24; DB 9; Length 24; Pred. No. 0.58;
                                                                                                                                                                                                                    100.0%; Score 24; DB 9; Length 24; 100.0%; Pred. No. 0.58;
                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                            Sequence 24 BP; 2 A; 6 C; 13 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP; 2 A; 6 C; 13 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fouron Y;
                                                                                                                                                                                                                                                                                                 24
                                                                                                                                                                                                                                                                       1 GGGGTCCAGCGTGCGCCATGGGGG 24
                                                    Disclosure; Page 10; 229pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 6; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunostimulatory nucleic acid #72
                                                                                                                                                                                                                                                                                        1 GGGGTCCAGCGTGCGCCATGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                  ADB36458 standard; DNA; 24 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-FEB-2000; 2000US-0179991P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-FEB-2001; 2001US-00776479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bratzler RL, Petersen DM,
                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BRATZLER R L.
PETERSEN D M.
FOURON Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-657977/62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2003087848-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24
                                                                                                                                                                                                                                                                                                                                                                                                                   04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PETE/) (FOUR/)
                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                           ADB36458
                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BRAT/)
                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suppressing allergies, including asthma, rhinitis, urticaria and atopic dermatitis, in a subject, comprises administering a first and second dose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             ss, antiasthmatic, antiallergic, dermatological, antiinflammatory, antibacterial, virucide, immunoglobulin E antagonist, allergy, immunostimulator, asthma, rhinitis, urticaria, dermatitis, bacterial infection, viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 24 BP; 2 A; 6 C; 13 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 81; 235pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of an immunostimulatory nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGGGTCCAGCGTGCGCCATGGGGG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eggerccaecerececcareege 24
24
                                               24
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GGGGTCCAGCGTGCGCCATGGGGG
                             GGGGTCCAGCGTGCGCCATGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
                                                                                                                                                                                               ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-FEB-2000; 2000US-0179991P.
02-FEB-2001; 2001US-00776479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-APR-2004; 2004US-00831778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ86577 standard; DNA; 26
                                                                                                                                                                                               ADU89397 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bratzler RL, Petersen DM,
                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 КD
Ч.Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-833006/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BRATZLER F
PETERSEN I
FOURON Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2004235774-A1
                                                                                                                                                                                                                                                                                                           10-FEB-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
AAQ86577
ID AAQ8
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WO200047778-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primer;
26-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA50259;
                                                                                                                                      field
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
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                                                                                                                                                                                                                                                                                                                      The signal sequence was isolated from barley alpha-amylase cDNA by PCR using the primers given in AAQ86577-78. The product was cloned into BBLUBSCTIPILI together with a mouse MHC II alpha chain mature peptidenenceing sequence to obtain plasmid pSM155, for expression in tobacco cv. SRI transformants. (Updated on 25-MAR-2003 to correct PN field.) (Updated
                                                                                                                                                                                                                                                                  Expressing a mammalian antigen in transformed plants to provide a source of plant material - for oral or enteral admin. to a mammal to produce tolerance to the antigen.
                                                                      Barley; Hordeum vulgare; alpha-amylase; signal peptide; PCR; primer; polywerase chain reaction; major histocompatibility complex; MHC; transgenic plant; allograft rejection suppression; plasmid pSM155; tobacco; Nicotiana tabacum; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 filamentous fungus; Bcl-2; herbicide;
Colletotrichum gloeosporioides f.sp. aeschynomene; food production;
drug production; paper; pulp industry; agriculture; bioremediation;
                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                        71.7%; Score 17.2; DB 2; Length 26; 86.4%; Pred. No. 5.8e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 26 BP; 4 A; 8 C; 12 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                            (UNLO ) UNIV HOSPITAL LONDON HEALTH ASSOC.
                                                    Alpha-amylase signal sequence primer.
                                                                                                                                                                                                                                                                                                                                                                      on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Bcl-2 PCR primer SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                            23
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGATCCGGCGCGCCCATGGGG 23
                                                                                                                                                                                                                                                                                                       Example 2; Page 17; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGTCCAGCGTGCGCCATGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP
                                                                                                                                                                          94WO-CA000530
                                                                                                                                                                                                                                Stiller
                                                                                                                                                                                           93GB-00019429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADR29366 standard; DNA; 30
                         (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human; PCR; primer; ss
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                Ma S,
                                                                                                                                                                                                                                                  WPI; 1995-139392/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2004072225-A2.
                                                                                                                                     WO9508347-A1
                                                                                                                                                                          21-SEP-1994;
                                                                                                                                                                                           21-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                Jevnikar AM,
                         25-MAR-2003
25-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-NOV-2004
                                                                                                                                                      30-MAR-1995.
                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
         AAQ86577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADR29366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
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The present invention describes a filamentous fungus (I) comprising an exogenous polynucleotide capable of expressing a Bcl-2 polypeptide or its active portion, and exhibiting accelerated growth as compared to a wild-crype filamentous fungus. Also described: (1) enhancing (M1) growth of filamentous fungus. Involving providing the filamentous fungus with a Bcl cilamentous fungus; (2) enhancing (M2) the viability and/or pathogenicity of a filamentous fungus stored at sub-optimal temperature; (3) increasing (M3) the resistance of a filamentous fungus to stress; (4) a fungal collumentous fungus stored at sub-optimal temperature; (3) increasing (M3) the resistance of a filamentous fungus comprising Bcl-2 culture medium (II) suitable for growth of fungus, comprising Bcl-2 culture medium (II) suitable for growth of fungus, comprising Bcl-2 culture medium (II) suitable for growth of fungus, comprising Bcl-2 culture medium (II) suitable for growth of fungus, comprising Bcl-2 colletotrichum gloeosporioides f.sp. aeschynomene. (M1) is useful for eradicating an unwanted weed growing in a crop field, which involves correspondention, paper and prupindustry apprassion and pulp industry applications, such as food and drug production, paper and pulp industry agriculture and confidention. (I) remains viable in storage for a time period longer than the wild-type filamentous fungus when grown on solid media. (I) stress, as compared to the wild-type filamentous fungus. The present culture are exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                Novel filamentous fungus having exogenous polynucleotide expressing Bcl-2 polypeptide, and exhibiting accelerated growth compared to wild- type filamentous fungus, useful for eradicating unwanted weed growing in crop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene; human; episome; transfection; selection; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 30 BP; 7 A; 8 C; 13 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 2; 57pp; English
                                                                                                                                                                       (UYRA-) UNIV RAMOT AT TEL AVIV LTD
                                                                                                                                                                                                                                                             Sharon A, Goldstein-Barhoom S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
10-FEB-2004; 2004WO-IL000132.
                                                                                      12-FEB-2003; 2003US-0446513P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGCGTGCGCCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAGCGTGCGCCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bcl2 gene 5' PCR primer
                                                                                                                                                                                                                                                                                                                                               WPI; 2004-625842/60.
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Gaps

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OB 3; Lens O. 2e+03; O; Indels

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The present invention relates to the use of apoptotic genes in the the production of transgenic plants with improved resistance characteristics. The present sequence is the mutagenic PCR primer Bc12-5. This primer was used with primer Bc12-3 (AAA48985) to introduce a 5' Ncol site and a 3' Xbal site in the human apoptotic gene bc1-2. Specifically the primer introduced an Ala residue between the Met (position 1) and His (position 2) residues of the native protein. The altered bc1-2 sequence was used in the creation of the final vector used to transform plants. The improved resistance characteristics of the plants helps protect against bacterial, viral and other pathogens. Resistance to abiotic challenges may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid regulatory sequences, which are able to regulate expression of a gene operably linked to a promoter, useful for regulating the expression of transgenes and for treating e.g., cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vanH promoter; androgen receptor promoter; AR promoter; human epidermal growth factor receptor 2 promoter; her2 promoter; beta lactamase promoter; Bla promoter; transgene; cancer; breast cancer; colon cancer; immunological disorder; prostate cancer; cytostatic; autoimmune disease; HBV pre-2 promoter; HBV-X promoter; Enterococcus infection; immunosuppressive; antibacterial; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyclin D1 promoter; CD40L promoter; hepatitis B virus promoter;
HBV promoter; vancomycin-resistant enterococci promoter; VRE promoter;
Transgenic plants with improved resistance characteristics comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene expression modulator; multiple sclerosis; MS; chronic hepatic insufficiency; cirrhosis; hepatocellular carcinoma; systematic lupus erytheatecous; SLE; graft-vs-host disease; GVHD; familial adenomatous polyposis; rheumatoid arthritis; PCR; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laurance ME, Michelotti EF;
mas RL, Kongpachith A, Sheppard LT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human epidermal growth factor receptor 2 (Her2), primer #2.
                                                                                                                                                                                                                                                                                                                                                                             Seguence 33 BP; 3 A; 9 C; 12 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 16; DB 3
Pred. No. 2e+0
0; Mismatches
                       nucleic acids encoding apoptotic proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tam AW, Daus.
Thomas RL,
                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                      66.7%; Scor.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENE-) GENELABS TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABK29920 standard; DNA; 35 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUN-2001; 2001WO-US018343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUN-2000; 2000US-0209549P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21
                                                              Example 3; Page 58; 109pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-APR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 CCAGCGTGCGCCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 ccaecerececares
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Velligan MD, Latour DR,
Lim MY, Bruice TW;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.
nes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-130595/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Starr DB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transgenic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200194600-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-DEC-2001
                                                                                                                                                                                                                                                                                                                                      conferred
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK29920;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABK29920,
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present 5' primer was used with the 3' primer given in AAA50260 for the PCR amplification of Bel2 DNA, introducing a 5' BaiMI site and a 3'

Nhel site. The PCR product was incorporated into an episome to demonstrate a method of the invention. The method relates to the maintenance and selection of episomes in transfected eukaryotic cells in viron or in vivo, e.g. for gene therapy. It involves transfecting the cells with an episome under conditions in which cells that survive are successfully transfected with the episome. The resulting cells express a first protein whose expression causes cell death and a second protein whose expression causes cell death and a second protein whose expression and each of the first protein. In an example of the method, bcl2 and bad, and dff45 and first protein. In an example of the method allows the rapid establishment used to transfect 293E cells. The method allows the rapid establishment of eukaryotic cells that stably and reliably express a gene of interest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                Stably transfecting eukaryotic cells with at least one episome for the production of a desired protein in vitro and for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apoptosis; bcl-2; resistance; bacterial; viral; pathogens; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mutagenic PCR primer Bc12-5 targeted to anti-apoptotic gene bc1-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3; Length 33; 2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 33 BP; 9 A; 9 C; 10 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                   Example 1; Page 29; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.7%; Scor.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEBRASKA-LINCOLN
                                           11-FEB-2000; 2000WO-US003547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0106321P.
99US-0138303P.
                                                                                       99US-00249585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US025522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 ccaecerececcares 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA48984 standard; DNA; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 ccaccerececcares
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                 (PHAR-) PHARMACOPEIA INC.
                                                                                                                                                                             Chelsky D;
                                                                                                                                                                                                                       WPI; 2000-515062/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-365634/31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYNE-) UNIV
                                                                                       11-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-JUN-1999;
17-AUG-2000
                                                                                                                                                                           Horlick RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dickman MB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA48984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA48984/c
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The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immunos response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Th2 to a Th1 immune response and to activate immune cells. Note: the
              Vaccinating against tumors, infectious diseases, allergies and asthmausing immunostimulatory Py-rich and TG nucleic acids.
                                                                 Disclosure; Page 40; 338pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-566690/60.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABS77606;
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABS77606
   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                          The invention describes an isolated nucleic acid regulatory sequence for a cyclin DI promoter, a CD40L promoter, vancomycin-resistant enterococci (VRE) promoter, and TRA promoter, human epidermal growth factor receptor 2 (HER2) promoter, or a beta lactamase regulate expression of the endogenous, autologous or heterologous genes operably linked to the promoter, and may be incorporated into heterologous nucleic acid constructs for use in regulated expression of transgenes. Regulated expression of cyclin DI can be used in cancer therapies, such as breast, colon or pancreatic cancers and familial adenomatous polyposis. Regulation of the activity of CD40L gene promoter may be used in the treatment of immunological disorders, such as uctoimmune diseases e.g. multiple sclerosis (MS), systematic lupus erythematosus (SLE), graft-ve-host disease (GVHD) and rhematoid autoimmune diseases e.g. multiple sclerosis (MS), systematic lupus erythematosus (SLE), graft-ve-host disease (GVHD) and rhematoid arthitis. Regulated expression of genes under the control of the HBV (hepaticis B)-specific core, pre-S and X promoters can be used in the therapy of HBV disease, chronic hepatic insufficiency, cirrhosis, hepatocellular carcinoma, and in the regulated expression of the androgen receptor gene can be used in the treatment of Enterococcus infection, while regulated expression of the androgen receptor gene can be used in the invention to determine the regulatory regions involved in gene expression, collectine corribed in the method of the invention may are promoter region used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vaccine, cytostatic, virucidal, bactericidal, fungicidal, anti-parasitic, immunostimulatory, tumour, viral infection; bacterial infection; fungal infection, parasitic infection, cancer, asthma, infections allergy, immune deficiency, phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 35 BP; 3 A; 13 C; 14 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunostimulatory nucleic acid #81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vollmer J;
                                   Example 6; Page 52; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGTCCAGCGTGCGCCATGG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGTCCAGCCGGAGCCATGG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.3%;
85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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immunological diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-273485/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200122972-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-APR-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF98965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to inhibiting angiogenesis in a subject, comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; oSler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound granulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
                                                                                                                                  Length 16;
                                                                                                                                                                                                      0; Indels
present sequence may have a phosphorothioate backbone
                                                             Sequence 16 BP; 3 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
                                                                                                                                     62.5%; Score 15; DB 4; Le 100.0%; Pred. No. 5.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Angiogenesis inhibitory oligonucleotide #90.
                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (COLE-) COLEY PHARM GROUP INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-DEC-2001; 2001WO-US048458.
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                                                                                                                                                                                                                                                                              5 TCCAGCGTGCGCCAT 19
                                                                                                                                                                                                                                                                                                                                            rccaecerececar 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABS77606 standard; DNA; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                      Local Similarity 100.
nes 15; Conservative
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present sequence is an immunostimulatory oligonucleotide described in the

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               included is a kit comprising a first container housing the antianglogenic included is a kit comprising a first container housing the antianglogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis, dabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler Webber Syndrome, myocardial angiogenesis, plaque meovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to methods for treating or preventing cancer, involving administering to a subject having or at risk of developing cancer immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies. The methods are useful for treating or preventing cancer such as basal cell carcinoma, bladder cancer, bone cancer, brain and central nervous system (CNS) cancer, breast cancer, cervical cancer, colon and rectum cancer, connective tissue cancer, oseophageal cancer, eye cancer, kidney cancer, larynx cancer, leukaemia, liver cancer, lung cancer, kidney cancer, larynx Hodgkin's lymphoma, melanoma, melanoma, cancer, rabdomycaarcoma, skin cancer, pancreatic cancer, postate cancer, rhabdomycaarcoma, skin cancer, stomach cancer, testicular cancer, and uterine cancer. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treating or preventing cancer, such as basal cell carcinoma, comprises administering immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies to a subject having or at risk of
    administering at least one antiangiogenic nucleic acid molecule. Also
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer, such as basal cell carcinoma,
                                                                                                                                                                                                                                                                                                                                 Score 15; DB 6; Length 16;
Pred. No. 5.4e+03;
                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                          Sequence 16 BP; 3 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunostimulatory nucleic acid SEQ ID NO: 533.
                                                                                                                                                                                                                                                                                                                                            100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       angiogenesis; metastasis; cytostatic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 231; 312pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JUN-2001; 2001WO-US020154.
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                                                                                                                                                                                                                                                                                                                                 62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                   5 TCCAGCGTGCGCCAT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                          rccaecerececar 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL39111 standard; DNA; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                          15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-154611/20.
                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
This sequence represents an immunostimulatory nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes a method of treating non-allergic inflammatory disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases, such as
                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                     Immunostimulatory, antiinflammatory, dermatological, antipsoriatic; antiulcer; gene therapy, vaccine; non-allergic inflammatory disease; psoriasis; eczema; allergic contact dermatitis; latex dermatitis; latex in inflammatory bowel disease; ulcerative colitis; crohn's disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating non-allergic inflammatory diseases, such as psoriasis, ecze allergic contact dermatitis, latex dermatitis or inflammatory bowel disease by administering an immunostimulatory nucleic acid.
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                                                            Length 16;
                                                                                           0; Indels
                              Sequence 16 BP; 3 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
                                                          Score 15; DB 6; Le
Pred. No. 5.4e+03;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16 BP; 3 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 10; 229pp; English,
                                                                                                                                                                                                                                                                                                                                         Immunostimulatory nucleic acid #84.
exemplification of the invention
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100.0%; Pre-
                                                                                                                                                                                                                                          BP
                                                                              100.08;
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                                                             62.5%;
                                                                                                                          5 TCCAGCGTGCGCCAT 19
                                                                                                                                            TCCAGCGTGCGCCAT 15
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                                                                                                                                                                                                                                                                                                       25-SEP-2003 (first entry)
                                                                                           15; Conservative
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                                                                           Best Local Similarity
Matches 15; Conserv
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Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KRIE/) KRIEG A M. (BERG/) BERG D J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2003050268-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                        ACD99398;
                                                            Query Match
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ACD99398
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RESULT 16

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23-APR-2004; 2004US-00831778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-OCT-2003 (first entry)
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 TCCAGCGTGCGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cross-species comparison.
                                                                                  'nΣ
                                                                                                                                                                WPI; 2004-833006/82.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AFFY-) AFFYMETRIX
                                                                                (BRAT/) BRATZLER |
(PETE/) PETERSEN |
(FOUR/) FOURON Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2003104410-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mittmann MP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a method of treating or preventing allergy or asthma which comprises administering to a subject a poly-G nucleic acid in an aerosol formulation. The methods and compositions of the present invention are useful for diagnoshing and/or treating asthma and allergy especially in a hypo-responsive subject. The present sequence represents an immunostimulatory nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                         Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          se; antiasthmatic; antiallergic; dermatological; antiinflammatory;
antibacterial; virucide; immunoglobulin E antagonist; allergy;
immunostimulator; asthma; rhinitis; urticaria; dermatitis;
bacterial infection; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                        ds; allergy; asthma; poly-G nucleic acid; aerosol formulation; hypo-responsive subject; immunostimulatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.5%; Score 15; DB 9; Length 16; 100.0%; Pred. No. 5.4e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16 BP; 3 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Allergic response suppressor oligonucleotide #90.
                                                                                                                                                                                                                                                                                                                                                                       Fouron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Page 6, 221pp, English.
                                                                                                 Immunostimulatory nucleic acid #81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.55,
100.0%; FIE
0; N
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              ADB36467 standard; DNA; 16 BP
                                                                                                                                                                                                                                                       02-FEB-2001; 2001US-00776479.
                                                                                                                                                                                                                                                                                   03-FEB-2000; 2000US-0179991P.
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                                                                                                                                                                                                                                                                                                                                                                       Petersen DM,
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                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                          (BRAT/) BRATZLER R L.
(PETE/) PETERSEN D M.
(FOUR/) FOURON Y.
                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-657977/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                               US2003087848-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2004235774-A1.
                                                                                                                                                                                                                                                                                                                                                                    Bratzler RL,
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                                                                      04-DEC-2003
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                                                                                                                                                                       Synthetic.
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                                            ADB36467;
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ADU89406
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  ADB36467
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The invention relates to a method of suppressing a symptom of an allergic response in a subject by administering a first and second dose of an immunostimulatory nucleic acid that comprises a nucleotide sequence comprising 5'-cg-3', and where the second dose is administered from 1 day to 8 weeks after the first dose. The methods and compositions of the present invention are useful for the treatment or prevention of asthma and allergy, including rhinitis, urticaria and atopic dermatitis, using an immunostimulatory nucleic acid alone or in combination with other medicaments. They can also be used in preventing bacterial and viral infections. This sequence represents an oligonucleotide used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suppressing allergies, including asthma, rhinitis, urticaria and atopic dermatitis, in a subject, comprises administering a first and second dose of an immunostimulatory nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 90; 235pp; English.
                                                                                                                                                                                                                                                                                                        Bratzler RL, Petersen DM, Fouron Y;
03-FEB-2000; 2000US-0179991P.
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in manitoring gene expression levels by hybridisation to a DNA library, compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence or specific cutations of any gene, in mapping the 5' termini of mRNA molecules by crimate extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been containing segments of DNA that have been contained and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence date for this patent can also be obtained in electronic format directly from USPTO at sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fas-associated protein; tumour necrosis factor receptor; PTP-BAS; apoptosis; PAP; cell surface protein; autoimmune disease; HIV virus; hybridoma; cell death; DNA primer; PCR; polymerase chain reaction; s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.5%; Score 15; DB 9; Length 25; 78.3%; Pred. No. 5.5e+03;
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                                       sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                            Claim 1; SEQ ID NO 96172; 9pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Bcl-2 forward DNA primer.
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Best Local Similarity 78.3.
Best Local 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-049689/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reed JC, Sato T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9534661-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-DEC-1996
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New Fas associated proteins PTP-BAS types 4 and 5 - involved in

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the signal sequence causing a transmembrane transport of the nucleic acid in a biological system. The invention also relates to a vector containing the nucleic acid and a biological system. The invention also relates to a vector containing the nucleic acid, a host organism containing at least the nucleic acid or the vector, a method of producing the nucleic acid, the vector, a pharmaceutical composition comprising the nucleic acid, the vector or the host organism and optionally a pharmaceutical carrier and/or diluent and a kit comprising the nucleic acid, the vector or the host organism and optionally a pharmaceutical carrier and/or diluent and a kit comprising the nucleic acid, the vector or the host organism. The nucleotide sequence further contains at least one second nucleotide acquainted and/or one or mare components accordently linked and/or second nucleotide sequence, where the covalently linked and/or second nucleotide sequence. Where the covalently linked and/or complexed components are biologically active. The nucleic acid, vector or host organism is useful for preparing a pharmaceutical composition for treating genetically based disorders. This sequence represents a signal sequence-containing
                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                      for
programmed cell death, used for modulating apoptosis, e.g. for treating cancer, and for identifying other modulators.
                                                                                              The cDNA sequence encoding the cytoplasmic domain of human Fas (AA 191-335) was modified by PCR mutagenesis using this primer along with the corresponding reverse primer (AAT18389) and another forward (AAT18386) and reverse (AAT18337) primer set. It was then subcloned in frame into plasmid pEG202 to produce plasmid pEG/Fas(191-135). The cDNA sequence the cytoplasmic domain of human Fas was then subcloned into the ECORI site of pEG202, in-frame with the upstream LexA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a nucleic acid comprising a first nucleotide
                                                                                                                                                                                                                                                                                                                                                    Gaps
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0
                                                                                                                                                                                                                                                                                                          Length 27;
                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                   Seguence 27 BP; 7 A; 6 C; 10 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                          Score 15; DB 2; Le
Pred. No. 5.5e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful for treating genetically based disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal sequence-containing oligonucleotide #5.
                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wuensche W,
                                                            Disclosure; Page 42; 84pp; English.
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                                                                                                                                                                                                                                                                                                       Match 62.5%; Scc
Local Similarity 100.0%; Pr
les 15; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYSC-) UNIV SCHLESWIG-HOLSTEIN
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                                                                                                                                                                                                                                                                                                                                                                                           20
                                                                                                                                                                                                                                                                                                                                                                                                                 21 CCAGCGTGCGCCATG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADY71779 standard; DNA; 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2005-223387/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cellular transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2005024033-A2
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                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                    datches
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(first entry)

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Novel expression vector comprising reporter gene and a reporter genetranscription promoting enhancer sequence that has a variable number of tandem repeat and is found in 3'non-coding region of human dopamine
                                                                                                                                                                                                                                                                                               human; ds; dopamine transporter; DAT; enhancer; expression vector; reporter gene; antiparkinsonian; neuroleptic; antidepressant; Parkinson's disease; schizophrenia.
                                                                                                                                                                                                                                                     Human dopamine transporter enhancer SEQ ID NO:1.
                                                                                                 ADF70717 standard; DNA; 40 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-2001; 2001GB-00026268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-2001; 2001GB-00026268.
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                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                      12-FEB-2004
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                                                                                                                                                      ADF70717;
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                                                  RESULT 22
ADF70717/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a nucleic acid comprising a first nucleotide sequence having at least one signal sequence unit or a mixture of units, the signal sequence causing a transmembrane transport of the nucleic acid in a biological system. The invention also relates to a vector containing the nucleic acid, a host organism containing at least the nucleic acid or the vector, a method of producing the nucleic acid, the vector, a pharmaceutical composition comprising the nucleic acid, the vector or the host organism and optionally a pharmaceutical carrier and/or diluent and a kit comprising the nucleic acid, the vector or the host organism. The nucleotide sequence further contains at least one second nucleotide sequence further contains at least one second nucleotide sequence to be transported and/or one or more components covalently linked and/or second nucleotide sequence. Where the covalently linked and/or complexed components are biologically active. The nucleic acid, vector or host organism is useful for preparing a pharmaceutical composition for treating genetically based disorders. This sequence represents an oligonucleotide used in the scope
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                                                                                                                                                         Gaps
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                                                                                                    Score 15; DB 14; Length 28;
Pred. No. 5.5e+03;
                                                                                                                                                      0; Indels
oligonucleotide used in the scope of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 28 BP; 6 A; 10 C; 7 G; 5 T; 0 U; 0 Other;
                                                    Sequence 28 BP; 3 A; 9 C; 8 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Overhoff M;
                                                                                    62.5%; Sco...
100.0%; Pred. No. ...
... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                      ADY71781 standard; DNA; 28 BP
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                                                                                                                                                                                                                                     CCAGCGTGCGCCATG 19
                                                                                                                                                                                                        6 ccadcerececare 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Control oligonucleotide #18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                            Query Match
Best Local Similarity 100.0
Matches 15, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cellular transport; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2005-223387/23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2005024033-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                   ADY71781;
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                                                                                                                                                                                                                                                                                                                                                         ADY71781

THE PROPERTY OF THE 
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                                                                                                               The invention relates to a novel expression vector comprising an enhancer sequence and a reporter gene. The enhancer sequence comprises a variable number of tandem repeat (VWTR) and is found in the 3' non-coding region of the human dopamine transporter (DAT) gene. The enhancer sequence is capable of promoting the transcription of the reporter gene. An expression vector of the invention has antiparkinsonian, neuroleptic, and antidepressant activity, and may act as a dopamine transporter gene expression vector is useful for identifying a compound capable of regulating the expression of a target gene (preferably human dopamine transporter gene) that comprises an enhancer sequence. A compound of the transporter gene) that comprises an enhancer sequence. A compound of the transporter gene) that required parkinson's disease and schizophrenia that are associated with reduced and increased levels of dopamine, respectively. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.5%; Score 15; DB 10; Length 40; 78.3%; Pred. No. 5.5e+03; ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 40 BP; 8 A; 15 C; 12 G; 5 T; 0 U; 0 Other;
                                                            Claim 1; SEQ ID NO 1; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGCCCTGCATGCGTCCTGGGG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGGGTCCAGCGTGCGCCATGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
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ID ABN86431 standard; DNA; 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 18; Conserv
transporter
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6 CCAGCGTGCGCCATG 20

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15, Conservative

Matches

Local Similarity

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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation to a DNA library, or at least one target sequence. The method of analysis comprises of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The morphisms, or family members of a gene and a cross-species comparises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acid further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening CDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been containing sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at sequence thm!
                                                                                                                                                                                              New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 60.8%; Score 14.6; DB 9; Length 25; Best Local Similarity 81.0%; Pred. No. 8.2e+03; Matches 17; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human microarray DNA oligonucleotide SEQ ID NO 87909.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 25 BP; 2 A; 7 C; 9 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 35445; 9pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GICCAGCGTGCGCCATGGGGG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grecacrerectechiesers 21
16-MAR-2001; 2001US-0276759P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-MAR-2002; 2002US-00098263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACI87918 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-OCT-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cross-species comparison.
                                               (AFFY-) AFFYMETRIX INC
                                                                                                                                                 WPI; 2003-567953/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2003104410-A1
                                                                                                 Mittmann MP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUN-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapeutic protein production, characterized by the utilization of sequence motifs for restriction endonucleases NotI or NcoI to connect the gene segments (including promoter regulatory regions) with the gene segments (including structural fragments of the gene coding the required protein). The method is useful for preparing an expression vector for therapeutic protein production, in particular human erythropoietin (BPO). The vector produced by the method is useful for BPO expression in suitable transfected eukaryotic cells or in the mammary gland of transgenic organisms. The present sequence represents a translational consensus WAP-EPO sequence with NotI modification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to the preparation of an expression vector for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Preparing vectors for therapeutic protein production in transgenic animals, based on utilization of modified translational Kozak consento connect promoter regulatory sequences with coding structural gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                       Translational consensus WAP-EPO with NotI modification sequence.
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                                                                          Therapeutic; erythropoietin; EPO; transgenic; WAP; ss.
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                                                                                                                                                                                                                                                                                                                                                                               (BIOP-) BIOPHARM VU BIOFARMACIE A VETERINARNICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 1; 32pp; English.
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in analysis of genetic variation or in hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dotblot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence date for this patent can also be obtained in electronic format directly form the directly of the microarray.
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                                                                                                                 New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                              Claim 1; SEQ ID NO 87909; 9pp; English.
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Best Local Similarity 81.0'
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(AFFY-) AFFYMETRIX INC
                                                                              WPI; 2003-567953/53
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                                       Mittmann MP
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its configuration, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one target sequence. The method of analysis comprises of at least one or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence or specific or probes is useful in in situ hybridisation, in Southern, Northern or dotor hybridisation to identify or detect the sequence or specific or mutations of any gene, in mapping the 5' termini of mRNA molecules by cylmer extensions or in screening solwa or genomic libraries or subclones or solational subclones containing segments of DNA that have been consolated in netering or the sequence presented is one of the concleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at sequence thml
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                                                                               New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
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                                                                                                                                                                        Claim 1; SEQ ID NO 55179; 9pp; English
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ses 17; Conservative
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                                         WPI; 2003-567953/53.
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                                                                                             The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in analysis of genetic variation or in hybridisation to a DNA library, or at least one target sequence. The method of analysis comprises compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one target sequence. The method of analysis comprises in hybridising at least one or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the cucleic acids further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence or specific or mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the containing patent can also be obtained in electronic format directly
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                      New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
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ligand internalisation; cell transduction; library screening;
gene therapy; PCR primer; ss.
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                                                                         Claim 1; SEQ ID NO 87293; 9pp; English.
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Best Local Similarity 81.0'
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WPI; 2003-567953/53
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17-NOV-1998;
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The present sequence is a PCR primer used to amplify the EGF sequence in COS cells infected with non-targeted M13 phage and EGF-phage. The maplification primers have sequences located on each side of the EGF sequence in the gene III coding sequence. The PCR products were digested with restriction endonucleases and ligated into a new phage vector and used to transform competent bacterial cells by electroporation. Plaques cover analysed via PCR using oligonucleotides which included the present sequence. Four rounds of selection were sufficient to enrich the targeted EGF-phage to 100%. This selection procedure is a useful example of a novel method of selecting internalising ligands displayed on a genetic package carries a gene encoding a detectable product expressed on internalisation. The method is referred to as Ligands Ingands that may be useful as antibacterial agents or in gene therapy. The method is also useful for studying protein interactions that the ligands. (Updated on 15-SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                             Selecting internalized ligands displayed on a genetic package by contacting them with a cell, where each package carries a gene encoding detectable product expressed on internalization, useful for identifying
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81.0%; Pred. No. 8.3e+03;
Live 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 47 BP; 6 A; 10 C; 18 G; 13 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 19; Page 65; 112pp; English
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                                                                                                                                              Kassner P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baird A;
                                                                     (SELE-) SELECTIVE GENETICS INC.
99US-00258689.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 81.0%;
ses 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     ligands for gene therapy.
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                                                                                                                                              Baird A,
                                                                                                                                                                                                                WPI; 2000-387775/33
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(KASS/) KASSNER P.
(BAIR/) BAIRD A.
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bacterial infections, and cancer, e.g. biliary tract cancer, breast
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modified_base
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                                                                                                                                                                   The invention relates to a method for selecting ligands that internalise and facilitate transgene expression, comprising displaying on a phage carrying a transgene encoding a detectable product, and recovering a nucleic acid molecule encoding the ligands from the cell expressing the detectable product. The methods are useful in selecting and identifying ligands displayed on a phage that internalise and facilitate transgene expression, and also in identifying transduction facilitating peptides. Internalising ligands identified by the methods are useful in gene delivery methods and as anti-bacterial agents. The ligands and anti-ligands identified by the treatment of e.g., cancer and restenosis. The method is also useful in that it allows identification of molecules that are targets for new discovery. This sequence represents a PCR primer used to amplify a ligand gene III fusion of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New oligonuclectides, useful for treating allergy or asthma, viral and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                viral infection; bacterial infection; cancer; lymphoma;
intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;
carcinoma; sarcoma; gene therapy; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                           Genetic package display method useful for detecting and identifying protein-protein interactions that facilitate internalization and transgene expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 47 BP; 6 A; 10 C; 18 G; 13 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vollmer J, Uhlmann E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CpG immunostimulatory oligonucleotide #52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                       Example 19; Page 24; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGGTCCAGCGTGCGCCATGG 21
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2003US-0506108P.
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les 17; Conservative
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         WPI; 2003-776567/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jurk M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2004053104-A2
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modified_base
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25-SEP-2003;
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ADP86181
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                                                                                                                       The invention relates to a class of CpG immunostimulatory oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that care useful for stimulating an immune response. Oligonucleotides and compositions of the invention are useful for treating allergy or asthma, viral and bacterial infections and cancer e.g. biliary tract cancer, breast cancer, cervical cancer, choriocarcinoma, colon cancer, endometrial cancer, gastric cancer, hyphomas, intraepithelial neoplasms, liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma, neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer, rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, new CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer, testicular cancer, as well as other carcinomas and asrcomas. The invention is also useful in gene therapy. The present sequence is a CpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CpG immunostimulatory oligonucleotide; immune response; allergy; asthma; viral infection; bacterial infection; cancer; lymphoma; intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma; carcinoma; sarcoma; gene therapy; phosphorothioate; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60.0%; Score 14.4; DB 12; 93.8%; Pred. No. 1e+04; ive 0; Mismatches 1;
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                                                                  English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunostimulatory oligonucleotide.
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                                                                  Example; SEQ ID NO 52; 104pp;
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25-SEP-2003; 2003US-0506108P.
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/*tag= a
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cancer, cervical cancer
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nucleic acid; polypeptide or nucleotide probe, which

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agent interacts with or binds with a protein expressed by an abnormally spliced mRNA for use as a medicament or for the manufacture of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-OCT-1998;
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%$GGGGGGGGGGGGGGGGGGGGGG
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                                                The invention relates to a class of CpG immunostimulatory of objigonucleotides containing a 5TCG motif or a CG at or the 5' end that are useful for stimulating an immune response. Oligonucleotides and compositions of the invention are useful for treating allergy or asthma, viral and bacterial infections and cancer e.g. biliary tract cancer, breast cancer, cervical cancer, choricoarcinoma, colon cancer, endometrial cancer, gastric cancer, invaphomas, intraepithelial neoplasms, liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma, neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer, rectal cancer, sarcomas, thyroid cancer, renal cancer, brain and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer, testicular cancer, as well as other carcinomas and asrcomas. The invention is also useful in gene therapy. The present sequence is a CpG invariant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes a method of regulating apoptosis in a cell comprising targeting an abnormally or alternatively spliced mRNA, an abnormally or alternatively structured mRNA, or a product of either. Also described are: a nucleotide construct with a nucleotide sequence which is homologous to mRNA transcribed from an abnormally spliced gene; an agent selected from small molecule or protein; polypeptide; peptide; aptamer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Regulating apoptosis in a cell, useful for treating cancer, comprises targeting an abnormally or alternatively spliced mRNA, an abnormally or alternatively structured mRNA, or a product of either.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic; gene therapy; apoptosis modulation; pharmaceutical; cancer; cytostatic; neoplasm; Bcl-2; reverse transcriptase PCR; RT-PCR; primer;
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~hes 1; Indels
                                                                                                                                                                                                                                                                  Sequence 18 BP; 2 A; 8 C; 5 G; 3 T; 0 U; 0 Other;
                         Example; SEQ ID NO 53; 104pp; English.
                                                                                                                                                                                                                                         immunostimulatory oligonucleotide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Bcl-2 RT-PCR primer Bcl-2up.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                       15; Conservative
 cervical cancer
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ADW88846/c
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performant for the treatment of cancerous cell growth; a pharmaccutical composition comprising a nucleotide construct such as siRNA, anti-sense RNA, shrNA or markNA, or the agent cited above, and a pharmaccutical composition comprising a nucleotide construct such as siRNA, anti-sense RNA, shrNA or markNA, or the agent cited above, and a pharmaccutical cilluent or carrier; a DNA or RNA expression vector comprising an cilluent or carrier; a DNA or RNA expression vector comprising an uncleic acid sequence of the abnormally spliced gene element as given in the specification; a nucleic acid molecule which hybridizes to the nucleic acid sequence of (a); and a nucleic acid molecule which has a nucleic acid sequence which is degenerate because of the genetic code to the sequences in (a) and (b) and any sequence which is complementary to the above sequences, where the expression cassette is transcriptionally linked to a promoter sequence. The method is useful for regulating apoptosis in a cell or for treating cancer. The agent or nucleotide construct is useful as a medicament of the manifacture of a medicament for the treatment of cancerous cell growth. In addition, the nucleotide construct is a means for silencing the expression of an abnormally spliced gene for use as a medicament for treating cancerous cell growth. The DNA or RNA expression vector is used as a delivery means for a molecule that is used in the targeting of an abnormally spliced mile and the targeting of an abnormally spliced spliced spliced or represents and a reverse transferior entering the account of the angle of the angle or the plant or represents and and and and the plant of the targeting or reserved the plant or the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptide specific for pathogenic Neisseria useful in therapeutic or preventative vaccines and for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pathogenic strain; Neisseria; vaccine; Neisseria infection; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer used to isolate alternatively nspliced Bcl-2 polynucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ×
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR primer for a Neisseria pathogenic strain DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 14.4; DB 14; Length
Pred. No. 1e+04;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rokbi B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 26 BP; 6 A; 8 C; 9 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SERUMS & VACCINS SA. SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bouchardon A, Renauld-Mongenie G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 30; 187pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Query Local Similarity 93.00,
Best Local Similarity 93.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 CCAGCGTGCGCCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INMR ) PASTEUR MERIEUX
(INRM ) INSERM INST NAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perrin A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-365622/31.
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Gaps

.. 0

Length 31; Indels

60.0%; Score 14.4; DB 10; 93.8%; Pred. No. 1e+04;

0; Mismatches

AGCGTGCGCCATGGTG 16

8 AGCGTGCGCCATGGGG 15; Conservative

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Best Local Similarity Matches 15; Conserv

Query Match

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encoding a protein that is specific for pathogenic strains of Neisseria. The polynucleotides, polypeptides, or their antigenic fragments, are used in vaccines to treat or protect against Neisseria infections, particularly by N. meningitidis. The polynucleotide sequence is also used for recombinant production of the polypeptide and to produce attenuated Neisseria strains that overexpress it, or express it in a non-toxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New engineered human skin equivalent that becomes perfused in vivo after engraftment on an immunodeficient animal, useful for treating conditions involving impaired angiogenesis, e.g. diabetes, chronic leg ulcers or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bcl-2; endothelial cell; mutant; vascularisation; human; antidiabetic; antiulcer; vulnerary; cardiovascular; cell therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                          60.0%; Score 14.4; DB 3; Length 29; 75.0%; Pred. No. 1e+04; ive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                 Sequence 29 BP; 5 A; 8 C; 8 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caspase-resistant Bcl-2 5'-end terminal fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schechner JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; SEQ ID NO 3; 144pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                             24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGATCCAACCTGCTTCATGGGTG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GGGGTCCAGCGTGCGCCATGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADF28077 standard; cDNA; 31 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-APR-2003; 2003WO-US011371.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                               Local Similarity 75.0
nes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bothwell ALM, Pober JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-833725/77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYYA ) UNIV YALE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-FEB-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADF28077;
                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                         mutant
                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Human; D34A caspase-resistant Bcl-2; Bcl-2; mutant; vasotropic; vascularisation; angiogenesis; tissue transplantation; grafting; organ transplantation; gene; ss.

Human 5' end of Bcl-2 DNA SEQ ID NO:3.

(first entry)

03-APR-2002

ABA92890;

ВР

ABA92890 standard; DNA; 32

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The present invention describes a synthetic composition, which comprises collagen, fibronectin and at least one cell. Also described are: (1) a construct prepared by a method (MI) comprising; (a) preparing a solution comprising collagen and fibronectin; (b) suspending endothelial cells in the solution of step (a), where the suspended endothelial cells in the solution of step (a), where the suspended endothelial cells comprise a nucleic acid encoding a capsase-resistant Bel-2 polymetries, and (C) polymerising the collagen within the solution of step (b) to form a three construct produced by the method of [1]; (3) a method (M2) of a method (M3) for forming endothelial cells into tubbes within a comparint; (4) a method (M3) for producing endothelial cell tubules in vivo; (5) a method (M3) of producing endothelial cell tubules in vivo; (5) a method (M3) of producing endothelial cells into tubbes within a corresponded in the process of vascularisation; (7) a method (M7) of corrior in an argent, which modulates vascularisation or vascular cremodeling; and (8) the endothelial cell tubules produced by the method of (M4). The synthetic composition has vascuropic activity. The composition is useful in methods for forming cultured endothelial cells into tubes within a confinence-dimensional gel. This is partcularly, useful in the grafting of three-dimensional gel. This is partcularly, useful in the grafting of engineered skin onco recipients with impaired vascularisation or impaired caraftengered skin onco recipients with impaired vascularisation and organitarion and caraftengered in an example from the present invention
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comprise a nucleic acid encoding a caspase-resistant BC1-2 polypeptide, adjusting the solution of step (b) to about pH 7.0-8.0, and warming the solution of step (c) to about 25-40 °c; C to form a three-dimensional gel. The method of endothelial cell transplantation promotes wascularisation of human skin equivalents in vivo. Administration can be orthotopic or subcutaneous. The engineered human skin equivalents and methods are useful in treating diseases or conditions involving impaired angiogenesis, such as diabetes, chronic leg ulcers, wounds, cardiovascular disease or burnis. The present sequence represents a Caspase-resistant BC1-2 5'-end terminal fragment

Sequence 31 BP; 7 A; 10 C; 8 G; 6 T; 0 U; 0 Other;

The invention relates to an engineered human skin equivalent, where the skin equivalent becomes perfused in vivo after engraftment on an immunodeficient animal. The method involves implanting onto a skin surface wound of an animal a construct prepared by a method comprising: preparing a solution comprising collagen and fibronecth; suspending endothelial cells in the solution where the suspended endothelial cells

cells,

New synthetic composition comprising collagen, fibronectin and useful for forming cultured endothelial cells for tissue/organ transplantation or grafting onto recipients with impaired

Example 2; Page 55; 99pp; English.

vascularization.

Zheng

Schechner JS,

Pober JS,

Bothwell ALM,

(UYYA) UNIV YALE.

WPI; 2002-130568/17.

05-JUN-2001; 2001WO-US018034. 05-JUN-2000; 2000US-0208931P. 30-MAR-2001; 2001US-0279797P.

WO200193880-A1.

13-DEC-2001

Homo sapiens

Gaps

; 0

Indels

1;

Pred. No. 1e+04; Mismatches

93.8%;

Best Local Similarity 93.8 Matches 15; Conservative

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The invention relates to a hybrid oligomer comprising a cyclic AMP response element (CRE) sequence and a sequence that hybridises to the bcl response element (CRE) sequence and a sequence that hybridises to the bcl 2 pre-mRNA or mRNA. Also included are: (1) inhibiting the growth off cancer cells in vitro, which comprises contacting the cancer cells with a tybrid oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer. (2) treating or preventing cancer in a human, which comprises and a CRE decoy oligomer a hybrid oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer and (3) a pharmaceutical composition comprising a hybrid oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer and (3) a pharmaceutical composition of the invention is useful for preventing or treating cell-proliferative disorders e.g., cancer, byperplasia or tumourigenesis and also bacterial infection, viral infection, inflammation, anaphylaxis, allergy, arthritis, asthma, autoimmune disorders and parasitic infection. The CRE decoy oligomer and bcl-2 antisense oligomer are also useful for preventing or treating captening candidate transcription factors or other molecules e.g., gene screening candidate transcription factors or other molecules e.g., gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for diagnostic assays. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                    Antisense; ss; probe; Bcl-2; cell proliferative disorder; cancer; CRE; cAMP response element; bacterial infection; viral infection; inflammation; anaphylaxis; allergy; arthritis; asthma; cytostatic; autoimmune disorder; parastic infection; virucide; hyperplasia; tumourigenesis; hepatitis B infection; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and a
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hybrid oligomer comprises a cyclic AMP response element sequence sequence that hybridizes to the bcl-2 pre-mRNA or mRNA useful for preventing or treating cell-proliferative disorders e.g., cancer.
                                                                                  ö
                                      Score 14.4; DB 6; Length 32; Pred. No. 1e+04;
                                                                             1; Indels
Sequence 32 BP; 7 A; 10 C; 9 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 34 BP; 6 A; 12 C; 8 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                               Bcl-2/CRE hybrid antisense oligonucleotide #1.
                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  julatory proteins or for diagnostic assa;
-2/CRE hybrid antisense oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 25; 78pp; English
                                    60.0%;
93.8%;
                                                                                                                                                                                                                                                                      ABK90294 standard; DNA; 34 BP
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                                                                                                                                                                32 AĠĊĠŦĠĊĠĊĊAŦĠĠŦĠ 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JAN-2001; 2001US-0263244P
                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                         8 AGCGTGCGCCATGGGG
                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-590754/63.
                                      Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENT-) GENTA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200257480-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                      21-OCT-2002
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                                                                                                                                                                                                                                                                                                               ABK90294;
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60.0%; Score 14.4; DB 6; Length 34;

Query Match

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The invention relates to a hybrid oligomer comprising a cyclic AMP response element (CRE) sequence and a sequence that hybridises to the bcl 2 pre-mRNA or mRNA. Also included are: (1) inhibiting the growth of cancer cells in vitro, which comprises contacting the growth of cancer cells in vitro, which comprises contacting the cancer cells with a cancer cells in vitro, which comprises oligomer and a CRE decoy oligomer; (2) treating or preventing cancer in a human, which comprises administering a hybrid oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer; and (3) a pharmaceutical composition comprising a hybrid oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer and a CRE decoy oligomer; The pharmaceutical composition of the invention is useful for carrier. The pharmaceutical composition of the invention is useful for preventing or treating cell-proliferative disorders e.g., cancer, hyperplasia or tumourigenesis and also bacterial infection, viral infection, inflammation, anaphylaxis, allergy, arthritis, asthma, autoimmune disorders and parasitic infection. The CRE decoy oligomer and bcl-2 antisense oligomer are also useful for preventing or treating cancidate transcription factors or other molecules e.g., gene creening candidate transcription factors or other molecules e.g., gene creening candidate transcription assays. The present sequence is a Bcl-2 antisense oligomucleotide
                                                                                                                                                                                                                                                                                          Antisense; ss; probe; Bcl-2; cell proliferative disorder; cancer; CRE; cAMP response element; bacterial infection; viral infection; inflammation; anaphylaxis; allergy; arthritis; asthma; cytostatic; autoimmune disorder; parastic infection; virucide; hyperplasia; tumourigenesis; hepatitis B infection; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hybrid oligomer comprises a cyclic AMP response element sequence and sequence that hybridizes to the bcl-2 pre-mRNA or mRNA useful for preventing or treating cell-proliferative disorders e.g., cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Phosphorothioate backbone"
                                                                                                                                                                                                                                                         Bcl-2-targeting antisense oligonucleotide BK1-PS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 58; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mod_base= OTHER
                                                                                                                                        ABK90296 standard; DNA; 34 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-JAN-2002; 2002WO-US001967.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-JAN-2001; 2001US-0263244P.
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/*tag≈ a
                                                                                                                                                                                                                     (first entry)
                                     13 ccascerscsccarrs
6 CCAGCGTGCGCCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-590754/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENT-) GENTA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200257480-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
modified_base
                                                                                                                                                                                                                     21-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                           ABK90296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klem RE;
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Gaps

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Indels

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Pred. No. 1e+04;

93.8%;

Best Local Similarity

Mismatches

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Conservative

15;

Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a hybrid oligomer comprising a cyclic AMP response element (CRE) sequence and a sequence that hybridises to the 2-2 pre-mRNA or mRNA. Also included are: (1) inhibiting the growth of cancer cells in vitro, which comprises contacting the cancer cells with hybrid oligomer or a bol-2 antisense oligomer and a CRE decoy oligomer; (2) treating or preventing cancer in a human, which comprises administering a hybrid oligomer or a bol-2 antisense oligomer and a CRE decoy oligomer, and (3) a pharmaceutical composition comprising a hybrid oligomer or a bol-2 antisense oligomer and a cRE decoy oligomer and a carrier. The pharmaceutical composition of the invention is useful for preventing or treating call-probliferative disorders e.g., cancer, hyperplasia or tumourigenesis and also bacterial infection, viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infection, inflammation, anaphylaxis, allergy, arthritis, asthma, autoimmune disorders and parasitic infection. The CRE decoy oligomer and bcl.2 antisense oligomer are also useful for preventing or treating hepatitis B virus infection. The hybrid oligomers can also be used for screening candidate transcription factors or other molecules e.g., gene regulatory proteins or for diagnostic assays. The present sequence is a Bcl-2/CRE hybrid antisense oligomucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hybrid oligomer comprises a cyclic AMP response element sequence and a sequence that hybridizes to the bcl-2 pre-mRNA or mRNA useful for preventing or treating cell-proliferative disorders e.g., cancer.
                                                                                                                                                                                                                                                                                                                                                                                       Antisense; ss; probe; Bcl-2; cell proliferative disorder; cancer; CRE; cAMP response element; bacterial infection; viral infection; inflammation; anaphylaxis; allergy; arthritis; asthma; cytostatic; autoimmune disorder; parastic infection; virucide; hyperplasia; tumourigenesis; hepatitis B infection; human.
                                                                             Gaps
                                                                           ö
                                   60.0%; Score 14.4; DB 6; Length 34; 93.8%; Pred. No. 1e+04; ive 0; Mismatches 1; Indels
G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                          Bcl-2/CRE hybrid antisense oligonucleotide BK7-DE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 58; 78pp; English.
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                                                                                                                                                  ccaecerececarre 28
                                                                                                                CCAGCGTGCGCCATGG 21
                                                                                                                                                                                                                                             ABK90352 standard; DNA; 34
                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                           Conservative
   BP; 6 A; 12
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                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENT-) GENTA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200257480-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens
   Sequence 34
                                                                                                                                                                                                                                                                                                                     21-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JUL-2002
                                                                           15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                9
                                                                                                                                                                                                                                                                                  ABK90352;
                                                                                                                                                    13
                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ношо
                                                                             Matches
                                                                                                                                                                                                          RESULT 38
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receptor. Specifically, it comprises transformation of endocrine cell lines originating from mammalian hypothalamus and pancreatic islets, culturing the transformants and contacting with cells expressing the transformants and contacting with cells expressing the target receptor. The identification of those cells with a response reaction can be used for selecting a transformant cell line with the appropriate target activity that is expressing the novel transformed DNA. Accordingly, the present invention describes novel cell lines that are applicable in expression cloning systems of bloactive peptide precursor genes, and in screening GPCR ligands for use as drugs including agonists, antagonists and invesse agonists i.e. activators and inhibitors. Such cell lines can provide a highly enemative and convenient GPCR ligand assay system. This oligonucleotide sequence is a PCR primer used to amplify human GPCR cDNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to a novel method for obtaining a DNA that encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bioactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kishimoto K, Kunitomo H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endocrine cell lines originated from mammalian hypothalamus and pancreatic islet, applicable in expression cloning systems of bioactipeptide precursor genes, and in screening G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                     human, PCR; primer; ss; transformation; endocrine cell line; expression cloning system; bioactive peptide; GPCR ligand.
                                                                                                                                                                                                                      PCR primer used to amplify human GPCR G2A cDNA (SeqID 138)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 34 BP; 8 A; 14 C; 9 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yoshizawa M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 22; SEQ ID NO 138; 316pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGGTCCTGCGCCGCCAATGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saeki S,
                                                                                                                    ВР
                                                                                                                                                                                                                                                                                                                                                                                                             16-APR-2003; 2003WO-JP004840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                16-APR-2002; 2002JP-00113030.
                              13 ccAgcGrececarre 28
21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                    ADF50458 standard; DNA; 34
                                                                                                                                                                                    12-FEB-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Miura K,
Obinata M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-833737/77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 18; Conserv
                                                                                                                                                                                                                                                                                                                                            WO2003087366-A1
                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                            23-OCT-2003
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9
                                                                                                                                                    ADF50458;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                     ADF50458/c
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Matches
                                                                                    RESULT 39
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DB 6; Length 34;

Score 14.4;

60.08;

Query Match

Seguence 34 BP; 6 A; 12 C; 8 G; 8 T; 0 U; 0 Other;

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Homo sapiens.
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                                                                                                                05-JUL-2001
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                       of a gene that encodes cytochrome P450. The method involves using an oligomucleotide and/or a primer selected from those having sequences with at least 13 bases, including the base at position-21 in the base sequences represented by the oligos of 40-41 base pairs, or their complementary sequences, provided in the specification. The method is applicable in obtaining gene information, evaluation of drugs including safety and therapeutic efficacy, and screening drug candidates. This polymucleotide sequence represents one of the 40-41 base pair long oligos used in the gene polymorphism detection method of the invention.
                                                                                                                                                                                                                                                                                                                                                  cytochrome P450- encoded gene obtaining gene information,
                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel method for detecting gene polymorphisms
                                                                                            polymorphism; cytochrome P450; drug evaluation; safety; single nucleotide polymorphism; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                        Cytochrome P450 gene polymorphism detecting oligo, SEQ ID No 27.
                                                                                                                                                                              /standard_name= "Single nucleotide polymorphism"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 41 BP; 12 A; 13 C; 11 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                 Detecting gene polymorphism particularly of cytock with specific oligonucleotides, applicable obtains evaluation of drugs and screening drug candidates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 14.4; DB 1
Pred. No. 1e+04;
0; Mismatches
                                                                                                                                                                                                                                                                                                         Saito S;
                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 27; 144pp; Japanese
                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                         Iida A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human SNP oligonucleotide #7160.
ADK17713/c
ID ADK17713 standard; DNA; 41 BP.
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                                                                                                                                                                                                                                                                30-MAY-2002; 2002JP-00158237,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GGGGTCCAGCGTGCGC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGATCCAGCGTGCGC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60.0%;
93.8%;
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                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15; Conservative
                                                                                                                                                                                                                                                                                                        Sekine A,
                                                                                                                                                                                                                                                                                                                             WPI; 2004-043114/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                    (RIKE ) RIKEN KK
                                                                                                     screening;
                                                                                                                                                                                                 WO2003102181-A1
                                                                                                                           sapiens
                                                                                                                                                                                                                                                                                                        Nakamura Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JAN-2002
                                                   06-MAY-2004
                                                                                                                                                                                                                      11-DEC-2003
                                                                                            detection;
                                                                                                                                                         variation
                              ADK17713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                      drug
                                                                                                                           Ношо
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XX
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AC AAL3
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DT 24-JJ
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DB Humal
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XW Immul
XW Immul
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amyloid protein; angiopoietin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein, cytokome; kinesin; cytokine; interferon; interleukin; G-protein coupled receptor; thiosesterase; inflammation; multifactorial disease; autoimmune disease; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus errythromatosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse; lineage restricted precursor cell; neuron-restricted precursor; NRP; glial-restricted precursor; GRP; mouse neural tube; transplantation; antibody; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-protein coupled receptors and thioesterases. The present sequence is one such oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e.g. cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cyclins, polymerases, treating, e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                 multifactorial disease; autoimmune disease; infection; nervous system disease; 85.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 50 BP; 8 A; 24 C; 13 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymorphic nucleic acids encoding e.g. amylases, oncogenes and histones, useful for diagnosing and autoimmune diseases and infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 3440; 4143pp; English.
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27-DEC-2000; 2000US-00173419.
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-465210/50.
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nes 18; Conser
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its compounce, match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation to a DNA library, compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one target sequence. The method of analysis comprises of hybridising at least one or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid further comprises and a cross-species comparison. Each of the concleic acids further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence or specific or nucleic acids further comprises a tag sequence or specific or probes is useful in in situ hybridisation, in Southern, Northern or dotor hybridisation to identify or detect the sequence or specific or mutations of any gene, in mapping the 5' termini of mRNA molecules by containing segments of DNA that have been containing segments of DNA that have been consolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at sequence. html
           New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New array of nucleic acid probes, useful for in situ hybridization, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 84.2%; Pred. No. 1.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human microarray DNA oligonucleotide SEQ ID NO 94301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25 BP; 3 A; 9 C; 6 G; 7 T; 0 U; 0 Other;
                                                                                    Claim 1; SEQ ID NO 94919; 9pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCCAGCGTGCGCCATGGG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Grechergrecrecarded 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACI94310 standard; DNA; 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-567953/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides populations of lineage-restricted precursor cells from mouse neural tube and mouse embryonic stem cells. These populations are of neuron-restricted precursor cells (NRPs) and glial-restricted precursor cells (GRPs). These cell populations are useful in the development of new transplant techniques, for transplantation in diseases where neuronal or glial degeneration has occurred, in the identification of large which enhance the survival and proliferation of transplanted cells, to identify genes specific to selected stages of development, and in the generation of cell-specific
                                                                                                                                                                                                                                                                    New pure populations of neuron- or glial-restricted precursor cells and neuroepithelial stem cells from mouse neural tubes or embryonic stem cells for developing new drugs or techniques that enhance survival of transplanted cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ss; probe; expressed sequence tag; microarray; gene expression;
ic variation; biallelic marker; polymorphism; human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 14.2; DB 4; Length 19;
Pred. No. 1.2e+04;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human microarray DNA oligonucleotide SEQ ID NO 94919.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19 BP; 3 A; 5 C; 6 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                              Example 8; Page 22; 37pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-MAR-2001; 2001US-0276759P.
                                                                                        05-MAY-2000; 2000WO-US012446.
                                                                                                                           99US-0133159P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.2%;
84.2%;
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                                                                                                                                                             (UTAH ) UNIV UTAH RES FOUND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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hes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cross-species comparison
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                                                                                                                                                                                                                                  WPI; 2001-024863/03
                                                                                                                                                                                                   Mujtaba T, Rao MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2003104410-A1
                  WO200068359-A1
                                                                                                                           07-MAY-1999;
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                                                      16-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibodies
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

Also disclosed is a method of gene expression analysis. The array is used in analysis of genetic variation or in hybridisation to a DNA library, or nanalysis of genetic variation or in hybridisation to a DNA library, or monounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of a least one or more nucleic acids to at least two or mace nucleic acids probes are attached to a solid support. The analysis comprises monitoring concerning members of a gene and a cross-species or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence. The array of nucleic acid solutions of any gene, in mapping the 5' termin of mRNA molecules by comparisons or in screening cNNA or genomic libraries or subclones containing segments of DNA that have been containing acid probes in corporated in the microarray. Note: The sequence contains a for the melance are segmented in the microarray. Note: The sequence contains and previously sequenced in the microarray.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-acetylgalactosamine; N-acetylglucosamine; human; N-acteylglactosamine transferase; NGalNAc-T1; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated protein having specified amino acid sequence for enzyme used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            data for this patent can also be obtained in electronic format directly from USPTO at segdata.uspto.goc/sequence.html
Northern or dot-blot hybridization to identify or detect the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human N-acteylglactosamine transferase NGalNAc-T1 PCR primer #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 14.2; DB 9; Length 25; Pred. No. 1.2e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 25 BP; 3 A; 9 C; 6 G; 7 T; 0 U; 0 Other;
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(AMSH ) AMERSHAM BIOSCIENCES KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.2%; Scor.
84.2%; Pred. No. ...
                   of any gene
                                                    Claim 1; SEQ ID NO 94301; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 GTCCAGCGTGCGCCATGGG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sato T;
                   sequence or specific mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADK43158 standard; DNA; 31 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-AUG-2002; 2002JP-00236292.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-AUG-2003; 2003WO-JP010309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-203801/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oligosaccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       betal-4 linkage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2004016790-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR; primer.
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 Southern,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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ADK43158
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in producing oligosaccharides.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Capsule containing packaging cells that produce viral vectors for gene therapy - used as replaceable implants in treatment of cancer, atherosclerosis etc., providing localised, long-term vector delivery.
                                                                protein. The protein is useful for enzyme used in producing oligosaccharides. The inventive isolated protein has the activity of transferring N-acetylgalactosamine to N-acetylglucosamine via betal-4 linkage. The present sequence represents human N-acteylglactosamine transferase, NGalNAc-T1, PCR primer.
                                                The invention relates to an isolated N-acteylglactosamine transferase
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bcl-2 gene; anti-apoptotic gene; prevention; cell death; treatment; neurodegenerative disease; disease; Huntingdon's; Parkinson's; Alzheimer's; retroviral vector; LNXS; LNCX; live packaging cell; blocompatible capsule; release; viral vector; implant; gene therapy; tumour; PCR primer; amplify; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Kozak sequence which enhances translation
effeciency of bcl-2"
                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                 Length 31;
                                                                                                                                                                                                                                  Indels
                                                                                                                                                                Sequence 31 BP; 4 A; 12 C; 10 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR primer 1 used in RT-PCR to amplify bcl-2 cDNA.
                                                                                                                                                                                             Score 14.2; DB 12;
Pred. No. 1.2e+04;
0; Mismatches 3;
               Example 1; SEQ ID NO 16; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 5; Page 33; 45pp; English.
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                                                                                                                                                                                                                                                                   1 GGGGTCCAGCGTGCGCCAT 19
                                                                                                                                                                                                                                                                                                   GGGTCCACGCTGCGCCAT 31
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/note= "Kozak
                                                                                                                                                                                                 59.2%;
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                                                                                                                                                                                                                                                                                                                                                                                      AAV05322 standard; DNA; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-MAY-1998 (first entry)
                                                                                                                                                                                             Query Match 59.2'
Best Local Similarity 84.2'
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                       AAV05322;
                                                                                                                                                                                                                                                                                                    13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a vector system, for transfection and recombinant polypeptide expression in a mammalian host cell, comprising a first cisturon encoding a transactivator protein under control of a first promoter, and a second cistron encoding an appptosis-protective protein under the control of the first promoter or optionally under the control of a second promoter, where the first and the second cistron are contained in one or more vectors. The vector system is useful for transfecting and expressing recombinant polypeptide in mammalian cells. The present sequence represents a RT-PCR primer for cloning the hamster B -cell lymphoma 2 (bcl-2) cDNA.
The vectors are used to transfect live packaging cells which form the core of a biocompatible capsule. These packaging cells are able to secrete a viral vector which includes a heterologous gene (in this case bcl-2) encoding a biologically active compound e.g. antisense sequence, blood coagulation factor, or an enzyme. The biocompatible capsules are surrounded by a jacket of permeable material with a porosity that allows release of the viral vector. The biocompatible capsules are implanted, e.g. into the central nervous system, for use in gene therapy, particularly where the active compound is useful in the treatment of tumours, cancers and other cell proliferative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 Transfection; recombinant protein; vector; B-cell lymphoma 2; bcl-2; reverse transcriptase PCR; RT-FCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New vector system comprising cistrons encoding a transactivator gand an apoptosis-protective protein, useful for transfecting and expressing recombinant polypeptide in mammalian cells.
                                                                                                                                                                                                      ö
                                                                                                                                                                           59.2%; Score 14.2; DB 2; Length 33; 84.2%; Pred. No. 1.2e+04; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Hamster B-cell lymphoma 2 (bcl-2) cDNA cloning primer 26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 38 BP; 12 A; 8 C; 12 G; 6 T; 0 U; 0 Other;
                                                                                                                                                  Sequence 33 BP; 7 A; 10 C; 9 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 10; SEQ ID NO 36; 119pp; English.
                                                                                                                                                                                                                               CCAGCGTGCGCCATGGGGG 24
                                                                                                                                                                                                                                                         ccascerrescarseres 12
                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-DEC-2004; 2004WO-US043830
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                                                                                                                                                                                                                                                                                                                           AEB55627 standard; DNA; 38
                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                       Query Match
Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cricetulus longicaudatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yu B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KALO-) KALOBIOS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2005-506766/51.
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    셤
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Score 14.2; DB 14; Length 38; Pred. No. 1.2e+04;

59.2%;

Best Local Similarity

Query Match

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The invention relates to the use of a polynucleotide comprising a sequence of 3977, 2441 or 3410 base pairs, fully defined in the sequence of 3977, 2441 or 3410 base pairs, fully defined in the specification, its fragment or complement, foor diagnosis or treating contactual compound regularing the expression of the polynucleotide comprising: (a) bringing a test compound into contact with a cell capable of expressing the expression of the polypeptide in the cell, and (c) detecting the expression of the polypheptide in the cell, and (c) detecting the expression of the polypheptide in the cell, and (c) controlled to compared to a control. The polypucleotides and polypeptides are useful for diagnosing schizophremia, and for identification of subjects who are predisposed to schizophremia, and for identification of subjects who are predisposed to schizophremia, and for identification of subjects who are predisposed to schizophremia, and for evaluating the efficacy of drugs for such disorder, and monitoring the progress of patient symptoms involved in clinical trials for the progress of such disorder. This sequence corresponds to a hybridization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides and polypeptides, useful for diagnosing schizophrenia, and for identifying a compound modulating the activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treatment of such disorder. This sequence corresponds to a nyprinizar probe for the gene for the rat voltage-gated potassium channel Kv3.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat voltage-gated potassium channel Kv3.3 DNA hybridization probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis; schizophrenia; potassium channel; probe; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 45 BP; 8 A; 16 C; 14 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 9; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohashi Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22
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                                                                  6 CCAGCGTGCGCCATGGGGG 24
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                                                                                                                                                                                                                                                                                                                     BP
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Matches 16; Conservative
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16;
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                                                                                                                                                                                                                                                                                                                                                                                        ADY31048;
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ID AAV1
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Job time : 189.893 secs
                                      24-MAR-1994;
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US5734033-A.
                  31-MAR-1998
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                                                                                                                                                                                                                                                                                           Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful for treating cancers, e.g. lymphoma(s) and some leukaemia(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;
                                                                             Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;
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Pred. No. 1.5e+04;
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100.0%; Pred. No. ...
0; Mismatches
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                                                         Human bcl-2 antisense oligonucleotide 6.
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                                                                                                                                                                               94US-00217082
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14; Conservative
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                                                                                                                     Homo sapiens.
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Homo sapiens
                                                                                                                                                                               24-MAR-1994;
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21-FEB-1992;
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                                                               88US-00288692.
92US-00840716.
94US-00217082
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Matches 14, Conservative
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AZ619403 IM0451E09
AI619702 ty52a05.x
A1619403 IM0451E09
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CL2100842 W1266707
BES58242 3590 1 30
BWS90752 BWS90752
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BE376178 61028534
CZ1609359 W126C07 G
CZ1609359 W126C07 G
AU102361 AU102361
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BX893758 Arabidops
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AN65005 cv22e05.x
AA667773 AA6-2-7
BF938418 73-Ad-2-7
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A1254752 4489607.x
A134488 ti45e03.x
AA594397 n193q10.s
CZ55110 P070ED1 G
CR900779 Sus scrof
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CL521622 SAL3H08 F
AZ825200 ZM0106N11
AK216071 Mus muscu
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CG728115

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CZ295110

AZ54752

AA594337

CZ295110

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BI597957 603249661
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AA863355 oh04e09.s
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A135502 Qu15G02.x A1634365 te5940113.x C2918895 40210113.1 AA062214 ml67901.r AA86693 v494602.r AA446631 tj05605.x AZ586716 100392819 AG218131 Drosophil AJ58439 Arabidops AA88208 of66010.s AA98436 of65905.8 DN95483 Arabidops AA88208 of66010.s AA99426 of66010.s AA99426 of65905.3 AA594706 Arabidops AA661070 Arabidops AA840706 Arabidops AA840706 Arabidops AA84777 aj7700.c BA61949 ALK 0402 BA11949 SALK 0402 BA11940 ARABIA Alfandops AA854777 aj7700.c AI440092 ti56f07.x	N29994 Yx8201.81 CC178014 XC298 Bay AJ58745 ARABIGOSB AA6745 ARABIGOSB AA478678 Zv19204.r BW963171 BW963171 AZ83966.s AA101215 Zn37607.s BH171096 SALK_0037 BH171096 SALK_0175 AL181912 T. Erucei AU103724 AU103724 AU103724 AU103724 AU103724 AU103965 AU104815 AU104815 AU104815 AU104815 AU10696 AU105966 AU10596 AU105966 AU106765 AU106766 AU106765 AU106766 AU106766 AU106766 AU21815 AU106766 AU106766 AU106766 AU106766 AU106766 AU10696 AU106766 AU10696 AU106966 AU10696 AU106966 AU10696 AU106966 AU10696 AU106966 AU10696 AU106969 AU10696 AU
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A1457484 t173h02.x AU106874 AU106874 AZ352290 1M0090M10 A1466405 T. brucei AQ025266 EP (3) 3084 AZ389322 1M0149G18 AZ497161 1M0333622 B186166 60 60 3389356 H39876 y057f03.r1 AA14418 nf61e03.s AG194532 Pan troggl BG035308 60 2324932 AZ46541 1M0275D21 AA89568 am71f03.s AA285509 T684609.s AA285507 ZM0102B17 CC183089 XG218 Bay CC25220 XM220 Bay AA627090 ng66e10.s AA627090 ng66e10.s AA627090 ng66e10.s AA627090 ng66e10.s AA627090 ng66e10.s AA627090 ng66e10.s AA63763 of37b12.s AA847284 oe81b02.s AA103357 AU103359 AU103359 AU103359	AU103361 AU103361 AU103984 AU103984 AU103984 AU103984 AAS94651 n195909.8 CR297745 Au2bidops AA661707 or40e08.8 AZ774408 2M0003P09 AZ884299 2M0157M17 AL493292 T. brucei H04278 Yj50a08.81 BG250817 60238324 AJ734507 AJ734507 CZ467241 C01543c-5 AL4931313 T. brucei AA059057 Zf63b10.8 BG915507 602815734 CL301852 P001C09 G AZ656960 1M0532015 BH885197 SALK 0864 CC355236 XM091 Bay CG804917 111805461 CL64808 M0338706 G N6499 Za30a10.11 BG565805 602589152 AR68236 AU107939 AU107939 AU107939 AU107939 AU107939 AU107950 AU36647 AQ30601.8 CR295257 30DGS05 AZ861088 ZM0229G21 AJ46642 AJ746642 AA865336 CG889408.8
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	JUDINAL EMBO Rep. 2 (5), 388-393 (2001) FUBMED 11375929 COMMENT Contact: Yutaka Suzuki Contact: Yutaka Suzuki Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Emall: ysuzukiains.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997). FEATURES Location/Qualifiers	Source 150 Corganism="Homo sapiens" Corganism="Homo sapiens" Amol type="mRNA" Ab_xref="taxon:9606" Alone="LNG15924" Alone="LNG15924" Alone="LNG15924" Alone Sapiens CDNA library" Clone_lib="Sugano Homo sapiens CDNA library" Query Match	Qy 2 GGGTCCAGCGTGCGGG 24	Z _ X	Hominidae, Homo. REFERENCE 1 (bases 1 to 50) AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Morishita,S., Okubo,K., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S. TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites JOURNAL EMBO Rep. 2 (5), 388-393 (2001) PUBMED 11375929 COMMENT Contact: Yutaka Suzuki	Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minacoku, Tokyo 108-8639, Japan Email: ysuzuki@ims.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997). FEATURES 150 /organism="Homo sapiens" /mol_type="mRNA"
A2473927 1M0290M03 H92936 yt92e04.rl CL520163 SAJ3D11 F CN757501 1D0AAA1DC CV93334 PMpcm 104 AQ025518 EP(X) 1587 AZ802142 2M0061105 AA630952 nq76e01.8 AA630950 od75h11.8	BM046304 603625308 BM047185 603627544 CD530897 08102 Ara CN973499 20998 45- BX121223 DANÍO rer CL213837 M042B03 G C20871 HUMGS000493 AZ812913 2M0079M19 AU103440 AU103440 AU103444 AU103444 AU103444 AU103444 AU103444 AU103444	AU106655 AU106655 AU107016 AU107016 AZ323931 1M0045F09 AA09237 0108c04.8 CZ474839 0405611-5p AI287706 qv07d12.x AI357706 qv17901.x CG718745 1119054C1 AA868659 ak499C2.8 AI262512 qk41f11.x AB082692 Drosophil	AL462237 T. brucei AZ784718 2M0027K01 AL938116 Arabidops CV064406 WNEL10f1 DN652373 S383 cDNA AU256510 AU256510 BG292849 602389872 AJ599761 Arabidops	AL760976 Arabidops AL940456 Arabidops AAB78864 of 89405.5 BE296536 601174028 AA680963 LIMFPAM057 AA509356 vgl8809.r BH639962 1008033A0 BH625517 1007110D0 A1423979 tf36h03.x BG86682 602785673	BXC20428 N47451 Yy09c10.s1 C2194596 PST3619-N AL464182 T. brucei BH810609 SALK 0509 AA447140 0448b04.s AA867748 vx16a12.r AI793579 fc51d05.x	mENA linear EST 28-JÄN-2004 library Homo sapiens cDNA clone
11 45.8 44.8 8 11 45.8 44.8 8 11 45.8 44.10 11 45.8 44.5 7 11 45.8 45.9 11 45.8 45.9 11 45.8 46.1 11 45.1 11 45.8 46.1 11 45.8 46.1 11 45.8 46.1 11 45.8 46.1 11 45.1 11 45.1 11 45.1 11 45	2552 2553 2554 2555 2556 2559 2559 2559 2559 2559 2559	11 45.8 50 1 10.8 45.0 19 9 10.8 45.0 25 1 10.8 45.0 25 1 10.8 45.0 28 1 10.8 45.0 28 1 10.8 45.0 29 10 10.8 45.0 33 1	10.8 45.0 33 11 10.8 45.0 35 9 10.8 45.0 35 10 10.8 45.0 36 8 10.8 45.0 36 8 10.8 45.0 38 10	283 10.8 45.0 38 10 284 10.8 45.0 38 10 286 10.8 45.0 40 2 287 10.8 45.0 41 1 288 10.8 45.0 41 1 289 10.8 45.0 41 1 280 10.8 45.0 41 9 290 10.8 45.0 42 9 291 10.8 45.0 43 1 292 10.8 45.0 43 1	10.8 45.0 44 5 10.8 45.0 44 10 10.8 45.0 44 11 10.8 45.0 44 11 10.8 45.0 45 11 10.8 45.0 46 11 10.8 45.0 46 11	RESULT 1 ALIGNMENTS RU107435 LU107435 LUCUS DEFINITION AU107435 Sugano Homo sapiens cDNA libra. LNG15924, mRNA sequence. LNG15924, mRNA sequence. ACCESSION AU107435.1 GI:13556956 KEYWORDS SOURCE Homo sapiens (human)

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Contact: Andrew R. Cossins
Laboratory for Environmental Gene Regulation
Contact: Andrew R. Cossins
Laboratory for Environmental Gene Regulation
University of Liverpool.
School of Biological Sciences, The Biosciences Building, Crown
Street, Liverpool, United Kingdom, L69 72B
Tel: +44(0)151-795-4510
Fax: +44(0)151-795-4431
Email: cossinselly.ac.uk
Vector has been trimmed from this EST.
Plate: 34 row: a column: 07
Seq primer: Triplex 5' LD (5'-CTCGGGAAGCGCCCATTGTTGTTGTTGTT-
High quality sequence stop: 47
POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="DH10B"
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Average insert size 0.8 kb."
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Cyprinus carpio

Cyprinus carpio

Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Cyprinus.

I (bases I to 47)

Gracey, A. Y., Fraser, B. J., Li, W., Fang, Y., Taylor, R.R., Rogers, J., Brass, A. and Cossins, A.R.

Coping with cold: An integrative, multitissue analysis of the transcriptome of a poikilothermic vertebrate

Proc. Natl. Acad. Sci. U.S.A. 101 (48), 16970-16975 (2004)
                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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                                                                                                                                              unknown library type
Trace considered overall poor quality
Trace considered overall poor quality
Seq primer: -40ml3 fwd. ET from Amersham
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
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/tissue_type="hepatic adenoma"
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/mol_type="mRNA"
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/organism="Homo sapiens"
                                                                                                     Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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AJ796516.1 GI:51111844
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicotyledons,
asterids, lamiids, Lamiales, Plantaginaceae, Antirrhineae,
Antirrhinum.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bey,M., Stueber,K., Fellenberg,K., Schwarz-Sommer,Z., Sommer,H.,
Saedder,H. and Zachgo,S.
Characterization of Antirrhinum Petal Development and
Identification of Target Genes of the Class B MADS Box Gene
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                                                                                                            50;
                                                                                                                                                         5; Indels
                                                                                                            Length
                                                                                                          62.5%; Score 15; DB 1; I 78.3%; Pred. No. 7.3e+04; ive 0; Mismatches 5;
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MPI fuer Zuechtungsfersebinng
Carl-von-Linne Weg 10, D-50829, Germany.
Location/Qualifiers
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Contact: Schwarz-Sommer
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AA878878.1 GI:2987843
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Homo sapiens
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Gaps

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EST 20-AUG-1998

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/clone_libe_Sugano mouse liver mlia"
/clone_libe_Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME185-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); lst strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCTACTGG], digested
and cloned into distinct DraIII sites of the pME185-FL3
vector [5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGGG and 3' end
primer CGACCTGCAGCACA."
                                                                                                                                                                                                                                                                                                                                                                          Mustayota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi, Muroidea, Muridae, Murinae, Mus.

1. (Dases 1 to 49)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                AI098584 140 mRNA linear EST 20.

AL098587.X. Sugano mouse liver mlia Mns musculus cDNA clone
IMAGE:1481821 3' similar to SW.A2HS MOUSE P29699
ALPHA-2-HS-GLYCOPROTEIN PRECURSOR ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marxa M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.7%; Score 13.6; DB 1; Length 49; 80.0%; Pred. No. 2.9e+05; tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .49
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="IMAGE:1481821"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
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  24
                                33 CCTTCCTGCGCCATGGGGG 15
                                                                                                                                                                                                                                                                                      AI098584.1 GI:3448109
  6 CCAGCGTGCGCCATGGGGG
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Best Local Similarity
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                                                                                                                                                                                    DEFINITION
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                                                                                                                                          AI098584/c
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JOURNAL
COMMENT
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AUTHORS
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KEYWORDS
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                     / sex="Wale & female"
/ tissue type="Muscle"
/ dev_stage="Adult"
/ dev_stage="Adult"
/ lab host="E.coli Bectromax DH10B"
/ clone_lib="Carp muscle library 1"
/ note="Vector: Piriplexy; site 1: $fil GGCGATTACGGCC;
Site 2: $fil GGCGCTCGGCC; Serially subtracted cDNA
library prepared from muscle of warm, cold and hypoxia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.inh.gov
This clone is available royalty-free through LLNL; contact the mAGE Consortium (info@image.lnh.gov) for further information.
Trace considered overall poor quality
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA993146 49 bp mRNA linear EST 03-JUN-1
ot77a10.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone
IMAGE:1622778 3' similar to SW:FBRL_HUMAN P22087 FIBRILLARIN ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae, Homo.
1 (bases 1 to 4049)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP ttp://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                        59.2%; Score 14.2; DB 6; Length 47; 84.2%; Pred. No. 1.6e+05; ive 0; Mismatches 3; Indels
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Pred. No. 1.6e+05;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:1622778"
/dev_stage="8-9 weeks"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
'db xref="taxon:7962"
                                                                                                                                                                                                                                       challenqed animals<sup>n</sup>
                                                                                                                                                                                                                                                                                                                                                                                                        4 GTCCAGCGTGCGCCATGGG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                     47 GTCCAGAGAGTGCCATGGG 29
                        34a07
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84.2%;
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Best Local Similarity 84.2
Matches 16; Conservative
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Matches 16; Conserv
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Gaps

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RESULT 8 AU102746/c

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DEFINITION

ACCESSION

KEYWORDS

ORGANISM

REFERENCE AUTHORS JOURNAL PUBMED

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TITLE

FEATURES

ORIGIN

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/note="PCN varies" in the DNA of primary transformants of Orysa sativa plants. The DNA fragment(s) resulting of PCN were directly sequenced from the left border to determine the genomic sequence flanking the insertion.

T-DNA derived sequences were removed Information to order the corresponding mutant line and a link to a datebase providing a graphical display is available from june 2004 at http://genoplante.info.infobiogen.fr/oryzatagline/.

This sequence has been generated in the framework of the French plant genomics program Genoplante (http://www.genoplante.org and http://genoplante.org and http://genoplante.org and http://genoplante.info.infobiogen.fr)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Not-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae, Homo.

1 (Jases, Homo.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Gancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                   /organism="Oryza sativa (japonica cultivar-group)"
/mol type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone lib="Flanking Sequence Tag of Oryza sativa T-DNA insertion lines"
                                                              TA 40/03 ave Agropolis 34398 Montpellier cedex 5 FRANCE Tel: 33467615629 Fax: 33467615605 Fax: 33467615605 Easil: emmanuel.guiderdoni@cirad.fr Class: TDNA tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.8%; Score 13.4; DB 10; 73.9%; Pred. No. 3.5e+05; iive 0; Mismatches 6;
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Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. .40
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AI800161.1 GI:5365633
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 73.9
Matches 17; Conservative
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Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Entartophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Entartoideae; Oryzeae; Oryza.

Entartoideae; Oryzeae; Oryza.

I (bases 1 to 37)

Entartoideae; Oryzeae; Oryza.

Entartoideae; Oryza.

Entartoideae; Oryza.

Droc,G., Regad F., Bes,M., Piffanelli,P., Piegu,B.,

Ghesquiere,A., Delseny,M., Glaszmann,J.C. and Guiderdoni,E.

High throughput T-DNA insertion mutagenesis in rice: A first step towards in silico reverse genetics

Contact: Guiderdoni

Contact: Guiderdoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ysuzuki@ins.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
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                                                                                                                                                                                                                AU102746 Sugano Homo sapiens CDNA library Homo sapiens CDNA library Homo sapiens CDNA clone
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hominidae, Homo.

1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Tangai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
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/mol_type="mRNA"
/db_xref="twxnon:9606"
/db_xref="twxnon:9606"
/clone="cAs09562"
/clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 13.6; DB 1; Length 50;
Pred. No. 2.9e+05;
0; Mismatches 4; Indels
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EMBO Rep. 2 (5), 388-393 (2001)
11375929
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             GGTCCAGTGTCCCCCATGTG 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.7%;
80.0%;
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Best Local Similarity 80.0
Matches 16; Conservative
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CL517576
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LOCUS

ACCESSION

VERSION KEYWORDS

ORGANISM

AUTHORS

REFERENCE

JOURNAL

COMMENT

TITLE

CL517576/c

RESULT 9

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Gaps

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us-09-669-187a-81.szlm50.rst

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Mus musculus (house mouse)
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GSS.
                                                                                                Query Match
Best Local Similarity 73.9%;
Matches 17; Conservative C
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COMMENT
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AUTHORS
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                                                ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CBAP clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
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/clone lib="NCI CGAP Kid3"
/note="Corgan: Kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI; lst
strand cDNA was primed with a Not I - oligo(dT) primer,
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT7T3 vector: mRNA
source: 2 pooled kidneys. Library went through one round
                                                                /clone=IMAGE:219917"
/tissue_type="tumor, 5 pooled (see description)"
/lab host="DH10B"
/clone=lib="NCI_CGAP_Ov23"
/note="organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.35 kb. Tumor types include: mixed
Mullerian tumor, papillary serous, clear cell, spindle
cell. All are primary tumors, metastasis positive. Life
Technologies catalog #: 11534-013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Bmall: cgapbs-römail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hominidae, Homo.

1 (bases 1 to ...)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP ttp://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                             55.8%; Score 13.4; DB 1; Length 40; 73.9%; Pred. No. 3.5e+05; ive 0; Mismatches 6; Indels
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'organism="Homo sapiens"
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'organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:1456840"
                  /mol_type="mRNA"
/db xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GGGTCCAGCGTGCGCCATGGGGG 24
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                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 73.9
les 17; Conservative
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Unpublished (1997)
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VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwm742 (gil4732114 gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ434579 33 bp DNA linear GSS 03-OCT-2000 IM0221I10F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0221I10 F, genomic survey sequence.
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of normalization. Library constructed by Bento Soares and
M. Fatima Bonaldo. "
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
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/lab host="B. Coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jacksor
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Dunn,D., Acyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                           ö
                                                                                                                                  Length 43;
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                                                                                                                                     Score 13.4; DB 1;
Pred. No. 3.5e+05;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plate: 0221 row: I column: 10
Seq primer: CGTTGTAAAACGACGGCCAGT
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/strain="C57BL/6J"
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/clone="UUGC1M0221110"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                          17 degeccháceerreccheedes 39
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Contact: Yutaka Suzuki
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
length-enriched and a S'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
                                               AU104320 AUGano Homo sapiens CDNA library Homo sapiens CDNA clone
                                                                                                                                                                                                                                                                                                                                                      Hominidae, Homo.

1 (Dases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,

Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,

Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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EMBO Rep. 2 (5), 388-393 (2001)
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                                                                                                                     HEP06849, mRNA sequence
                                                                                                                                                                           AU104320.1 GI:13553841
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Homo sapiens
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Best Local Similarity
Matches 16; Conserv
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I (bases 1 too 38)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L (Dubblished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

CDNA Library Preparation: Michael J. Brownstein (LIML)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:

http://image.llh.gov

Plate: LLAMI1656 row: g column: 03

High quality sequence stop: 38.

Location/Qualifiers
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603188912F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5260442 5',
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adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                        Length 33;
                                                                                                                                                    Score 13; DB 9; I
Pred. No. 5.1e+05;
0; Mismatches 5;
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76.2%;
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Suzuki, Y., Taira, H., Tsunoda, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakaura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
                                                                                                                                                                                                                                                       Gaps
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/mol_type="mRNA"
|db_xref="taxon:9606"
|clone="HEP06849"
|clone_lib="Sugano Homo sapiens cDNA library"
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Department of Mirology
Institute of Medical Science, University of Tokyo
Tratitute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                                                                                                                                                                                    54.2%; Score 13; DB 1; Length 50; 76.2%; Pred. No. 5.1e+05;
                                                                                                                                                                                             Score 13; _______Pred. No. 5.1e+05; _______ 5; Indels
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FEATURES

ORIGIN

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50 bp mRNA linear EST 28-JAN-2004 AU107885 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HSI05714, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
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AU107886 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
AU107886
                                                                                                                                                                                                                                                        Hominidae, Homo...

1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., 1sogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
EMBO Rep. 2 (5), 388-393 (2001)
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedal Minatoku, Tokyo 108-8639, Japan
Banil: yeuzukidoims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleo
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                     Email: ysuzuki@ims.u-tokyo.ac.jp
Suzukik,Y., Ysbiticomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,

Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,

Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
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/db_xref="taxon:9606"
                                                                                                                                                 location/Qualifiers
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AU107884.1 GI:13557406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Yutaka Suzuki
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                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 76.2.
The 16; Conservative
                                                                                                                         149-156 (1997).
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Matches 16; Conserv
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BF384787
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                                                                                                                                                                                                                                                                                                                                                                                                                                             R85071 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:180595 5' similar to gb:J05096_rna1 SODIUM/POTASSIUM-TRANSPORTING ATPASE_ALPHA-1 CHAIN (HUMAN);, mRNA
                                                                                                                                                                                                                                                                            ö
Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares adult brain N2b4HB55y"
/note="Organ: brain; Vector: pT773D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; lst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insert Size: 2244
High quality sequence starts: 1
High quality sequence storis: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 2244 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae; Homo.

1 (bases 1 to 50)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Hutenan,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilson, K.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                         /clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                                                                                                                    Length 50;
                                                                                                                                                                                                                                                                          5; Indels
                                                                                                                                                                                                                                  Score 13; DB 1; I
Pred. No. 5.1e+05;
0; Mismatches 5;
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organism="Homo sapiens"
                                                                                                    /organism="Homo sapiens"
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/db xref="GDB:3827242"
                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:180595"
                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  1 GGGGTCCAGCGTGCGCCATGG 21
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                                            149-156 (1997)
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602046279F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:4195795 5',
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-remail.nih.gov
Tissue procurement: Jeffrey B. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
High quality sequence stop: 34.
High quality sequence stop: 34.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="INAGE:4195795"
/lab.host="DH10B (T1 phage-resistant)"
/lab.host="DH10B (T1 phage-resistant)"
/clone lib="WCI CGAP Li9"
/note="Organ: liver; Vector: pCWV-SPORT6; Site_1: Not1;
Site_2: Sall; cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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76.2%; Pred. No. 5.1e+05;
tive 0; Mismatches 5;
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Mus musculus
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/strain="FVB/N"
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LOCUS

ACCESSION VERSION KEYWORDS SOURCE

RESULT 21 AI755616

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AUTHORS REFERENCE

TITLE JOURNAL COMMENT

FEATURES

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/tissue_type="hypothalamus"
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/lab_host="DH10B"
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/clone_lib="hypothalamus"
/clone_lib="hypothalamus"
/clone_lib="hypothalamus"
/clone_lib="hypothalamus"
/clone_lip="hypothalamus"
/clone_lip="hypothalamus"
/clone_lip="hypothalamus"
/clone_lip="hypothalamus"
/clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein
(NIMM/NHGRI, National Institutes of Health). Note: this is
                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae, Homo.

In (bases 1 to 38)

NH-MGC http://mgc.nci.nlh.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.inh.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

CDNA Library Preparation: Michael J. Brownstein (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Llocation/Qualifiers

Llocation/Qualifiers
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Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and
BIS97957 38 bp mRNA linear EST 07-SEP-2001
603249661F1 NIH_MGC_96 Homo sapiens CDNA clone IMAGE:5301590 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AJ683869 CSEQRAN04 Sus scrofa cDNA clone C0001803_F11, mRNA
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/organism="Homo sapiens"
/mol_type="mRNR"
/db xref="taxon:9606"
/clone="IMAGE:5301590"
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Sus scrofa
                                                                                       mRNA sequence.
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/lab_host="SOLR E. coli"
/clob host="SOLR E. coli"
/clob host="Vector: Bluescript SK-; Site_1: EcoRI; Site_2:
/hote="Vector: Bluescript SK-; Site_1: EcoRI; Site_2:
/hote="Vector: Bluescript SK-; Site_1: EcoRI; Site_2:
/hote="Vector swere obtained from in vitro sporulated
and excysted occysts of E. tenella grown in chickens.
conA was synthesized from poly mRNA using an oligo-dr
primer containing a XhoI site. Following second strand
synthesis, EcoRI adapters were ligated to the cDNA and
products were size-selected on Sephacryl S500. cDNAs were
digested with EcoRI/XhoI and cloned into lambda Zap II
(Stratagene) . Clones were converted to phagemids by mass
excision using ExAssist helper phage and SOLR cells
(Stratagene) . Insert sizes range from 1.2-2.9 kb."
                                                                                                                                                                                                                                                                                                                                       A1755616
37 bp mRNA linear EST 18-JAN-2000 ELESTea38h12.yl Eimeria S5-2 Sporozoite stage Eimeria tenella cDNA 5' similar to TR:Q28583 Q28583 KAP5.4 KERATIN PROTEIN. ;, mRNA
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Contact David Sibley (toxoest@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
Dessible reversed clone: similarity on wrong strand
Seg primer: -40RP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liberator, P., Diaz, C., Tang, K., Marra, M., Hillier, L., Kucaba, T., Liberator, P., Diaz, C., Tang, K., Steptoe, M., Thelsing, B., Anlarim, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Florence, N., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., Wilson, R. and
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Unpublished (1999)
Contact: David Sibley, Ph.D.
Washu-Merck Eimeria tenella project
Washu-Merck Eimeria tenella project
Washington University School of Medicine
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
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                                                                                                                              B GGGCCCAGCTGGGCCCACTCGGG 31
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                                                    GGGGTCCAGCGTGCGCCATGGGGG
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/strain="LS18"
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Best Local Similarity 70.83
Matches 17; Conservative
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Gaps

RESULT 22 BI597957

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ORIGIN

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Homo sapiens
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                                                                                           Roslin Institute
Roslin Midlothian, EH25 9PS, UNITED KINGDOM
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
Single pass sequencing. Bases called and trimmet he -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Sitel: EcoRI
R. Site2: NotI S, Seq Primer M1F Rormalised library constructed
Firm pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
Location/Qualifiers
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/mol trype="mmna"
/db xref="teaxon:9823"
/clone="clone="clone"
/tissue trype="terus"
/clone lib="CSEQRAN04"
/note="vector: pBlueScriptII(KS+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."
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(bases 1 to 40)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Ralam, D., Aoyagi, A., Gongacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Thomas, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Duouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ998247
2M0285P03F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0285P03 F, genomic survey sequence.
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embryo development in pigs and cattle Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
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Insert Length: 10000 Std Exror:
Plate: 0.285 row: P column: 03
Seg primer: CGTTGTAAAACGACGGCCAGT
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/mol_type="genomic DNA"
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High quality sequence stop: 40.
Location/Qualifiers
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Mus musculus
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Fax: 801 585 7177
Email: ddunn@genet
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Best Local Similarity
Matches 17; Conserve
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AZ998247/c
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwd2 (gql/4732114/gbl/AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (bases 1 to 41)

S NIH-WGC http://mgc.nci.nih.gov/.

SNIH-WGC http://mgc.nci.nih.gov/.

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The 1.M.A.G.E.

Clone distribution: MGC clone distribution information can be
found through the 1.M.A.G.E. Consortium/LINL)

Flowed through the 1.M.A.G.E. Consortium/LINL at:

http://mage.llnl.gov

Plate: LLAM1752 row: j column: 15
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                                                                                                                                        /lab host="E. coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/G (female) was obtained from the Jackson Laboratory Mouse DNA Resource
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0285P03"
/sex="Female"
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/lab_host="DH10B"
/clone_lib="NIH_MGC_97"
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/db_xref="taxon:9606"
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Best Local Similarity 70.8%
Matches 17; Conservative
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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.05 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were
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S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Ungey, A., von Dublasmid inserts

L Unpublished (2000)

C Ontact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT 84112, USA
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1M0240A01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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                                                                                                                                                                                                                                                                                                                                                          0; Gaps
'note="Organ: testis; Vector: pBluescriptR (modified
                                                                                                                                                                                                                                                                                                     Query Match 53.3%; Score 12.8; DB 3; Length 41; Best Local Similarity 70.8%; Pred. No. 6.2e+05; Matches 17; Conservative 0; Mismatches 7; Indels
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Pax: 801 585 7177

Email: ddunm@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0240 row: A column: 01
Seq primer: CACACAGGAAACAGCTATGACC
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/strain="C57BL/6J"
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/clone="UUGC1M0240A01"
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High quality sequence stop: 44.
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AZ444974.1 GI:10594347
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ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwns2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored to the insert adaptors and complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored the complement E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (Dases 1 to 48)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Rallam, H., Longacre, S., Mahmud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Dlasmid inserts

Unpublished (2000)
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1M0355P08R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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/clone_11b="Mouse 10kb plasmid UUGCNM library"
/note="Vector: PWD42nr; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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70.8%; Pred. No. 6.2e+05;
iive 0; Mismatches 7;
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Insert Length: 10000 Std Error: C
Plate: 0355 row: P column: 08
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC1M0355P08"
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Location/Qualifiers
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Mus musculus
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Fax: 801 585 7177
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Best Local Similarity
Matches 17; Conserv
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BB616279
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AU106561
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/mol_type="mRNA"
/db_raref="taxon:9606"
/clone="tMAGE:1518200"
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/clone_lib="Ncl CGAP GC4"
/note="Vector: pT713D-pac (Pharmacia) with a modified
polylinker; lst strand cDNA was prepared from 3 pooled
germ cell tumors, and was prepared from 3 pooled
germ cell tumors, and was prepared from 3 pooled
germ cell tumors on a proper of the primed with a not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT773
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo. "
polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AR129072.1), a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XI10-Gold (Stratagene) cells and selected for ampicillin resistance."
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CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

Clound through the I.M.A.G.E. Consortium/LINL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 555 Std Brror: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hominidae, Homo.

1 (bases 1 to 49)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                               Score 12.8; DB 9; Length 48;
Pred. No. 6.2e+05;
0; Mismatches 7; Indels
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AA903627.1 GI:3038750
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1 Similarity 70.8%;
17; Conservative 0
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BB616279 RIKEN full-length enriched, adult male testis Mus musculus cDNA clone 4931436G19 5', mRNA sequence.
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AU106561 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT03341, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
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Bail: Suzuki, Minatoku, Tokyo 108-8639, Japan
Bmail: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Bugano, S. Construction and characterization of a full
Inength-enriched as S'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997)
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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1 (Dases 1 Homo.)

2 (Dases 1 Homo.)

3 (Dases 1 Homo.)

4 (Dases 1 Homo.)

8 (Dases 1 Homo.)

9 (Dases 1 Homo.)

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Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
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/db_xref="texcon:9606"
/dbome="xtr03341"
/clone_lib="Sugano Homo sapiens cDNA library"
Score 12.8; DB 1; Length 49;
Pred, No. 6.2e+05;
0; Mismatches 7; Indels
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87.5%; Pred. No. 6.2e+05;
ive 0; Mismatches 2; Indels
                                                                                              0; Mismatches
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53.3%;
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    Query Match
Best Local Similarity 70.8<sup>†</sup>
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 87.5
Matches 14; Conservative
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24

1 GGGGTCCAGCGTGCGCCATGGGGG

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COMMENT

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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 175-1771 (200)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library Genome Res. 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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/lab_host="SOLR"

/clome lib="Rolk" lill-length enriched, adult male testis"

/note="Site 1: XhoI; Site_2: BamHI; cDNA library was

/note="Site and sequenced in Mouse Genome Encyclopeddia

project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5
Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, K., Sano, H., Sasaki, B., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takaka, Y., Tanaka, T., Toya, T., Muramatsu, M., and Hayashizaki, Y. Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                      Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
1-1: 81-45-503-9216
Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: genome_res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected CONAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matsuira,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIKEN. Division of Experimental Animal Research in Riken
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Location/Qualifiers
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/strain="C57BL/6J"
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FEATURES

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/lab hose="E. coli strain XL10-Gold, Tl-resistant, F-"
/lab hose="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nt; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically shaared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose get a 9.5 to
10.5 kb range using preparative agarose gfrom a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid RI. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli X110-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                  AZ982659
2M0263J03R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0263J03 R, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases) Lt o 50)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plate: 0263 row: J column: 03
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/strain="C57BL/6J"
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/clone="UUGC2M0263J03"
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Location/Qualifiers
16 GCGGCCGTGCGGAGCCATGGCGG 39
                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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Matches 17; Conserv
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0; Gaps

53.3%; Score 12.8; DB 2; Length 50; 70.8%; Pred. No. 6.2e+05; ive 0; Mismatches 7; Indels

Query Match 53.3 Best Local Similarity 70.8 Matches 17; Conservative

CL521622/c DEFINITION

ð 8 ORGANISM

VERSION KEYWORDS SOURCE

ACCESSION

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

FEATURES

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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil #4732114[gb] AR129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chamically-competent E. coll Xili0-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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45 bp mRNA linear HTC 23-NOV-200 MRNA us musculus cDNA, clone:YZG0137P14, strand:plus, reference:ENSEMUs.Mouse-Transcript-ENST:ENSMUST0000040729, based on BLAT search.
                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                              1 (bages 1 to 28)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.5%; Score 12.6; DB 9; Length 28; 78.9%; Pred. No. 7.5e+05; tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0106 row: N column: 11
Seg primer: CACACAGGAAACAGCTAATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .28
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="UUGC2M0106N11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Class: plasmid ends
High quality sequence stop: 28.
Location/Qualifiers
                   Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GGTCCAGCGTGCGCCATGG 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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                                                                                                                                                         REFERENCE
                                                                                                                                                                                  AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Ehrhartoideae; Oryzae, Dillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae, Oryza,
I (basea; I to SO)
Sallaud, C., Gay, C., Larmande, P., Bes, M., Piffanelli, P., Piegu, B.,
Droc, G., Regad, F., Bourgeois, E., Meynard, D., Perin, C.,
High throughput T-DNA insertion mutagenesis in rice: A first step
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ829200
2M0106N11R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0106N11 R, genomic survey sequence.
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Fax: 33467615605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  French plant genomics program Genoplante
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (http://www.genoplante.org and
http://genoplante-info.infobiogen.fr)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: emmanuel.guiderdoni@cirad.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24
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                           1 GGGGTCCAGCGTGCGCCATGGGGG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Class: TDNA tagged.
Location/Qualifiers
                                                                        32 degerccadecrresagadeses 9
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Contact: Guiderdoni
UMR PIA Biotrop program
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AZ829200.1 GI:12999108
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Best Local
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AZ829200/c
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Gaps . 0 HTC 23-NOV-2004

DEFINITION ACCESSION VERSION

ORIGIN

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http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
CELL_LINE&KEY=XE347
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Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: walbot@stanford.edu

Sossible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.

Plate: 1119098 row: 39
                                                       /clone lib="1119 - RescueMu Grid AA" /note="Organ: leaf; Vector: RescueMu (engineered from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="Embryonic stem cell"
/clone_lib="BayGenomics Gene Trap Library pGT1Lxf"
/note="Vector: pGT1Lxf"
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/cultivar="mixed background W23/A188/B73/K55"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
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855 California Ave, Palo Alto, CA 94304, USA
TTE1: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 12.6; DB 9;
Pred. No. 7.5e+05;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="mRNA"
/strain="129 ola"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Zea mays"
                                                                                                                                                                                                                                                                                          Location/Qualifiers
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Location/Qualifiers
                         http://baygenomics.ucsf.edu/
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 GGTCCAGCGTGCGCCATGG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 GGGCCCGGCTGCGCATGG 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:37768518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.5%;
78.9%;
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Walbot, V.
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Contact: Walbot V
                                                                                                                                                                                                                                                                     Class: Gene Trap
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CG728115
CG728115.1 GI:3
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Best Local Similarity
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CG728115/c
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Nakamura, M., Sasaki, D., Arakawa, T., Kawai, J., Harbers, M.,
Hayashizaki, Y. and Carninci, P.
Libraries enriched for alternatively spliced exons reveal splicing
patterns in melanocytes and melanomas
Nat. Nethods 1, 233-239 (2004)
2 (bases 1 to 45)
Arakawa, T., Carninci, P., Fukuda, S., Harbers, M., Hayatsu, N.,
Hori, F., Inocani, K., Kawai, J., Kondo, S., Murata, M., Nakamura, M.,
Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC183529 45 bp mRNA linear GSS 08-MAY-2003 XE347 BayGenomics Gene Trap Library pGT1Lxf Mus musculus cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (15-SEP-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-reseggsc.riken.jp, URL:http://genome.gsc.riken.jp, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alternative Splicing Libraries (ASL8) are prepared by: Preparating of single-stranded DNA using a RNA template from full length CDNA libraries, hybridizating of single-stranded DNA, removing of remaining single-stranded DNA, aligesting of regions comprising double-stranded DNA by a set of 4 bp-cutters, capturing of DNA hybrids with loop structures (alternative spliced exon), ligating of r-shaped primers to isolated DNA hybrids with loop structures and that continuous structures, PCR amplification of ligation products and their cloning into PFLCI vector. (Reference).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_line="mixture of B16-F10Y and melan-c"
/cell_type="mixture of melanoma cell and melanocyte cell"
/colne_lib="Alternative Splicing Library L3"
/note="strand:plus, reference:ENSEMBL:Mouse-Transcript-
ENST:ENSMUST00000040729, based on BLAT search"
                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sclurognathi; Muridae; Murinae; Mus.
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/db_xref="taxon:10090"
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Mus musculus
                                                                   Mus musculus (house mouse)
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                                                                                        Mus musculus
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                   A1254752 AL NCI CGAP CO14 Homo sapiens DNA clone IMAGE:1962469 3' gimilar to SW:WASP WOUSE P70315 WISKOTY-ALDRICH SYNDROME PROTEIN HOMOLOG; contains element MSR1 repetitive element; mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 2)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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    .49
    /organism="Homo sapiens"

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/db_xref="taxon:9606"
/clone="IMAGE:1962469"
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                                                                                 16 GGTGGAGCCTGGGCCATGG 34
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                                               3 GGTCCAGCGTGCGCCATGG
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| Mol_type="mRNA" |
| Ab_xref="taxon:9606" |
| Alone="mRNA" |
| Alone="mRNA" |
| Alone="mrna" |
| Alone | Mora |
| 
pBlueScript backbone); Site 1: BamHI; Site 2: BgIII; RescueMu is a 4.9 kb, modified maize Mu transposon Messigned to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.rmdb.iastate.edu' and follow the links for RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BHHIOB cells were transformed and then screened on LB plates with ampicillin."
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603062308F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5211864 5',
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAMIS31 row: o column: 01
High quality sequence stop: 48.
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1 (bases 1 to 48)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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Matches 15; Conservative
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P070E01 GGTC Gene Trap Library GV18C05 Mus musculus cDNA clone
CZ295110
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Bmail: info@genetrap.de
FlipROSACeoC42 gene trap. Sequence tag generated by 5'RACE.
Additional sequence information can be found at:
'http://genetrap.gsf.de/project/web_new/databbase/result_clone.html?
'clone id=P070E01' ES cell line harboring insertion mutation of target gene is available at:
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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Hansen, J., Floss, T., van Sloun, P., Fuchtbauer, E.M., Vauti, F.,
Hansen, J., Schnutgen, F., Wurst, W., Von Melchner, H. and Ruiz, P.
A large-scale, gene-driven mutagenesis approach for the functional
analysis of the mouse genome
Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
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                                                                                                                         Trace considered overall poor quality Insert Length: 1930 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 1. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.5%; Scor.
78.9%; Pred. No. /...
0; Mismatches
                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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/strain="129 Sv"
/db_xref="taxon:10090"
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Mus musculus
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CZ295110
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                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: capabs.remail.nih.gov
Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
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/clone_lib="NCI_CGAP_Lym12"
/note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1:
Salf; Site_2: NotI, Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015"
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cDN Library Preparation: M. Bento Soares, Ph.D.
cDN Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                            Hominidae, Homo.

1 (bases 1 to 49)

Noti-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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1. (Dases 1 to .0, www. ncbi.nlm.nih.gov/ncicgap.
NCI-CASP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Umpublished (1997)
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
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    .49
    /organism="Homo sapiens"

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/db_xref="taxon:9606"
/clone="IMAGE:2133436"
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78.9%;
   Homo sapiens (human)
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Best Local Similarity 78.5.
Local Similarity 78.5.
Local Similarity 78.5.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi, Muziodae, Muzinae; Mus.

1 (bases 1 to 23)

2 (bases 1 to 23)

3 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ619403 23 bp DNA linear GSS 13-DEC-2000 1M0451E09R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0451E09 R, genomic survey sequence.
                                                                                                                                                                                                Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Sensen, C.W., Gordon, P.M.K. and Moore, S.S.
Gene Expression Profiling of the Bovine Gastrointestinal Tract Gene Expression Profiling of the Bovine Gastrointestinal Tract Gene Expression Moore
Beef Genomics Laboratory
Dept of ARNS, University of Alberta
410 Agri, For, Dept of ARNS, U of A, Edmonton, AB, T6G 2P5, Canada Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae, Bovinae, Bos.

1 (bases 1 to 50)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Bos taurus"
/mol_type="mRNA"
/db xref="taxon:9913"
/tissue_type="Roll muscle"
/tissue_type="Simple columnar epithelial"
/dev_stage="Young adult"
/lab host="X11-BluoRRF'strain"
/lone_lib="Bos taurus Duodenum #1 library"
/note="Gorgan: Intestine/duodenum; Vector: Uni-2ZAPXR;
Site_1: EcoRI; Site_2: Xho I"
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.larity 78.9%; Pred. No. 7.5e+05;
Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               Bmail: stephen.moore@ualberta.ca
Insert Length: 50 Std Brror: 0.00
POLYA=No.
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                                    CB221472.1 GI:28291986
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                                                                             Bos taurus (cow)
Bos taurus
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Submitted (18-NOV-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CB221472 50 bp mRNA linear EST 10-FEB-2003 1Duo13A09 Bos taurus Duodenum #1 library Bos taurus cDNA, mRNA
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Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                                 GSS 23-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Construction of a swine BAC library: application to the characterization and mapping of porcine type C endoviral elements Cytogenet. Cell Genet. 85 (3-4), 205-211 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                     Gaps
                  /sex="Male"
/cell type="Embryonic stem cell"
/cell_line="Es cells [C57BL/6J x 129S6/SvEvTac] F1"
/clone lib="GGTC Gene Trap Library GV18CO5"
/note="Vector: FlipROSACeoC+2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 49)
Rogel-Gaillard,C., Bourgeaux,N., Billault,A., Vaiman,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 49)
Chardon, P., Iannuccelli, N., Roig, A., Dossat, C., Demars, J.,
Rogel-Gallard, C., Roy, A., Schibler, L. and Milan, D.
A physical map of the swine genome
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="fibroblast"
/clone_lib="SBAB"
/note="Genoscope sequence ID : IH0AAA28BF12FM1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.5%; Score 12.6; DB 11; Length 49; 78.9%; Pred. No. 7.5e+05; tive 0; Mismatches 4; Indels (
                                                                                                                                                                     52.5%; Score 12.6; DB 10; Length 49; 78.9%; Pred. No. 7.5e+05; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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GSS; Bac-end sequence BES; Genome Survey Sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                 CR900779 49 bp DNA
Sus scrofa BES, genomic survey sequence.
CR900779
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/mol_type="genomic DNA"
/strain="Large White"
/db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="b10280E04"
clone="P070E01"
                                                                                                                                                                                                                                                            CCAGCGTGCGCCATGGGGG 24
                                                                                                                                                                                                                                                                                                       8 chagcegececechededed 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="male"
                                                                                                                                                                         Query Match
Best Local Similarity 78.9
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 49)
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15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa
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CR900779/c
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Gaps

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us-09-669-187a-81.szlm50.rst

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Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ434030 45 bp DNA linear GSS 03-OCT-2000 IM0220B14F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0220B14 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="mAGRs:2282672"
/tissue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
/lab host="DHI08"
/clone_lib="NCI_CGAP_Ut2"
/clone_lib="NCI_CGAP_Ut2"
/note="Corgan: uterus, Vector: pCMV-SPORT6; Site_l: SalI;
/note="Corgan: uterus"
/cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Butheria; Buarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Murinae; Mus.

1 (bases i to, 45)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 51.7%; Score 12.4; DB 1; Length 37; Best Local Similarity 72.7%; Pred. No. 9.1e+05; Matches 16; Conservative 0; Mismatches 6; Indels
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 45.
Location/Qualifiers
                                                                                                                Trace considered overall poor Insert Length: 2109 Std Erro Seq primer: -40UP from Gibco High quality sequence stop: 1 POLYA-NO.
                                                                                                                                                                                                                                                            Location/Qualifiers
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AZ434030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 /done lib="Mouse lobb plasmid UUGCIM library"
/rloonellib="Mouse lobb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/67 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gal
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gql 4732114|gp|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XIIO-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Email: gapbs.r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDM Library Preparation: Life Technologies, Inc.
cDM Library Arrayed by: Greg Lennon, Ph.D.
DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 37)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP ttp://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                       'sex="Male"
'lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Flate: 0451 row: E column: 09
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
                                                                                                                                                                                                                                                         /organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                               db_xref="taxon:10090"
clone="UUGC1M0451E09"
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Unpublished (1997)
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16; Conservative
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Best Local (
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AI619702/c
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/mol type="genomic DNA"
/mol type="genomic DNA"
/mol type="genomic DNA"
/mol type="genomic DNA"
/mol type="leaf"
/fissue type="leaf"
/fissue type="leaf"
/dev_stage="adult"
/dev_stage="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47 bp DNA linear GSS 17-DEC-2002
3590 1 30 1 H08.2EL x 1 3590 - RescueMu Grid M Zea mays genomic,
genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 227
Fax: 650 725 8227
Fax: 650 725 8227
Bmail: walbotdestanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 3590_1_30_1 column: 14
Class: transposon-tagged.
Location/Qualifiers
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1 Similarity 72.7%; Pred. No. 9.1e+05;
16; Conservative 0; Mismatches 6;
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Stanford University
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clone="W126F07"
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                                  /sex="Male"
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Walbot, V.
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                                                                                                                                                                                                                                                      (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalvel (gif 4712114) [pl]AR129072.1), a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pribetageo gene trap. Sequence tag generated by 5'RACE. Additional sequence information can be found at: 'http://generrap.gsf.de/project/web_new/database/result_clone.html?'-clone id=WileF07' ES cell line harboring insertion mutation of target gene is available at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm
1' Inhouse Sequence Identifier: 08571
Class: Gene Trap.
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1 (bases 1 to 46)

1 (bases 1 to 46)

Arnold, H.H., Schnutgen, F., Wurst, W., Von Melchner, H. and Ruiz, P. A large-scale, gene-driven mutagenesis approach for the functional analysis of the mouse genome

Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
                                                                                            /lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G51BL/6J (male) was obtained from the Jackson
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Pred, No. 9.1e+05;
0; Mismatches 6;
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Email: info@genetrap.de
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   /db_xref="taxon:10090"
/clone="UUGC1M0220B14"
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Mus musculus
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/strain="129 Sv"
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Best Local Similarity 72.7%;
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Search completed: February 15, 2006, 21:10:23 Job time : 1612.3 secs
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                                                                                                                                BW590752 Yutaka Satou unpublished cDNA library (csef2) Ciona savignyi cDNA clone csef029n10 5', mRNA sequence.
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/clone_lib="Yutaka Satou unpublished cDNA library (csef2)"
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                                                                                                                                                                                                                                                                  Ciona savignyi
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 48)
Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
Expressed genes in Ciona savignyi (Satou, Shin-i, Kohara, Satoh)
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMAJUGLS1 SOARES NFL T GBC S1 HOMO SADIENS CDNA CLONE IMAGE:1504849 3' Similar to TR:P94909 P94909 HYPOTHETICAL 58.7 KD AMAGE:15, mRNA sequence.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 49)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 1605 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: yutaka@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4095
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'organism="Ciona savignyi"
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/db_xref="taxon:51511"
/clone="csef029n10"
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                          16 GCGCCCAGCGCCGCCATGCGG 37
2 GGGTCCAGCGTGCGCCATGGGG 23
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Department of Zoology
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Best Local Similarity 66.7"
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/mol_type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:1504849"
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libraries (fetal lung NbHL19W, testis NHT, and B-cell
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI CGAP GCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as trace; in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
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CORRESPONDENCE ADDRESS:

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US-09-396-196G-96521
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ALIGNMENTS

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US-08-617-874-1

Sequence 1, Application US/08617874

Patent No. 6338850

GENERAL INFORMATION:

APPLICANT: Jevnikar, Anthony M.
APPLICANT: Stiller, Calvin R.

TITLE OF INVENTION: METHODS AND PRODUCTS FOR CONTROLLING

TITLE OF INVENTION: INMUNE RESPONSES IN MAMMALS

NUMBER OF SEQUENCES: 10
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LOCATION: (1). [33)
OTHER INFORMATION: oligonucleotide used for RT-FCR amplification of Bcl2
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§ Sequence 11, Application US/09249585A

§ Patent No. 6417002

§ GENERAL INFORMATION:

APPLICANT: Horlick, Robert

TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES

FILE REFERENCE: 0867/0D905

CURRENT APPLICATION NUMBER: US/09/249,585A

CURRENT FILING DATE: 1999-02-11

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin version 3.0

SEQ ID NO 11

LENGTH: 33
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ADDRESSEE Burns, Doane, Swecker & Mathis, L.L.P.
STREET: George Mason Building, 699 Prince Street
CITY: Alexandria
STATE: Virginia
STATE: Virginia
COUNTRY: USA
Z19: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,874
FILING DATE: 21-MAY-1996
CLASSIFICATION NUMBER: 30,427
REGISTRATION COMPATION:
NAME: Rea, Teresa Stanek
REGISTRATION UNDRER: 30,427
REFERENCE/DOCKET NUMBER: 024916-002
TELECOMMUNICATION:
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Pred. No. 6.6e+02;
); Mismatches 3;
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100.0%; Pred. No. 8e+02;
ive 0; Mismatches 0;
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DESCRIPTION: /desc = "DNA - primer"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: artificial sequence
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Matches 18; Conservative
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Matches 16; Conservative
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STRANDEDNESS: single
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Score 15.2; DB 3;
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; Sequence 13, Application US/08410804
; Patent No. S62294
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
APPLICANT: Sato, Takaaki
; TITLE OF INVENTION:
; WUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-875-453B-69/c
; Sequence 69, Application US/09875453B
; Patent No. 6838556
                                                                                                                                                                                                                                                           3 GGTCCAGCGTGCGCCATGGG 22
                                                                                                                                                                                                                                                                                                                       1 Griccagccircaccarada 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kim, Jungsuh P.
APPLICANT: Starr, Douglas B.
APPLICANT: Tam, Albert W.
APPLICANT: Laurance, Megan E.
APPLICANT: Michelotti, Emil F.
APPLICANT: Velligan, Mark D.
                                                                                                               Query Match 63.3%;
Best Local Similarity 85.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 85.0%;
Matches 17; Conservative
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                    , ORGANISM: mus musculus
US-09-396-196G-107962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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RESULT 3
US-08-650-726-1/c
is Sequence 1, Application US/08650726
j Patent No. 6027721
structure 1, Application US/08650726
j Patent No. 6027721
j APPLICANT: Hammang, Joseph P
j APPLICANT: Aebischer, Patrick
TITLE OF INVENTION: DEVICE AND METHOD FOR ENCAPSULATED GENE
j TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
j ADDRESSEE: FISH & NEAVE
STREET: 1251 Ave. of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65.8%; Score 15.8; DB 3; Length 33;
89.5%; Pred. No. 9.8e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPTONEN: BEADABLE FORM:

MEDIUM TYPE: Floppy disk

COMPTONEN: DEACHTIN Release #1.0, Version #1.30

SUSTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATE:

APPLICATION NUMBER: US/08/650,726

FILING DATE: 20-MAY 1996

CLASSIFICATION: 514

ATTORNEY AGENT INFORMATION:

NAME: Elifi, IVOR R

REFERENCE POCKET NUMBER: CTI-35

REFERENCE POCKET NUMBER: CTI-35

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 107962, Application US/09396196G
Patent No. 6821724
GENERAL INPORMATION:
APPLICANT: Michael Mittmann
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Cockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-15
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 107962
TYPE: DNA
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Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ANTI-SENSE: NO
US-08-650-726-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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APPLICANT: Thomas, Rita L.
APPLICANT: Thomas, Rita L.
APPLICANT: Thomas, Rita L.
APPLICANT: Thomas, Rita L.
APPLICANT: Sheppard, Liana T.
APPLICANT: Lim, Moon Young
APPLICANT: Lim, Moon Young
TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
TITLE OF INVENTION: PROMOTERS: VS/09/875,453B
CURRENT APPLICATION NUMBER: US/09/875,453B
CURRENT FILING DATE: 2001-6-06
PRIOR APPLICATION NUMBER: US 60/209,549
FRIOR APPLICATION OF SEQ ID NOS: 246
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS: 246
Length 25;
                                               3; Indels
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Gaps
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                                                                                                             Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPAGE: IBM PC compatible
COMPUTER: IBM PC compatible
COMPAGE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,514
FILIAG DATE: 14-JUN-1994
CIASSIFICATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-LJ 9954
TELECAMUNICATION INFORMATION:
FELEPHONE: (619) 535-9949
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
                                                                                                                                                                                                                                                                                                                                 US-08-259-514-13/c
| Sequence 13, Application US/08259514|
| Sequence 13, Application US/08259514|
| Patent No. 274-13/c
| Patent No. 374-13/c
| APPLICANT: Reed, John C.
| APPLICANT: Sato, Takaaki
| TITLE OF INVENTION: FAS ASSOCIATED PROTEINS |
| NUMBER OF SEQUENCES: 22 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: CALBYIN Campbell |
| STREET: 4370 La Jolla Village Drive, Ste 700 |
                                                                                                        Score 15; DB 2; L. Pred. No. 2.2e+03; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          % Sequence 13, Application US/08858311

Patent No. 5876939

GENERAL INFORMATION:

APPLICANT: Reed, John C.

APPLICANT: Reed, John C.

APPLICANT: Resto, Takaaki

TILE OF INVERTION: FAS ASSOCIATED PROTEINS

NUMBER OF SEQUENCES: 22
                                                                                                        Query Match 62.5%; Sc
Best Local Similarity 100.0%; P
Matches 15; Conservative 0;
                                                                                                                                                                                                       6 CCAGCGTGCGCCATG 20
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STATE: California
COUNTRY: United States
ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: CDNA
           ; STRANDEDNESS: Sin
; TOPOLOGY: linear
US-08-607-269-8
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APPLICANT: Reed, John C.
APPLICANT: Sato, Takaaki
TITLE OF INVENTION: Interaction of Proteins Involved in a
TITLE OF INVENTION: Cell Death Pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.5%; Score 15; DB 2; Length 27; 100.0%; Pred. No. 2.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/607,269
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Preα. ...
tive 0; Mismatches
                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,804
FILING DATE: 27-MAR-1995
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,514
FILING DATE: 14-JUN-1994
ATTORNEY/AGENT INPORMATION:
NAME: Campbell, Cathryn
REGISTRATION NUMBER: 91,818
REFREENCE/POCKET NUMBER: P-LJ 1389
TELECHONE: (619) 535-9091
TELECHONE: (619) 535-8049
INPORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9882
TELECOMMUNICATION INFORMATION:
TELEPAX: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTER STICS:
LENGTH: 27 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/226,876
FILING DATE: 13.APR-1994
ATTORNEY/AGENT INFORMATION:
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 8, Application US/08607269
; Patent No. 5702897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 CCAGCGTGCGCCATG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.C
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
US-08-607-269-8/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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Gaps

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| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Larocca, David
| APPLICANT: Baird, Andrew
| APPLICANT: Baird, Andrew
| APPLICANT: Rasener, Paul
| APPLICANT: Rasener, Paul
| APPLICANT: Rasener, Paul
| APPLICANT: Rasener, Paul
| TITLE OF INVENTION: DETECTING AND IDENTIFYING PROTEIN-PROTEIN
| TITLE OF INVENTION: INTERACTIONS THAI FACILITATE INTERALIZATION
| TITLE OF INVENTION: COMPETENT FOR THE SAME AND METHODS FOR EVOLVING
| TITLE OF INVENTION: GENE DELIVERY VECTORS
| TITLE OF INVENTION: GENE DELIVERY VECTORS
| TITLE OF INVENTION: GENE DELIVERY VECTORS
| CURRENT APPLICATION OF SEQ 10 NOBER: 2001-05-24
| NUMBER OF SEQ 1D NOS: 18
| SOFTWARR: Patentin Ver: 2.0
| SEQ 1D NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 47;
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Pred. No. 2.2e+03;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.8%; Score 14.6; DB 3;
illarity 81.0%; Pred. No. 3.2e+03;
Conservative 0; Mismatchan
REFERENCE/DOCKET NUMBER: FP-LJ 1361
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                          62.5%; Scor.
v 100.0%; Pre
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                                       TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEO ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) OTHER INFORMATION: PCR Primer US-09-258-689-5
                                                                                                                                                                                                                                                                                                                                                                             6 CCAGCGTGCGCCATG 20
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Marches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                              linear
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US-09-258-689-5
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; Sequence 8, Application PC/TUS9504600
GENERAL INFORMATION:
; TITLE OF INVENTION: Interaction of Proteins Involved in TITLE OF INVENTION:
; TITLE OF INVENTION: Interaction of Proteins Involved in TITLE OF INVENTION:
; TITLE OF INVENTION: A Cell Death Pathway; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STRTE: California
COUNTRY: USA
ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.5%; Score 15; DB 2; Length 27; 100.0%; Pred. No. 2.2e+03;
                                                                                                                                       COMPUTER READLE FORM:
MEDTIM TYPE: FORPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
SOURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,311
FILING DATE: US/08/858,311
FILING DATE: 195
APPLICATION NUMBER: US/08/410,804
FILING DATE: 14-UN-1994
FILING DATE: 14-UN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1389
TELEPAN: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER FEACHBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PATENTIN BATA:
APPLICATION NUMBER: PCT/US95/04600
FILING DATE: 12-APR-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Imbra, Rachard J.
REGISTRATION NUMBER: 37,643
                        ADDRESSEE: Cathryn Campbell
STREET: 4370 La Jolla Village Drive. Ste 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.5.,
100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ccaecerececcare 7
                                                                                          STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15; Conservative
  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                    San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-858-311-13
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Gaps

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3 GGTCCAGCGTGCGCCATGG 21
                                      GGTCCAGCATTTGCCATGG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (408) 436-2075
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 CCAGCGTGCGCCAT 19
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Best Local Similarity 100.(
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: San Jose
STATE: California
COUNTRY: U.S.A.
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US-08-217-082A-9
                                                                                                              RESULT 15
US-08-217-082A-9
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Sequence 127, Application US/09830433A

Patent No. 6835384

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: Mucleic acids and polypeptides specific for pathogenic
TITLE OF INVENTION: Mucleic acids and polypeptides specific for pathogenic
TITLE OF INVENTION: Mucleic acids and polypeptides specific for pathogenic
TITLE OF INVENTION: Mucleic acids and polypeptides specific for pathogenic
CURRENT APPLICATION: WUMBER: US/09/830,433A

CURRENT APPLICATION NUMBER: FR 98 13 693

FRIOR APPLICATION NUMBER: FR 98 13 693

NUMBER OF SEQ ID NOS: 129

SOFTWARE PATENT OF 129

SOFTWARE PATENT OF 129

SEQ ID NO 127

LENGTH: 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Rao, Mahendra S.
APPLICANT: Rao, Mahendra S.
TITLE OF INVENTION: Lineage-Restricted Neuronal Precursors
FILE REFERENCE: T5530.CIP
CURRENT APPLICATION NUMBER: US/09/109,858
CURRENT APPLICATION NUMBER: US/09/109,435
EARLIER APPLICATION NUMBER: US 08/909,435
BARLIER FILING DATE: 1997-07-04
NUMBER OF SEQ ID NOS: 14
SOFTWARE: WordPerfect 8.0
SEQ ID NO 14
LENGTH: 19
                                                                                                                                                       Query Match 60.8%; Score 14.6; DB 3; Length 47; Best Local Similarity 81.0%; Pred. No. 3.2e+03; Matches 17; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.0%; Score 14.4; DB 3; Length 29; 75.0%; Pred. No. 3.9e+03; Live 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 59.2%; Score 14.2; DB 3; Length 19; Best Local Similarity 84.2%; Pred. No. 4.8e+03; Matches 16; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 14, Application US/09109858
; Patent No. 6787353
                                                                                                                                                                                                                                                                                                  10 ĠĠĠŢŢĊĊĠĊĠŢĠĠĠĠĠĀŢĠĠ 30
                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                      ; OTHER INFORMATION: PCR Primer US-09-866-073A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Rattus norvegicus
US-09-109-858-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 60.0
Best Local Similarity 75.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              US-09-830-433A-127
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US-09-109-858-14
LENGTH: 47
                                                                   FEATURE:
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Sequence 9, Application US/08217082A

Patent No. 5734033

GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
TITLE OF INVENTION: GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
ADDRESSEE: P.C.
ADDRESSEE: P.C.
STREET: 224 Airport Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Patent No. 5734033
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE TITLE OF INVENTION: GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUW TYPE: FELPOPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSITCATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/88,692
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 33,600
REFERENCE/DOCKET NUMBER: 33,600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.3%; Score 14; DB 2; Lv 100.0%; Pred. No. 5.8e+03; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: other nucleic acid DESCRIPTION: Synthetic DNA
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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-UM-1995
CLASSIFICATION NUMBER: US/08/465,485A
FILING DATE: 05-UM-1995
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION NUMBER: US 07/886,692
PRIOR APPLICATION NUMBER: US 07/288,692
PRIOR APPLICATION NUMBER: US 07/288,692
RICHARD DATE: 22-DEC-1988
ATTONENTYAGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DESCRIPTION: Synthetic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
APPLICATION NUMBER: US/0
FILING DATE: 24-MAR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-217-082A-17
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Patent No. 5734033

GENERAL INFORMATION:
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
TITLE OF INVENTION: GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
TITLE OF INVENTION: GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
NUMBER OF SEQUENCE: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 224 Airport Parkway
CITY: San Jose
CITY: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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0
       CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 14; DB 2; Length 17;
Pred. No. 5.8e+03;
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                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
COMPUTER: APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-AMR-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTOMENYAGEN: IMPORMATION:
AMAN: ACCUPATION ANAMERICATION ANAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: FORTHER, Andrew D.

REGISTRATION NUMBER: 34,600

REFERENCE/DOCKET NUMBER: 3335-067-55 FWC

TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STARNDEDNESS: single
TOPOLLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.3%; Scc...
100.0%; Pred. No. ...
... 0; Mismatches
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DESCRIPTION: Synthetic DNA
                                                                                                                    224 Airport Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ccagcerececar 14
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Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                         San Jose : California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 95110
                                                                                                                                                                                                                                    U.S.A.
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US-08-217-082A-10
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US-08-217-082A-17
                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                         CITY:
STATE:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 58.3%; Score 14; DB 2; Le Best Local Similarity 100.0%; Pred. No. 5.8e+03; Matches 14; Conservative 0; Mismatches 0;
FILING DATE: 24-WAR-1994
CLASSIFTCATION 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cortney, Andrew
REFERENCE/DOCKET NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOM
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Gaps
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                                                                                                                                                                                                                                                                                                                                                             Sequence 17, Application US/09080285
; Sequence 17, Application US/09080285
; Patent No. 6040181
; GENERAL INFORMATION:
APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DEC.
; ADDRESSEE: P.C.
ADDRESSEE: P.C.
; TREET: 1755 S. Jefferson Davis Hwy., Suite 400
; TRY: Arlington
; TATE: Virgina
; COUNTRY: U.S.A.
Last two internucleoside linkages are phosphorothioates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 18;
                                                                                                  Length 18;
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100.0%; Pred. No. 5.8e+03;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.3%; Score 14; DB 3; Lo 100.0%; Pred. No. 5.8e+03; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                6 CCAGCGTGCGCCAT 19
                                                                                                                                                                                                                                                5 ccadcerececen 18
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                                                                                                Query Match
Best Local Similarity 100.0
Matches 14; Conservative
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LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
  j OTHER INFORMATION:

j OTHER INFORMATION:

US-08-465-485A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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TOPOLOGY:
US-09-080-285-17
                                                                                                                                                                                                                                                                                                                                            US-09-080-285-17
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| Sequence 24, Application US/08465485A |
| Patent No. 5831066
| GENERAL INPORMATION: |
| APPLICANT: Reed, John |
| TILLE OF INVENTION: Regulation of bc1-2 Gene Expression |
| NUMBER OF SEQUENCES: 29 |
| CORRESPONDENCE ADDRESS: 29 |
| CORRESPONDENCE ADDRESS: ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, STREET: 1755 S. Jefferson Davis Hwy., Suite 400 |
| CITY: Arlington | STREET: D. COMPUTER: US-NA. |
| COUNTRY: U.S.A. |
| ZIP: 22202 S.A. |
| ZIP: 22202 S.A. |
| ZIP: 22202 S.A. |
| COMPUTER: IBM PC Compatible |
| OFFWATING SYSTEM: PC-DOS/MS-DOS |
| SOFTWARE: Patent In Release #1.0, Version #1.25 |
| CURRENT APPLICATION NUMBER: US/08/465,485A |
| FILING DATE: OS-JUN-1995 |
| FILING DATE: OS-JUN-1995 |
| PRIOR APPLICATION NUMBER: US 07/840,716 |
| FILING DATE: 20-SEP-1993 |
| RIGH APPLICATION NUMBER: US 07/840,716 |
| FILING DATE: 1-FBB-1992 |
| RIGH APPLICATION NUMBER: US 07/288,692 |
| FILING DATE: 1-FBB-1992 |
| ATPORTEY NUMBER: US 07/288,692 |
| FILING DATE: 1-FBB-1992 |
| ATPORTEY NUMBER: US 07/288,692 |
| FILING DATE: 20-DEC-1988 |
| ATTORNEY ARBICATION NUMBER: US 07/288,692 |
| FILING DATE: 20-DEC-1988 |
| ATTORNEY ARBICATION NUMBER: US 07/288,692 |
| FILING DATE: 20-DEC-1988 |
| ATTORNEY ARBICATION NUMBER: US 07/288,692 |
| FILING DATE: 20-DEC-1988 |
| ATTORNEY ARBICATION NUMBER: US 07/288,692 |
| FILING DATE: 20-DEC-1988 |
| ATTORNEY ARBICATION NUMBER: US 07/288,692 |
| FILING DATE: 20-DEC-1988 |
| ATTORNEY ARBICATION NUMBER: US 07/288,692 |
| FILING DATE: 20-DEC-1988 |
| ATTORNEY ARBICATION NUMBER: US 07/288,692 |
| FILING DATE: 20-DEC-1988 |
| ATTORNEY ARBICATION NUMBER: US 07/288,692 |
| ATTORNEY ARBICATION NUMBER: US 07/28
                                                                                                                                                                                                                                                                          Length 18;
                                                                                                                                                                                                                                                                                                                       0; Indels
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100.0%; Pred. No. 5.8e+03;
iive 0; Mismatches 0;
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REGISTRATION NUMBER: 34,600
REPRENEUCE/POCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: Other nucleic acid; DESCRIPTION: Synthetic DNA
                    TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-465-485A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       6 CCAGCGTGCGCCAT 19
                                                                                                                                                                                                                                                                                                                                                                                                                     5 ccadcerececar 18
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Best Local Similarity 100.8
Matches 14, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
LOCATION:
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Gaps . 0

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APPLICANT: WRIGHT, Jim A.
APPLICANT: WRIGHT, Jim A.
APPLICANT: WRIGHT, Jim A.
APPLICANT: VOUNG, Alping H.
TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and
TITLE OF INVENTION: R2 Components of Ribonucleotide Reductase
FILE REPERENCE: 032396-040
CURRENT APPLICATION NUMBER: US/09/249,730
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 220
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 218
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1. Application US/09118220

Patent No. 6140051

GENERAL INFORMATION:

APPLICANT: Brown, Lauren R.

APPLICANT: APPLICANT: APPLICANT: APPLICANT: AND METHODS RELATED THERETO

TITLE OF INVENTION: AND METHODS RELATED THERETO

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson & Bear
                                                                                                                                                                                                                                                                                                                                                  Length 18;
                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                  Score 14; DB 3; Le
Pred. No. 5.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATION SYSTEM: Windows SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/118,220
                                                                                                                                                                                                                                                                                                                                       58.3%; Sco...
100.0%; Pred. No. ...
0; Mismatches
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INPORMATION:
NAME: BARTfeld, Neil S
REGISTRATION NUMBER: 39,901
REFERENCE/DOCKET NUMBER: GENT
TELECHONE: 619-235-8550
TELEPHONE: 619-235-0176
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IBM Compatible
svsTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 ccaecerececar 18
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Best Local Similarity 100.v
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LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U.S.A.
                                                                                                                                                                                                                                                                                      ORGANISM: Human
US-09-249-730-218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: CA
COUNTRY: U.
ZIP: 92660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER:
                                                                                                                                                                                                                                                                    TYPE: DNA
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                                          Sequence No. 6040181

Fatent No. 6040181

GENERAL INFORMATION:

APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:

ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Alington
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 16..17
OTHER INFORMATION: Last two internucleoside linkages are
OTHER INFORMATION: phosphorothioates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.3%; Score 14; DB 3; Length 18; 100.0%; Pred. No. 5.8e+03; 2ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATR:
APPLICATION NUMBER: US/09/080,285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3335-070-55 CONT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY AGENT INFORMATION:
NUMBER: CALLON NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
NRSCRIPTION: Synthetic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,60.
REFERENCY DOCKET NUMBER: 335-
TELECOMMUNICATION INPORMATION:
TELEFAN: (408) 436-2070
TELEFAX: (408) 436-2075
INPORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYRE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Modified base
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DESCRIPTION: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                     22202
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               RESULT 21
US-09-080-285-24
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DB 3;

58.3%; Score 14;

linear

MOLECULE TYPE:

US-09-118-220-1

Query Match

US-09-249-730-218; Sequence 218, Application US/09249730

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; Sequence 45, Application US/08960774
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US-09-286-098-104
                                                                         JS-09-286-098-59
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Schwartz, David A.
TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING
TITLE OF INVENTION: LES-ASSOCIATED DISORDERS
TITLE OF INVENTION NUMBER: 050/039/405
RRIOR APPLICATION NUMBER: 60/039/405
RRIOR APPLICATION NUMBER: 1997-02-28
NUMBER OF SEQ ID NOS: 65
SOFTWARE: FASTSEQ FOR Windows Version 3.0
SSOTWARE: FASTSEQ FOR Windows Version 3.0
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                   Sequence 55, Application US/08738652B
; Patent No. 6207646
; GENERAL INFORMATION:
    APPLICANT: Krieg, Arthur M.
    TITLE OF INVENTION:
    TILLE REFERENCE: C1039/7004 HCL
    CURRENT PAPLICATION NUMBER: US/08/738,652B
; CURRENT PILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER PILING DATE: 1996-07-15
; EARLIER PILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 18;
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
              Pred. No. 5.8e+03;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 58.3%; Score 14; DB 3; Ls 1 Similarity 100.0%; Pred. No. 5.8e+03; 14; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Synthetic oligonucleotide US-08-738-652-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: synthetic oligonucleotide
US-09-030-701-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 27, Application US/09030701B Patent No. 6214806
100.08; Fit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
                                                                         6 CCAGCGTGCGCCAT 19
                                                                                                               5 ccadecardececcar 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 CCAGCGTGCGCCAT 19
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            Best Local Similarity 100.
Matches 14; Conservative
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Best Local Similarity
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Best Local Similarity
Matches 14; Conserva
                                                                                                                                                                                           US-08-738-652-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-030-701-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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                                                                                                           임
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Sequence 59, Application US/09286098

Patent No. 6218371
GENERAL INFORMATION:
APPLICANT: Weiner, George
TITLE OF INVENTION: Methods and Products for Stimulating the
TITLE OF INVENTION: Twenter
FILE REFRENCE: 1039/7026/HCL
CURRENT APLICATION NUMBER: US/09/286,098
CURRENT PILING DATE: 1999-04-02
EARLIER APPLICATION NUMBER: US 60/080,729
BARLIER PILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 105
SEQ ID NOS: 105
SEQ ID NOS: 105
SEQ ID NOS: 105
SEQ ID NOS: 108
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GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Weiner, George
TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
TITLE OF INVENTION: Cytokines
TITLE OF INVENTION: UNWHER: US/09/286,098
CURRENT APPLICATION NUMBER: US/09/286,098
CURRENT APPLICATION NUMBER: US 60/080,729
EARLIER FILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NOS: 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Synthetic Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Synthetic Sequence US-09-286-098-104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 104, Application US/09286098 Patent No. 6218371
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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Matches 14; Conservative
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Best Local Similarity 100.
Matches 14; Conservative
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Sequence 51, Application US/09325193A

Patent No. 6406705

GRNERAL INFORMATION:
APPLICANT: Davis, Heather L.
APPLICANT: Schort, Joachim
APPLICANT: Krieg, Arthur M.
ITILE OF INVENTION: Unmethylated CpG Dinucleotide as an Adjuvant
ITILE OF INVENTION: Unmethylated CpG Dinucleotide as an Adjuvant
ITILE OF INVENTION: Unmethylated CpG Dinucleotide as an Adjuvant
ITILE OF INVENTION: Unmethylated CpG Dinucleotide as an Adjuvant
ITILE OF INVENTION: UNMERR: US/09/25,193A

CURRENT APPLICATION NUMBER: US 09/154,614

PRIOR APPLICATION NUMBER: US 09/154,614

PRIOR APPLICATION NUMBER: US 60/040,376

PRIOR FILING DATE: 1990-03-10

NUMBER OF SEQ ID NOS: 98

SEQ ID NO SI
ILENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.3%; Score 14; DB 3; Lo
100.0%; Pred. No. 5.8e+03;
:ive 0; Mismatches 0;
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                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: IBM Compatible
                                                                                                                  OPERATING SYSTEM: DOS 5.0
SOFTWARE: WORD PETFECT
CURRENT APPLICATION NUMBER: US/09/078,954
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: other nucleic acid HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                              08/856,374
                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE: 14-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: MATINE T. LATESON
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: 1NEX.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: (970) 668-2080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.3%; S
100.0%;
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Best Local Similarity 100.0
Matches 14; Conservative
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STRANDEDNESS: single
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Best Local Similarity
COUNTRY: USA
ZIP: 80443-5270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JS-09-325-193A-51
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APPLICANT: Hope, Michael J.
APPLICANT: Hope, Michael J.
APPLICANT: Ansell, Steven M.
APPLICANT: Cullis, Pieter
APPLICANT: Cullis, Pieter
APPLICANT: Geiser, Timothy
APPLICANT: Jon, Gerald
APPLICANT: Jon, Gerald
APPLICANT: Debeyer, Dan
TITLE OF INVENTION: High Efficiency Encapsulation of Charged Therapeutic Agents in
TITLE OF INVENTION: Lipid Vesicles
ANDRESEE: Oppedable Larson
ADDRESSEE: Oppedable Larson
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ZIP: 92337

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION IDMER: US/08/960,774
FILING DATE: 30-October-1997
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: U.S. Serial No. 6239116 08/738,652
FILING DATE: October 30, 1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
ATTORNEY/AGENT INFORMATION:
TELEPHONE: 619/678-5090
TELEFRAX: 619/678-5090
TELERGAT: 10 base pairs
TYPE: nucleic acid
STREE: APPLICATION INFORMATION:
TELERGAT: 10 base pairs
TYPE: nucleic acid
STREE: APPLICATION INFORMATION:
TELERGAT: 10 base pairs
TYPE: nucleic acid
STREE: APPLICATION INFORMATION:
TELERGAT: 10 base pairs
TYPE: nucleic acid
STREE: APPLICATION INFORMATION:
TELERGAT: 10 base pairs
TYPE: nucleic acid
                              GENERAL INFORMATION:
APPLICANT: Krieg et al.,
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID MOLECULES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 14 4225 Executive Square, Suite 1400
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.3%; Score 14; DB 3; Length 18; 100.0%; Pred. No. 5.8e+03; Live 0; Mismatches 0; Indels
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; Sequence 14, Application US/09078954
; Patent No. 6287591
; GENERAL INFORMATION:
APPLICANT: SEMPLE, Sean C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Oppedahl & Larson
PO Box 5270
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Klimuk, Sandra K.
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Best Local Similarity
Matches 14; Conserva
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            Patent No. 6239116
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CITY: F1
STATE: (
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58.3%; Score 14; DB 3; Length 18; 100.0%; Pred. No. 5.8e+03; ive 0; Mismatches 0; Indels
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Sequence 45, Application US/09136080E

GENERAL INFORMATION:

APPLICANT: Riley, Timothy A.

APPLICANT: Arnold, Lyle J.

TITLE OF INVENTION: COMBINATORIAL ANTISENSE LIBRARY

FILE REFERENCE: OASHO.003A

CURRENT APPLICATION NUMBER: US/09/136,080E

CURRENT FILING DATE: 1999-08-18

NUMBER OF SEQ ID NOS: 54

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 45

LENGTH: 18
                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: synthetic oligonucleotide US-09-191-170-53
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EARLIER APPLICATION NUMBER: US 08/960,774
EARLIER FILING DATE: 1997-10-30
EARLIER APPLICATION NUMBER: US 08/738,652
EARLIER FILING DATE: 1996-10-30
EARLIER FILING DATE: 1996-02-07
EARLIER FILING DATE: 1995-02-07
EARLIER FILING DATE: 1994-07-15
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 3.0
SSOFTWARE: FastSEQ for Windows Version 3.0
EENGTH: 18
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CURRENT FILING DATE: 2000-10-18
PRIOR APPLICATION NUMBER: PCT/FP00/02920
PRIOR PILING DATE: 2000-04-04
PRIOR APPLICATION NUMBER: 09/301,829
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Patent No. 6544518
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APPLICANT: Friede, Martin
APPLICANT: Gerard, Catherine
APPLICANT: Hermand, Philippe
TITLE OF INVENTION: Vaccines
FILE REFERENCE: B45181-1
                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                 TYPE: DNA
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                                                                                                                                                                                                                                                                                                                              FEATURE:
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US-09-191-170-53

Sequence 53, Application US/09191170

Sequence 54.29199

GENERAL INFORMATION:

APPLICANT: Krieg, Arthur M.

APPLICANT: Hartmann, Gunther

TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules

TITLE OF INVENTION: for Activating Dendritic Cells

FILE REPRENCE: C1039/7017

FURENT APPLICATION NUMBER: US/09/191,170

CURRENT PILING DATE: 1998-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.3%; Score 14; DB 3; Length 18; 100.0%; Pred. No. 5.8e+03; Live 0; Mismatches 0; Indels
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         0; Indels
                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of BCL-2 Gene Expression
FILE REFERENCE: 10412-024
CURRENT APPLICATION NUMBER: US/09/724,426
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.0
SEQ ID NO 17
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of BCL-2 Gene Expression
FILE REFERENCE: 10412-024
CURRENT APPLICATION NUMBER: US/09/724,426
CURRENT FILING DATE: 2000-11-28
NUMBER OF EAC ID NOS: 29
SOFTWARE: PatentIn version 3.0
       0; Mismatches
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                                                                                                                                                                                                          Sequence 17, Application US/09724426 Patent No. 6414134
                                                                                            5 ccaccerececen 18
                                                   6 CCAGCGTGCGCCAT 19
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Best Local Similarity 100.
Matches 14; Conservative
       14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-426-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
US-09-724-426-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 14; Conserva
                                                                                                                                                              RESULT 31
US-09-724-426-17
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US-09-724-426-24
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LENGTH: 18
       Matches
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Gaps

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TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 14; Conservative
; SEQ ID NO 218
; LENGTH: 18
; TYPE: DM;
; ORGANISM: Human
US-09-249-247-218
                                                                                                                                                                                                                                                                                                                                            US-09-337-619-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
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Sequence 218, Application US/09249247

Batent No. 6593305

GENERAL INFORMATION:
APPLICANT: WRIGHT, Jim A.
TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and TITLE OF INVENTION: R2 Components of Ribonucleotide Reductase
TITLE OF INVENTION: R2 Components of Ribonucleotide Reductase
FILE REFERENCE: 032336-023

CURRENT APPLICATION NUMBER: US 60/023,040

EARLIER APPLICATION NUMBER: US 60/039,959

EARLIER RILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: US 60/039,959

EARLIER APPLICATION NUMBER: US 60/039,959

EARLIER APPLICATION NUMBER: US 60/039,959

EARLIER FILING DATE: 1997-03-07

SEARLIER PLING DATE: 1997-03-07

SEARLIER APPLICATION NUMBER: US 60/039,950

EARLIER FILING DATE: 1997-03-07

SEARLIER PLING DATE: 1997-08-01

NUMBER OF SEQ ID NOS: 220
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                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                          Length 18;
                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                          Score 14; DB 3; Le
Pred. No. 5.8e+03;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Friede, Martin
APPLICANT: Hermand, Philippe
TITLE OF INVENTION: VACCINES
TITLE REFERENCE: B45181
CURRENT FILING DATE: 1999-04-29
PRIOR FILING DATE: 1999-04-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGINE 18
  PRIOR FILING DATE: 1999-04-29
PRIOR APPLICATION NUMBER: 9908085.8
PRIOR FILING DATE: 1999-04-19
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 2, Application US/09301829A; Patent No. 6558670; GENERAL INFORMATION:
                                                                                                                                                                                                                          58.3%; Scc.
100.0%; Pre
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCAGCGTGCGCCAT 18
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                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                         ) ORGANISM: Human
US-09-690-921-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 37
US-09-249-247-218
                                                                                                                                                                                                                                                                                    14;
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                                                                                                                                                            TYPE: DNA
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US-09-835-370-21

Sequence 21, Application US/09835370

Patent No. 677554

APPLICANT: UHLMANN, EUGEN
APPLICANT: UHLMANN, EUGEN
APPLICANT: WILL, DAVID W
TITLE OF INVENTION: PROCESSES FOR PREPARING THEM
TITLE OF INVENTION: PROCESSES FOR PREPARING THEM
FILE REPRERENCE: 02481.174-2 SEQUENCE LISTING
CURRENT APPLICATION NUMBER: US/09/835,370

CURRENT FILING DATE: 2001-04-17

NUMBER OF SEQ ID NOS: 64

SOFTWARE: Patentin Ver. 2.1

LENTH: 18
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Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                                 JUNEER OF INVENTION NUMBER: US 08/26,053

TITLE OF INVENTION: Immunostimulatory Oligonuclectides
CURRENT APPLICATION NUMBER: US 08/960,774
EARLIER FILING DATE: 1999-06-21
EARLIER FILING DATE: 1997-10-30
EARLIER FILING DATE: 1996-10-30
EARLIER PILING DATE: 1996-10-30
EARLIER PILING DATE: 1996-0-10-30
EARLIER PILING DATE: 1996-0-10-30
EARLIER PILING DATE: 1996-0-15
EARLIER PILING DATE: 1996-0-15
EARLIER PILING DATE: 1998-0-15
   DB 3; Le
5.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Synthetic Oligonucleotide US-09-337-619-45
                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                     Sequence 45, Application US/09337619; Patent No. 6653292; GENERAL INFORMATION:
   58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 CCAGCGTGCGCCAT 19
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GENERAL LINCKMALLIUM

J GENERAL LINCKMALLIUM

TITLE OF INVENTION: REGULATION OF BCL-2 GENE EXPRESSION

FILE REFERENCE: 04040/1200990-U57

CURRENT APPLICATION NUMBER: US/09/724,425

CURRENT FILING DATE: 2000-11-28

FRIOR APPLICATION NUMBER: US 09/375,514

PRIOR PILING DATE: 1999-08-17

PRIOR FILING DATE: 1999-08-17

PRIOR FILING DATE: 1999-08-17

PRIOR FILING DATE: 1999-06-18

PRIOR FILING DATE: 1995-06-05

PRIOR FILING DATE: 1995-02-18

PRIOR APPLICATION NUMBER: US 08/124,256

PRIOR PILING DATE: 1993-09-20

PRIOR FILING DATE: 1993-09-20

PRIOR FILING DATE: 1993-02-21

PRIOR FILING DATE: 1993-02-21

PRIOR FILING DATE: 1993-02-21

PRIOR FILING DATE: 1998-12-22

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PATENTIN VETSION 3.1
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    MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.3%; Score 14; DB 3; Le
100.0%; Pred. No. 5.8e+03;
tive 0; Mismatches 0;
                                                                                                        CUKKEN AFPLICATION DAMASE US/09/654,373

PRICATION NUMBER: US/09/654,373

FILING DATE: 01-Sep-200

CLASSIFICATION S. UDKNOWN>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/152,179

FILING DATE: SEPTEMBER 2, 1999

APPLICATION NUMBER: 09/078,954

FILING DATE: MAY 14, 1998

APPLICATION NUMBER: 08/856,374

FILING DATE: MAY 14, 1997

ATTORNEY/AGENT INFORMATION:

NAME: MAXINA T. LAZSON

REGISTRATION NUMBER: 32,038

REFERENCE/DOCKET NUMBER: 32,038

REFERENCE/DOCKET NUMBER: 1NEX.P-007

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: yes
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear _ MOLECULE TYPE: other nucleic acid
                        COMPUTER: IBM Compatible
OPBRATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17, Application US/09724425
Patent No. 6841541
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (970) 468-0104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 CCAGCGTGCGCCAT 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-654-373-14
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CRGANISM: HOR
US-09-724-425-17
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Scherrer, Peter
McIntosh, Deidre
Wong, Kim F.
TILE OF INVENTION: Small Multilamellar Oligodeoxynucleotide-Containing
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  nucleotide
; OTHER INFORMATION: Description of Artificial Sequence; nucleotic; OTHER INFORMATION: base sequence of PNA derivatives that bind to ; OTHER INFORMATION: viral and cellular targets
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GENERAL INCORMATION:

APPLICANT: Papisov, Mikhail, I.

TITLE OF INVENTION: DUG-CARRIER COMPLEXES AND METHODS OF

TITLE OF INVENTION: USE THEREOF

FILE REFERENCE: 0838.1003-001

CURRENT APPLICATION NUMBER: US/09/634,320

CURRENT FILING DATE: 2000-08-09

PRIOR APPLICATION NUMBER: US 60/147,919

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PASESEQ for Windows Version 4.0

SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lipid
Vesicles and Method of Making Same
                                                                                                                Query Match 58.3%; Score 14; DB 3; Length 18; Best Local Similarity 100.0%; Pred. No. 5.8e+03; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.3%; Score 14; DB 3; Length 18; ilarity 100.0%; Pred. No. 5.8e+03; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Synthetic Oligonucleotide US-09-634-320-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppedahl & Larson LLP
STREET: PO BOX 5068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SEMPLE, Sean C.
Klimuk, Sandra K.
Harasym, Troy O.
Dos Santos, Nancy
Ansell, Steven M.
Cullis, Pieter R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 41
US-09-654-373-14
; Sequence 14, Application US/09654373
; Patent No. 6835395
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/09634320
Patent No. 6822086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                     CCAGCGTGCGCCAT 18
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COUNTRY: USA
ZIP: 80435-5068
COMPUTER READABLE FORM:
                                                                                                                                                                                                            6 CCAGCGTGCGCCAT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 CCAGCGTGCGCCAT 19
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Best Local Similarity
....hes 14; Conserva
                                                                                                                                                                                                                                                                                                                             RESULT 40
US-09-634-320-7/c
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0; Indels
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100.0%; Pred. No. 5.8e+03;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                               Query Match 58.3%; Score 14; DB 3; Le Best Local Similarity 100.0%; Pred. No. 5.8e+03; Matches 14; Conservative 0; Mismatches 0;
                                                                                    REGISTRATION NUMBER: «Unknown»
REFERENCE/DOCKET NUMBER: «Unknown»
TELEPONUNICATION INFORMATION:
TELEPAX: «Unknown»
TELEFAX: «Unknown»
TELEFX: «Unknown»
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , OTHER INFORMATION: ANTISENSE OLIGONUCLEOTIDE US-10-002-884A-6
                                                                                                                                                                                                                                                                           ANTI-SENSE: yes
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-895-480A-14
                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 46
US-09-108-673A-34
Sequence 34, Application US/09108673A
Patent No. 6887906
GENERAL INFORMATION:
APPLICANT: Ching-Leou Teng and Gri
FILING DATE: 29-Jun-2001
CLASSIFICATION: <Unknown>
                                                   FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 CCAGCGTGCGCCAT 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100."
Matches 14; Conservative
                                                                             NAME: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-002-884A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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                                                                                                                                                  Length 18;
             Score 14; DB 3; Length 18;
Pred. No. 5.8e+03;
                                         0; Indels
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/895,480A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 14; DB 3; Le
Pred. No. 5.8e+03;
      58.3%; Sco. 100.0%; Pred. No. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 58.3%; Scc
Best Local Similarity 100.0%; Pr
Matches 14; Conservative 0;
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COMPUTER READABLE FORM:
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                                                                   6 CCAGCGTGCGCCAT 19
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     Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-425-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
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US-09-724-425-24
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Sequence 6, Application US/10002884A

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Sequence 6, Application US/10002884A

Sequence 6, Application US/10002884A

Sequence 6, Application

Retent No. 6867043

APPLICANT: Stein, Cy A

APPLICANT: Benimetskaya, Lyuba

APPLICANT: Guzzo-Pernell, Nancy

TITLE OF INVENTION: PEC-PECTEIN EXPRESSION IN CELLS

TITLE OF INVENTION: PRC-PROTEIN EXPRESSION IN CELLS

FILE REFERENCE: 0579/63293

CURRENT APPLICATION NUMBER: US/10/002,884A

CURRENT FILING DATE: 2001-11-02

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PatentIn version 3.1

SEQ ID NO 6

LENGTH: 18
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                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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Length 18;
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Gaps
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APPLICANT: Stefan Bauer
APPLICANT: Grayson B. Lipford
APPLICANT: Hermann Wagner
TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF
TITLE OF INVENTION: CpG-BASED IMMUNO-AGONIST/ANTAGONIST
FILE REFERENCE: C1041/7016 (AMS)
CURRENT APPLICATION NUMBER: US/09/954,987B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-672-126B-110

| Sequence 110, Application US/09672126B
| Patent No. 6949520
| Patent No. 6949520
| GENERAL INFORMATION:
| APPLICANT: Hartmann, Gunther
| APPLICANT: Hartmann, Gunther
| APPLICANT: Hartlann, Gunther
| TITLE OF INVENTION: Methods Related to Immunostimulatory
| TITLE OF INVENTION: Methods Related to Immunostimulatory
| TITLE OF INVENTION: Methods Related to Interferon
| FILE REFERENCE: C1039/7044
| CURRENT APPLICATION NUMBER: US/09/672,126B
| CURRENT FILING DATE: 1999.09-29
| PRIOR FILING DATE: 1999.09-29
                                                                                    Query Match 58.3%; Score 14; DB 3; Length 18; Best Local Similarity 100.0%; Pred. No. 5.8e+03; Matches 14; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 5.8e+03;
tive 0; Mismatches 0;
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US-09-954-987B-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/233,035
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-01-13
PRIOR FILING DATE: 2001-01-23
PRIOR FILING DATE: 2001-05-17
PRIOR FILING DATE: 2001-05-17
PRIOR FILING DATE: 2001-05-17
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 230
SOFTWARE: PSESEQ for Windows Version 3.0
SSOFTWARE: PSESEQ for Windows Version 3.0
SEQ ID NO 115
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 110
LENGTH: 18
, OTHER INFORMATION: of PNA targeting CMV US-09-835-371-21
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 115, Application US/09954987B Patent No. 6943240
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Best Local Similarity 100.
Matches 14; Conservative
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US-09-954-987B-115
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Fatent No. 6905820

GENERAL INFORMATION:

APPLICANT: URLAANN, Eugen

APPLICANT: WILL, David W

TITLE OF INVENTION: PROCESSES FOR PREPARING THEM

FILE REFRENCE: 02481.1743 SEQUENCE LISTING

CURRENT APPLICATION NUMBER: US/09/835,371

CURRENT APPLICATION NUMBER: US/09/835,371

SOFTWARE: PALENTING DATE: 2001-04-17

NUMBER OF SEQ ID NOS: 53

SOFTWARE: PALENTIN Ver. 2.1

SEQ ID NO 21

LENGTH: 18
                               NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6887906ris LLP
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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  Oligonucleotides Via the Alimentary Canal 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.3%; Score 14; DB 3; Length 18; 100.0%; Pred. No. 5.8e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: 1910

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: WORDPERFECT 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/108,673A

FILING DATE: July 1, 1998

CLASSIFICATION: 514

PRIOR APPLICATION 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/886,829

FILING DATE: 01-UUL-1997

ATTORNEY/AGENT INFORMATION:

REFERENCE/DOCKET NUMBER: 15IS-3105

TELLEPHONE: (215) 568 3439

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LEBRGTH: 18 base pairs

TELENGTH: 18 base pairs

TELENGTH: 18 base pairs

TERNORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LEBRGTH: 18 base pairs

TERNORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LEBRGTH: 18 base pairs

TERNORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LEBRGTH: 18 base pairs

TYPELENGTH: 18 base pairs

TYPELENGTH: 18 base pairs

TYPELENGTH: 18 base pairs
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PUBLICATION INFORMATION:
DOCUMENT NUMBER: WO 95/08350 (SEQ ID NO:17)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 20-SEP-1994
; PUBLICATION DATE: 30-MAR-1995
US-09-108-673A-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 CCAGCGTGCGCCAT 19
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Matches 14; Conservative
        TITLE OF INVENTION:
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                                                                                                                                                                                               USA
                                                                                                                                          CITY: Phil
STATE: PA
                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-835-371-21
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US-09-634-320-8

Sequence 8, Application US/09634320

Sequence 8, Application US/09634320

SEREAL INFORMATION:
APPLICANT: Papisov, Mikhail, I.
TITLE OF INVENTION: USE THEREF.
TITLE OF INVENTION: USE THEREF.
TITLE REPERENCE: 0938-1003-0.1
CURRENT FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: US 60/147,919
PRIOR RILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 13
SOFTWARE FastSEQ for Windows Version 4.0
SEQ ID NO 8
IENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
FORTURE:
COTHER INFORMATION: Cindicates an RNA base
US-09-634-320-8
                                                                         Query Match 58.3%; Score 14; DB 3; Length 18; Best Local Similarity 100.0%; Pred. No. 5.8e+03; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-672-126B-110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 CCAGCGTGCGCCAT 19
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Search completed: February 15, 2006, 21:14:18 Job time : 57.9504 secs

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Sequence

Sequence 35445, A Sequence 55179, A Sequence 87299, A Sequence 165784, Sequence 773179, Sequence 5, Appli Sequence 52, Appli Sequence 52, Appli Sequence 53, Appli Sequence 21, Appli Se

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US-10-719-900-91312

US-10-098-263B-33445

US-10-098-263B-33445

US-10-098-263B-87293

US-10-098-263B-87293

US-10-719-900-765784

US-10-719-900-765784

US-10-719-900-765785

US-10-151-204-5

US-10-10-17-900-217604

US-11-036-317-941810

US-10-098-263B-94199

US-10-098-263B-94199

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US-10-098-263B-94199

US-10-098-263B-94199

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US-10-19-900-345118

US-11-07-729-51

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US-09-824-468-59

US-09-962-116A-77

US-09-965-116A-98

US-09-965-116A-98

US-09-965-116A-98

US-09-965-116A-98

US-09-800-266A-51

US-09-805-07A-51

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Sequence 200607,
Sequence 240612,
Sequence 69, Appl,
Sequence 533, App
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90, Appl
90, Appl
96172, A
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Sequence 368311,
Sequence 107962,
Sequence 200607,
                                                                                       01:43:22 ; Search time 348.298 Seconds (without alignments) 569.815 Million cell updates/sec
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9: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
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              GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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US-09-776-479-81
US-09-776-479-81
US-10-112-653-75
US-10-017-995-81
US-10-314-578-81
US-10-314-578-81
US-10-005-073-1
US-10-005-073-1
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US-11-036-317-240612
US-10-956-157-200607
US-11-036-317-827644
US-09-875-453-69
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US-09-776-479-90
US-10-112-653-84
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Maximum Match 100%
Listing first 300 summaries
                                                               sw model
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                                                               nucleic search, using
                                                                                         February 16, 2006,
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                          Copyright
                                                                                                                                                                                                                                                                                       seq length: 0
seq length: 50
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                                                                                                                                                                                                                                                                      OTHER INFORMATION: Synthetic oligonucleotide
CURRENT APPLICATION NUMBER: US/09/888,326
CURRENT FILING DATE: 2001-06-22
PRIOR PILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 848
SOFTWARE: PastSEQ for Windows Version 3.0
SOFTWARE: 24
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                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
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APPLICANT: Bratzler, Robert L.
APPLICANT: Petersen, Deanna M.
TITLE OF INVENTION: Treatment of Asthma and Allergy
TITLE OF INVENTION: Treatment of Asthma and Allergy
FILE REFERENCE: C1037/7013 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/776,479
FRIOR APPLICATION NUMBER: US/09/776,479
FRIOR PETING DATE: 2001-02-03
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 81
LENGTH: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 24; DB 3; Length 24; Best Local Similarity 100.0%; Pred. No. 1.7; Matches 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 81, Application US/09776479
Publication No. US20040067902A9
GENERAL INFORMATION:
APPLICANT: Bratzler, Robert L.
APPLICANT: Petersen, Deanna M.
APPLICANT: Fouron, Yve8
TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Treatment of Asthma and Allergy
FILE REFERENCE: C1037/7013 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/776,479
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APPLICANT: Weiner, George
APPLICANT: Hartmann, Gunther
TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
TITLE OF INVENTION: Cell Lysis and Treating Cancer
FILE REFERENCE: C1039/7052 (AWS)

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RESULT 7
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                                                                                                                                                                                                                                                                                                                              Gaps
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APPLICANT: Krieg, Arthur M.
APPLICANT: Berg, Daniel J.
TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
FILE REPERENCE: C01039/70060(AMS)
CURRENT APPLICATION NUMBER: US/10/112,653
CURRENT APPLICATION NUMBER: US 60/279,642
PRIOR FILING DATE: 2002-03-29
NUMBER OF SEQ ID NOS: 1040
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 75
LENGTH: 24
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Sequence 81, Application US/10017995

Publication No. US20030055014A1

GENERAL INFORMATION:

APPLICANT: Bratzler, Robert L.

TITLE OF INVENTION: Inhibituch MARIO

FILE REFERENCE: C1037/7025 (HCL/MAT)

CURRENT APPLICATION NUMBER: US/10/017, 995

CURRENT FILING DATE: 2001-12-18

PRIOR PILING DATE: 2001-12-14

NUMBER OF SEQ ID NOS: 1093

SEQ ID NO 8: SEQ ID NO 8: 1093

LENGTH: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , OTHER INFORMATION: Synthetic Oligonucleotide US-10-112-653-75
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: US 60/179,991
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 81
LENGTH: 24
                                                                                                                                                                                                                      CTHER INFORMATION: Synthetic Sequence US-09-776-479-81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
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24; Conserva
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US-10-112-653-75
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Best Local 
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sequence 81, Application US/10831778

publication No. US20040235774A1

sequence 81, Application No. US20040235774A1

septicant: No. US20040235774A1

septicant: Brataler, Robert L.

APPLICANT: Petersen, Deanna M.

APPLICANT: Petersen, Deanna M.

APPLICANT: Petersen, Deanna M.

TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Immunostimulatory Nucleic Polyonal (HCL/MAT)

CURRENT APPLICATION NUMBER: US 60/179,991

PRIOR FILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 1093

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 81

LENGTH: 24
                                                                                                                     Length 24;
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| Sequence 81, Application US/10314578
| Publication No. US20030212026A1
| Publication No. US20030212026A1
| GENERAL INFORMATION:
| APPLICANT: Krieg, Arthur M.
| APPLICANT: Volumer, Jorg
| TITLE OF INVENTION: Immunostimulatory Nucleic Acids
| FILE REFERENCE: C1039/7035 (HCL/MAT)
| CURRENT APPLICATION NUMBER: US/10/314,578
| CURRENT FILING DATE: 1099-09-25
| PRIOR PILING DATE: 1999-09-25
| PRIOR PILING DATE: 1999-09-25
| PRIOR FILING DATE: 1999-09-25
| PRIOR FILING DATE: 1999-09-25
| PRIOR PILING DATE: 1999-09-37
| PRIOR FILING DATE: 1999-09-37
| PRIOR PILING DATE: 1999-09-37
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                                                                                                                 100.0%; Score 24; DB 5;
100.0%; Pred. No. 1.7;
tive 0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: Synthetic Sequence US-10-314-578-81
) OTHER INFORMATION: Synthetic Sequence US-10-017-995-81
                                                                                                                                                                                                                                                                                                                         1 GGGCTCCAGCGTGCGCCATGGGGG 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
                                                                                     Query Match
Best Local Similarity 100.v
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Best Local Similarity 100.0
Matches 24; Conservative
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TITLE OF INVENTION: Methods of Genetic Analysis of Rat FILE REFERENCE: 3527.1

CURRENT APPLICATION NUMBER: US/10/719,956

CURRENT FILING DATE: 2003-11-20

PRIOR FILING DATE: 2002-11-20

NUMBER OF SEQ ID NOS: 699466

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
                                                                                                                                                                                                                           TYPE: DNA
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                                                                                                                                                                                                        RESULT 8
US-10-005-073-1
; Sequence 1, Application US/10005073
; Publication No. US2002090371A1
; GENERAL INFORMATION:
    APPLICANT: Jevnikar, Anthony M.
    APPLICANT: Jevnikar, Anthony M.
    Stiller, Calvin R.
    Stiller, Calvin R.
    TITLE OF INVENTION: METHODS AND PRODUCTS FOR CONTROLLING IMMUNE RESPONSES IN MAMMALS
. TITLE OF INVENTION: METHODS AND PRODUCTS FOR CONTROLLING IMMUNE RESPONSES IN MAMMALS
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                                        DB 8; Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
STREET: George Mason Building, 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.5%; Score 16.2; DB 5;
85.7%; Pred. No. 3.4e+03;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/005,073
FILING DATE: 07-Dec-2001
CLASSIFICATION: cluknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/617,874
FILING DATE: 21-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: REA, TEACES STANEK
REGISTRATION NUMBER: 30,427
TELECOMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-620
                                      100.0%; Score 24; DB 8
100.0%; Pred. No. 1.7;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DESCRIPTION: /desc = "DNA - primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: other nucleic acid
                                                                                                                    1 GGGGTCCAGCGTGCGCCATGGGGG 24
                                                                                                                                           1 GGGGTCCAGCGTGCGCCATGGGGG 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                   Query Match
Best Local Similarity 100.0
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 85.7.
Conservative
US-10-831-778-81
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; Sequence 368311, Application US/10719956 ; Publication No. US20040146910A1 ; GENERAL INFORMATION:

US-10-719-956-368311/c

RESULT 9

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APPLICANT: Wyeth
APPLICANT: Wounts, William
APPLICANT: Mounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 200607
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                                                                       Length 25;
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                                                                                                                       Indels
                                                            64.2%; Score 15.4; DB 7;
illarity 94.1%; Pred. No. 7.4e+03;
Conservative 0; Mismatches 1:
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Michael Mittmann; APPLICANT: Michael Mittmann; APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 310.1.1
CURRENT APPLICATION NUMBER: US/10/809,189
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: US/09/396,196
PRIOR APPLICATION NUMBER: 05/00-15
PRIOR PILING DATE: 1998-09-17
NUMBER OF SEQ. ID NOS: 127806
SOFTWARE: FASESEQ for Windows Version 4.0
LENGTH: 25
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                          ; Sequence 107962, Application US/10809189; Publication No. US20050048531A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-956-157-200607/c; Sequence 200607, Application US/10956157; Publication No. US20050118625A1; GENERAL INFORMATION:
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                                                                                                                                                                       3 GGTCCAGCGTGCGCCAT 19
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; ORGANISM: Rattus norvegicus US-10-719-956-368311
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Matches 17; Conservative
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                                                  Query Match
Best Local Similarity
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Query Match
Best Local Similarity
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APPLICANT:
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## Sequence 240612, Application US/11036317

## Publication No. US20050214823A1

## SEQUENCE INCOMMATION:

## APPLICANT: Williams, Alan

## PLICANT: Blume, John

## TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

## FILE REFERENCE: 3654.1

## CURRENT APPLICATION NUMBER: US/11/036,317

## CURRENT APPLICATION NUMBER: US 60/536,639

## PRIOR FILING DATE: 2004-01.13

## NUMBER OF SEQ ID NOS: 991174

## SOFTHARE: Microarray Probe Sequence Listing Generator V 1.1

## SEG ID NO 240612

## LENGTH: 25
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; Sequence 827644, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REPRESENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; LENGTH: 25
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                                                                                                     Length 25;
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                                                                                                     Score 15.2; DB 9;
Pred. No. 9e+03;
0; Mismatches 3;
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85.0%;
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                                                                                                            Query Match
Best Local Similarity 85.0
Matches 17; Conservative
; LENGTH: 25
; TYBE: DM:
; ORGANISM: Probe Sequence
US-10-956-157-200607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Mus musculus
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US-11-036-317-240612/c
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, LOCATION: (0)...(0) ...(0) ; OTHER INFORMATION: chimeric phosphorothioate/phosphodiester backbone ; OTHER INFORMATION: with phosphorothioate at 5' and 3' ends US-09-888-326-533
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FILE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
FILE REFERENCE: 4600-0135.30
CURRENT APPLICATION NUMBER: US/09/875,453
CURRENT APPLICATION NUMBER: US 60/209,549
PRIOR PILLING DATE: 2000-06-06
PRIOR FILING DATE: 2000-06-06
NUMBER: OF SEQ ID NOS: 78
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 533, Application US/0988326

Publication No. US20030026801A1

GENERAL INFORMATION:

APPLICANT: Weiner, George

TITLE OF INVENTION: Methods for Enhancing Antibody-Induced

TITLE OF INVENTION: Methods for Enhancing Cancer

TITLE OF INVENTION: Methods for Enhancing Cancer

FILE REFERENCE: C1039/7052 (AWS)

CURRENT FILING DATE: 2001-06-22

PRIOR FILING DATE: 2000-06-22

NUMBER OF SEQ ID NOS: 848

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 16
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Pred. No. 8.3e+03;
0; Mismatches 3;
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Sequence 69, Application US/09875453 Publication No. US20030027320A1 GENERAL INFORMATION:
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Thomas, Rita L.
Kongpachith, Ana
Sheppard, Liana T.
Lim, Moon Young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 85.0%;
Matches 17; Conservative
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                                                                                                                                        Laurance, Megan E.
Michelotti, Emil F
Velligan, Mark D.
                                                                  APPLICANT: Kim, Jungsuh P. APPLICANT: Starr, Douglas B. APPLICANT: Tam, Albert W.
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Gaps

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0; Indels

0; Mismatches

15; Conservative

Matches

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15; Conservative
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Best Local Similarity
Matches 15; Conserv
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Best Local Similarity
Matches 15; Conserv
                   US-10-112-653-84
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APPLICANT: Petersen, Deanna M.
APPLICANT: Petersen, Deanna M.
APPLICANT: Fouron, Yves
TITLE OF INVENTION: Treatment of Asthma and Allergy
FILE REFERENCE: C103/7013 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/776,479
PRIOR APPLICATION NUMBER: US 60/176,479
PRIOR APPLICATION NUMBER: US 60/176,991
PRIOR PRILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: PastSEQ for Windows Version 3.0
LENGTH: 16
                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Brataler, Robert L.
APPLICANT: Petersen, Deanna M.
APPLICANT: Petersen, Deanna M.
APPLICANT: Fourcon, Yves
TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
TITLE OF INVENTION: Treatment of Asthma and Allergy
FILE REFERENCE: C1037/7013 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/776,479
PRIOR APPLICATION NUMBER: US 60/179,991
PRIOR FILING DATE: 2000-02-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.5%; Score 15; DB 3; Length 16; 100.0%; Pred. No. 1.2e+04; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.5%; Score 15; DB 3; Length 16; 100.0%; Pred. No. 1.2e+04; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 90
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Synthetic Sequence US-09-776-479-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Synthetic Sequence US-09-776-479-90
                                                                                                 RESULT 16
US-09-776-479-90
; Sequence 90, Application US/09776479
; Publication No. US20030087848A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 90, Application US/09776479 Publication No. US20040067902A9 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
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5 TCCAGCGTGCGCCAT 19
                        1 TCCAGCGTGCGCCAT 15
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Best Local Similarity 100.0
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15, Conservative
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                                                             APPLICANT: Krieg, Arthur M.
APPLICANT: Berg, Daniel J.
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
TITLE OF INVENTION: TREATWENT OF NON-ALLERGIC INFLAMMATORY DISEASES
FILE REFERENCE: C01039/70060(AWS)
CURRENT APPLICATION NUMBER: US/10/112,653
CURRENT FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: US 60/279,642
NUMBER OF SEQ ID NOS: 1040
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-017-995-90

is sequence 90, Application US/10017995

is gequence 90, Application US/10017995

is publication No. US20030055014A1

is GENERAL INFORMATION:

if TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids

if TITLE OF INVENTION: Inhibition of Angiogenesis by CURRENT APPLICATION NUMBER: US/10/1017,995

is CURRENT APPLICATION NUMBER: US 60/255,534

is PRIOR APPLICATION NUMBER: US 60/255,534

is PRIOR FILING DATE: 2000-12-14

is NUMBER OF SEQ ID NOS: 1093

is SOFTWARE: PastSEQ for Windows Version 3.0

is SEQ ID NO 90
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100.0%; Pred. No. 1.2e+04;
iive 0; Mismatches 0;
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Pred. No. 1.2e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) OTHER INFORMATION: Synthetic Oligonucleotide US-10-112-653-84
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Sequence 84, Application US/10112653 Publication No. US20030050268A1 GENERAL INFORMATION:
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
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oligonucleotide
Description of Artificial Sequence:
oligonucleotides, linkages between positions 1
to 18 are phosphorothioates, linkages between
positions 18 to 26 are phosphodiasters
positions 19 to 29 carry 2'-OCH3 modified ribosyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/09817387
Fatent No. US20010039263A1
GENERAL INFORMATION:
APPLICANT: Max-Delbruck-Centrum fur Molekulare Medizin
TITLE OF INVENTION: Chimeric Oligonucleotides and the Use Thereof
FILE REFERENCE: 101195-24
CURRENT APPLICATION NUMBER: US/09/817,387
CURRENT FILING DATE: 2001-03-26
FRIOR APPLICATION NUMBER: DE 197 20 151.2
FRIOR PILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver. 2.1
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Sequence 91312, Application US/10719900

Publication No. US20050026164A1

GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

FILE REFERENCE: 3528.1

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT PELLON DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,808

PRIOR FILING DATE: 2002 11 20

NUMBER OF SEQ ID NOS: 982914
                PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 96172
LENGTH: 25
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                                                                                                                                                                                                                                                                                    Length 25;
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                                                                                                                                                                                                                                                                                    62.5%; Score 15; DB 5; I
78.3%; Pred. No. 1.1e+04;
tive 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                           1 GGGGTCCAGCGTGCGCCATGGGG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                       24 GGAGTCCACAGTCCGCCACGGGG 2
  2003-01-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 78.33
Matches 18; Conservative
                                                                                                                                                                                   TYPE: DNA
CORGANISM: Homo sapien
US-10-098-263B-96172
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  CURRENT FILING DATE:
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US-09-817-387-12
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LENGTH: 29
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Sequence 90, Application US/10831778

Publication No. US20040235774A1

GENERAL INFORMATION:

APPLICANT: Petersen, Deanna M.

CURRENT APPLICATION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Treatment of Asthma and Allergy

FILE REFERENCE: C1037/7013 (HCL/MAT)

CURRENT APPLICATION NUMBER: US/10/831,778

PRIOR FILING DATE: 2000-02-03

FRIOR FILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 1093

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 16
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APPLICANT: Vollmer, Jorg
TITLE OF INVENTION: Immunostimulatory Nucleic Acids
FILE REPERENCE: C1039/7035 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/10/314,578
CURRENT FILING DATE: 2002-12-09
FRIOR APPLICATION NUMBER: US 60/156,113
PRIOR APPLICATION NUMBER: US 60/156,135
PRIOR APPLICATION NUMBER: US 60/156,135
PRIOR PRILING DATE: 1999-09-27
PRIOR PILING DATE: 1999-09-27
PRIOR FILING DATE: 1999-09-27
PRIOR FILING DATE: 1099-09-27
PRIOR FILING DATE: 1099-09-27
PRIOR FILING DATE: 1099-09-27
PRIOR FILING SATE: 2000-08-23
NUMBER OF SEQ ID NOS: 1145
SOFTWARE: FRAEKEQ for Windows Version 3.0
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US-10-098-263B-96172/C
Sequence 96172, Application US/10098263B
Sequence 96172, Application US/10098263B
September of US20030104410A1
GENERAL INFORMATION:
APPLICANT: Mittman, Michael
TITLE OF INVENTION: Human Microarray
FILE REPERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/099,263B
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 15; Conservative
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LENGTH: 16
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Gaps

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Query Match
Best Local Similarity 81.0%;
Matches 17; Conservative C
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US-10-098-263B-87293
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US-10-098-263B-87909
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Matches 17; Conserv
                 RESULT 27
US-10-098-263B-87293
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                                                                                                                         61.7%; Score 14.8; DB 8; Length 25; 88.9%; Pred. No. 1.3e+04;
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81.0%; Pred. No. 1.6e+04;
ive 0; Mismatches 4; Indels
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APPLICANT: Mittman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION: NUMBER: US/10/098,263B
CURRENT PILING DATE: 2003-01-08
PRIOR PILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 55179
LENGTH: 25
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1 SEQ ID NO 91312
LENGTH: 25
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SOFTWARE Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 35445
LENGTH: 25
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                                                                                                                                                             Mismatches
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TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
                                                                                                                                                                                                                                                                                                           US-10-098-263B-35445
; Sequence 35445, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
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                                                                                                                                                             Conservative
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                                                   TYPE: DNA
CORGANISM: Mus musculus
US-10-719-900-91312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
CORGANISM: Homo sapien
US-10-098-263B-35445
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; ORGANISM: Homo sapien
US-10-098-263B-55179
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Best Local Similarity
....hes 17; Conserva
                                                                                                                                          Local Similarity
nes 16; Conserv
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es 17; Conserv
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US-10-098-263B-55179
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Matches 17,
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; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mitchael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 87909
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; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REPRENCE: 3528.1
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427, 808
; PRIOR APPLICATION NUMBER: 60/427, 808
; PRIOR PILING DATE: 2003-11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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                                                                     APPLICANT MACHAEL
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 87293
LENGTH: 25
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Pred. No. 1.6e+04;
0; Mismatches 4;
Sequence 87293, Application US/10098263B; Publication No. US20030104410A1; GENERAL INFORMATION:
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APPLICANT: BAIRCH, ADGREW
APPLICANT: BAIRCH, ADGREW
APPLICANT: BAIRCH, ADGREW
APPLICANT: KASSNET, PAUJ
TITLE OF INVENTION: METHODO USING GENETIC PACKAGE DISPLAY FOR
TITLE OF INVENTION: DETECTIONS THAT FACILITATE INTERNALIZATION
TITLE OF INVENTION: INTERACTIONS THAT FACILITATE INTERNALIZATION
TITLE OF INVENTION: COMPETENT FOR THE SAME AND METHODS FOR EVOLVING
TITLE OF INVENTION: GENE DELIVERY VECTORS
TITLE OF INVENTION: GENE DELIVERY VECTORS
TITLE OF INVENTION: GENE DELIVERY VECTORS
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 17
SEQ ID NO S: 17
LENGTHR: PATENTIN VEY: 2.0
SEQ ID NO 5:
LENGTH: 47
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Pred. No. 1.4e+04;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

60.8%; Score 14.6; DB 3; Length 47;
Best Local Similarity 81.0%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 4; Indels
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; Publication No. US20030148263A1
; GENERAL INFORMATION:
   APPLICANT: Larocca, David
; APPLICANT: Larocca, David
; APPLICANT: Barsner, Paul
; APPLICANT: Bars, Andrew
APPLICANT: Burg, Michael Alan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USING;
TITLE OF INVENTION: METHODS AND COMPOSITIONS
; TITLE OF INVENTION: GENETIC PACKAGE DISPLAY
; FILE REFERENCE: 760100 430C5
; CURRENT APPLICATION NUMBER: US/10/151,204
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5,
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US-10-735-592-52
; Sequence 52, Application US/10735592
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                                                                            Sequence 5, Application US/09866073
Patent No. US20020068272A1
GENERAL INFORMATION:
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81.0%;
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Best Local Similarity 81.0
Matches 17; Conservative
                                                                                                                                                                                   APPLICANT: Larocca, David
                        RESULT 32
US-09-866-073-5
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Fublication No. US2050214823A1

GENERAL INFORMATION:

APPLICANT: Milliams, Alan

TITLE OF INVENTION:

FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT PLING DATE: 2005-01-13

FRIOR PILING DATE: 2006-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: MICROARRAY Probe Sequence Listing Generator V 1.1

LENGTH: 25

LENGTH: 25
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US-10-719-900-765785

Sequence 765785, Application US/10719900

Publication No. US20050026164A1

CHERERAL INFORMATION:

APPLICANT: Xue Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

FILE REFERENCE: 3528.1

CURRENT FILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,808

FRIOR FILING DATE: 2003-11-20

NUMBER OF SEQ ID NOS: 992914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

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                                                                                                                                                                                       Length 25;
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                                                                                                                                                                                          Score 14.6; DB 8;
Pred. No. 1.6e+04;
                                                                                                                                                                                              Query Match 60.8%; Score 14.6; DB 8; Best Local Similarity 81.0%; Pred. No. 1.6e+04; Matches 17; Conservative 0; Mismatches 4
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CORGANISM: Mus musculus
US-11-036-317-773179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
, ORGANISM: Mus musculus
US-10-719-900-765785
                                                              TYPE: DNA
CORGANISM: Mus musculus
US-10-719-900-765784
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Best Local Similarity
Matches 17; Conserv
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US-11-036-317-773179/c
SEQ ID NO 765784
LENGTH: 25
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; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-217604
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: AFL, Krieg
APPLICANT: AC, Krieg
APPLICANT: AC, Ollmer
TILE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use
FILE REFREENCE: C1037.70038US01
CURRENT APPLICATION NUMBER: US/10/735,592
CURRENT FILING DATE: 2003-12-11
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn version 3.2
SEQ ID NO 52
LENGTH: 18
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; Sequence 217664, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; TITLE OF INVENTION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR APPLICATION NUMBER: 60/427,808
; NUMBER OF SEQ ID NOS: 982914
; SCPTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 217604
                                                                                                                                                                                                                                                                                                                                                                                Length 18;
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APPLICANT: Art, Krieg
APPLICANT: Joerg, Vollmer
TITLE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use
FILE REFERENCE: C1037, 70038US01
CURRENT PELLNG DATE: 2003-12-11
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin version 3.2
SEQ ID NO 53
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
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93.8%; Pred. No. 2.1e+04;
tive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 GTCCAGCGTGCGCCAT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GTCGAGCGTGCGCCAT 18
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Best Local Similarity 93.8°
Matches 15, Conservative
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Matches 15; Conservative
                                                                                                                                                                                                                                                                         ORGANISM: Artificial
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US-10-719-900-217604
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US-10-735-592-53
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Sequence 195172, Application US/11036317

Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

APPLICANT: Blume, John

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REPERENCE: 3664.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT PILING DATE: 2004-01-13

PRIOR FILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

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TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse FILE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse FILE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR APPLICATION NUMBER: US 60/536,639
NUMBER OF SEQ ID NOS: 991174
SEQ ID NO 228536
LENGTH: 25
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              Length 25;
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         DB 8;
                                          2e+04;
Query Match 60.0%; Score 14.4; D
Best Local Similarity 75.0%; Pred. No. 2e+0
Matches 18; Conservative 0; Mismatches
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; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
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Matches 15; Conservative
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US-11-036-317-195172
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US-11-036-317-228536
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2 GGGTCCAGCGTGCGCC 17
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US-11-036-317-874107
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| Sequence 313397, Application US/11036317
| Publication No. US20050214823A1
| GENERAL INFORMATION:
| APPLICANT: Williams, Alan
| APPLICANT: Williams, John
| TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
| FILE REFERENCE: 365410
| CURRENT APPLICATION NUMBER: US/11/036,317
| CURRENT FILING DATE: 2005-01-13
| PRIOR FILING DATE: 2004-01-13
| NUMBER OF SEQ ID NOS: 991174
| SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
| LENGTH: 25
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US-11-036-317-304181

Sequence 304181, Application US/11036317

Publication No. Us2005021482341

GENERAL INFORMATION:

APPLICANT: Williams, Alan

APPLICANT: Williams, John

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REPERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2005-50-13

PRIOR FILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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US-11-036-317-531172/c
US-11-036-317-531172, Application US/11036317
; Sequence 531172, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
    APPLICANT: Williams, Alan
    TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
    FILE REPRENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR PILING DATE: 2005-01-13
; PRIOR FILING DATE: 2004-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Best Local Similarity 93.8%;
Matches 15; Conservative (
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Best Local Similarity 93.8
Matches 15; Conservative
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CORGANISM: Mus musculus
US-11-036-317-304181
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US-11-036-317-313397
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Publication No. US20050214823A1
Publication No. US20050214823A1
Publication No. US20050214823A1
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Wethod of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 874107
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, NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 531172
; LENGTH: 25
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Pred. No. 2e+04;
0; Mismatches 1;
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93.8%; Pred. No. 2e+04;
tive 0; Mismatches 1;
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Pred. No. 2e+04;
0; Mismatches 1;
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Best Local Similarity 93.8<sup>3</sup>
Matches 15; Conservative
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Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 93.8
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-874107
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US-11-036-317-937038
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; ORGANISM: Mus musculus
US-11-036-317-531172
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RESULT 48
US-10-053-645A-35
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LENGTH: 32
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TITLE OF INVENTION: Nucleic acids and polypeptides specific for pathogenic TITLE OF INVENTION: Btrains of the Neisseria genius
FILE REFERENCE: P07180USOO/BAS
CURRENT APPLICATION NUMBER: US/10/909,436
CURRENT APPLICATION NUMBER: US/10/909,436
FILE REFERENCE: P07180USPER: P8 98 13 693
PRIOR FILING DATE: 1999ER: F8 98 13 693
PRIOR FILING DATE: 1999ER: F9 98 13 693
FRIOR FILING DATE: 1999ER: 1299
SOFTWARE: PATENTIN VET: 2.1
LENGTH: 29
                                                                                                                                                                                              APPLICANT: Williams, Alan
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REPERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENTH: 25
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                                                                                                                                     ; Sequence 942273, Application US/11036317; Publication No. US20050214823A1; GENERAL INFORMATION:
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4 GCGTCCAGCGTGCGCC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGGTCCAGCGTGCGCC 17
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ORGANISM: Artificial Sequence
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Best Local Similarity 93.8
Matches 15; Conservative
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                                                                                          RESULT 44
US-11-036-317-942273
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US-10-909-436-127
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APPLICANT: Robert E. Klem
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A
TITLE OF INVENTION: CELL-PROLIFERATIVE DISORDER USING CRE DECOY OLIGOMERS, BCL-2
TITLE OF INVENTION: CELL-PROLIFERATIVE DISORDER USING CRE DECOY OLIGOMERS, BCL-2
TITLE OF INVENTION: ANTISENSE OLIGOMERS, AND HYBRID OLIGOMERS THEREOF
FILE REFERENCE: 10412-022-99
CURRENT APPLICATION NUMBER: US/10/053,645A
CURRENT FILING DATE: 2002-01-22
PRIOR FILING DATE: 2001-01-22
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 33
LENGTH: 34
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Publication No. US20030176376A1
GENERAL INFORMATION:
APPLICANT: Robert E. Klem
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A
TITLE OF INVENTION: CELL-PROLIFERATIVE DISORDER USING CRE DECOY OLIGOMERS, BCL-2
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APPLICANT: Schechner, Jeffrey S.
APPLICANT: Zheng, Lian
TITLE OF INVENTION: Production and Use of Microvessels in a
TITLE OF INVENTION: Eibronectin-containing Gel
TITLE OF INVENTION: Eibronectin-containing Gel
FILE REFERENCE: 44574-5074-W0
CURRENT APPLICATION NUMBER: US/10/297,321
CURRENT FILING DATE: 2002-12-05
PRIOR APPLICATION NUMBER: US 60/208,931
PRIOR PILING DATE: 2000-06-05
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 60.0%; Score 14.4; DB 7;
Local Similarity 93.8%; Pred. No. 1.9e+04;
Nes 15; Conservative 0; Mismatches 1:
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; Sequence 33, Application US/10053645A
; Publication No. US20030176376A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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Matches 15; Conservative
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US-10-053-645A-41
                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of artificial sequence: Synthetic Antisense; OTHER INFORMATION: Oligionucleotide
US-10-053-645A-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: ANTISENSE OLIGOWERS, AND HYBRID OLIGOMERS THEREOF FILE REFERENCE: 10412-022-99
CURRENT APPLICATION NUMBER: US/10/053,645A
CURRENT FILING DATE: 2002-01-22
PRIOR PILING DATE: 2001-01-22
PRIOR FILING DATE: 2001-01-22
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-911-374-14
; Sequence 14, Application US/10911374
; Sequence 14, Application Wo. US20050003531A1
; GENERAL INFORMATION:
; APPLICANT: Rao, Mahendra S
; APPLICANT: Kalyani, Anjali J
; TITLE OF INVENTION: Lineage-Restricted Neuronal Precursors
; FILE REFERENCE: T5530.CIP
; CURRENT APPLICATION NUMBER: US/10/911,374
; CURRENT APPLICATION NUMBER: US/09/109,858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.0%; Score 14.4; DB 6; Length 34; 93.8%; Pred. No. 1.8e+04;
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                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Seguence
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Best Local Similarity
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US-10-053-645A-41
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Sequence 6, Appli Sequence 55, Appl Sequence 1, Appli Sequence 85, Appli Sequence 6, Appli Sequence 6, Appli Sequence 55, Appli

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Sequence 23991, A
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Sequence 402274,
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Sequence 1185838,
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Sequence 393938,
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Sequence 34498, A
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                                                           February 16, 2006, 02:03:53; Search time 223.736 Seconds (without alignments) 98.157 Million cell updates/sec
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Sequence 39338, Application US/11121849
Publication No. US20050272080A1
Publication No. US20050272080A1
Publication No. US20050272080A1
APPLICANTION:
APPLICANTION:
APPLICANTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT APPLICATION NUMBER: 605-63
CURRENT APPLICATION NUMBER: 605-63
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 24; DB 11; Length 24; Best Local Similarity 100.0%; Pred. No. 0.24; Matches 24; Conservative 0; Mismatches 0; Indels
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85.7%; Pred. No. 4.5e+02;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , OTHER INFORMATION: Synthetic oligonucleotide US-11-127-654-75
         THE REFERENCE: C1039 70060USO1
CURRENT APPLICATION NUMBER: US/11/127,654
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: US 10/112,653
PRIOR FILING DATE: 2002-03-29
PRIOR FILING DATE: 2002-03-29
PRIOR PILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 1040
SOFTWARE: PAERLIN VERSION 3.2
LENGTH: 24
INFLAMMATORY DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGGGTCCAGCGTGCGCCATGGGGG 24
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                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial seguence
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Best Local Similarity 85.7°
Matches 18; Conservative
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CORGANISM: Homo sapien
US-11-121-849-393938
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
US-10-310-914A-402269
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Sequence 73, Appl
Sequence 333, Appl
Sequence 378375,
Sequence 443158,
Sequence 518228,
Sequence 518228,
                          Sequence 8860, Ap
Sequence 8860, Ap
Sequence 81062, A
Sequence 40270,
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Sequence 490280,
Sequence 528482,
Sequence 95556,
Sequence 919624,
Sequence 1238304,
Sequence 1238304,
Sequence 1238304,
Sequence 16195, A
Sequence 16195, A
Sequence 238304,
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Sequence 124522,
Sequence 124619,
                                                                                                                    US-10-310-914A-362450

US-10-310-914A-402270

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US-10-310-914A-865051

US-10-310-914A-865051

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US-10-310-914A-916338

US-10-310-914A-91638

US-10-310-914A-91638
US-10-310-914A-1261001
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US-10-310-914A-362025
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US-10-310-914A-443158
US-10-310-914A-518228
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Gaps

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Sequence 402269, Application US/10310914A
Sequence 402269, Application US/10310914A
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bloinformatically detectable group of novel regulatory genes and
ITTLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patent In version 3.3
SEQ ID NO 402269
LENGTH: 25
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Indels
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                                                                                                               degarccadecadecarda 23
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APPLICANT: Krieg, Arthur M. APPLICANT: Berg, Daniel J. TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC

; Sequence 75, Application US/11127654; Publication No. US20050250726A1; GENERAL INFORMATION:

US-11-127-654-75

Length 25;

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APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S.
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S.
FILE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
PRIOR FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 235244
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 34498, Application US/10310914A

Fublication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac

APPLICANT: Bentwich, Isaac

TITLE OF INVENTION: Uses thereof

TITLE OF INVENTION: Uses thereof

FILE REFERENCE: 06097.0200.CPUS01

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 34498
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; Sequence 84, Application US/11127654
; Sequence 84, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Exteg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TILLE OF INVENTION: INFLAMMATORY DISEASES
; TITLE OF INVENTION: INFLAMMATORY DISEASES
; FILE REFERENCE: C1039, 70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
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89.5%; Pred. No. 6.6e+02;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.3%; Score 15.2; DB 7; 85.0%; Pred. No. 1.2e+03;
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                               US-11-121-849-235244/c
Sequence 225544/Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
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Query Match
Best Local Similarity 85.07
Matches 17; Conservative
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Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapien
US-11-121-849-235244
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Sequence 1185838

Sequence 1185838, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Biller, Kurzat

TITLE OF INVENTION: Uses thereof

TITLE OF INVENTION: Uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT FILING DATE: 2002-12-06

SOFTWARE: PATCHIN VONSE: 1888402

SOFTWARE: PatchIN version 3.3

SEQ ID NO: 1185838

LENGTH: 22

LENGTH: 22
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FILE REFERENCE: 30302
CURRENT APPLICATION NUMBER: US/11/201,322
CURRENT PILING DATE: 2005-08-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.7%; Score 16; DB 11; Length 30; 100.0%; Pred. No. 5.4e+02; ive 0; Mismatches 0; Indels
                                                                                 66.7%; Score 16; DB 7; Length 25; 70.8%; Pred. No. 5.48+02; ive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , OTHER INFORMATION: Single strand DNA oligonucleotide US-11-201-322-2
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                                                                                                                                                                                                            1 GGGGTCCAGCGTGCGCCATGGGGG 24
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Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                              Best Local Similarity 70.8 Matches 17; Conservative
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Matches 16; Conserv
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                   ) ORGANISM: Human
US-10-310-914A-402269
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ORGANISM: Human
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LENGTH: 30
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TYPE: RNA
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Sequence 46668, Application US/11121849
Sequence 46668, Application US/11121849
Sequence 46668, Application No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: JOHN PRIME
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
TITLE NEFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT APPLICATION NUMBER: 0505-05-03
FRIOR FILING DATE: 2005-05-03
NUMBER OF SEQ ID NOS: 673904
SEQ ID NOS: 673904
SEQ ID NOS: 673904
SEQ ID NO 46668
LENGTH: 25
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Publication No. US20050272080A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
MICROALRAY
TITLE OF INVENTION:
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TITLE OF INVENTION:
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TITLE OF INVENTION:
MICROALRAY
TITLE OF INVENTION:
MINMER: US/11/121,849
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: MICROALRAY Probe Sequence Listing Generator V 1.1
LENGTH: 25
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                           Indels
    1 Similarity 78.3%; Pred. No. 1.4e+03; 18; Conservative 0; Mismatches 5;
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                                                                   2 GGGTCCAGCGTGCGCCATGGGGG 24
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                                                                                              25 GGCCCAGCGTCCACCTTGGTGG 3
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78.3%;
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Best Local Similarity 78.3'
Matches 18; Conservative
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US-11-121-849-46868
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ORGANISM: Homo sapien
    Best Local Similarity
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US-10-310-914A-45418/c
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US-11-121-849-46868
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US-10-310-914A-94891/C

US-10-310-914A-94891/C

Sequence 94891, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Kvuzat
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: Patentin version 3.3

SEQ ID NO 94891
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Publication No. US20050272080A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Microarrays
FILE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR FILING DATE: 2004-05-03
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                                                                                                                                                                                                                                                                                     Length 16;
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 23997
LENGTH: 25
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                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                 62.5%; Score 15; DB 11; I
100.0%; Pred. No. 1.4e+03;
tive 0; Mismatches 0;
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PRIOR FILING DATE: 2002-03-29 PRIOR PEDLICALION NUMBER: US 60/279,642 PRIOR FILING DATE: 2001-03-29 NUMBER OF SEQ ID NOS: 1040 SEQ ID NO 84 LENGIH VERSION 3.2 LENGIH: 16
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                                                                                                                                                                                                                                                                                                                              15; Conservative
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Matches 18, Conservative
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ORGANISM: Homo sapien
US-11-121-849-23997
                                                                                                                                                                                                                                                                                                          Best Local Similarity
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US-11-121-849-23997/c
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ORGANISM: Human
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                                                                                                                                                       TYPE: DNA
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Sequence 895311/C

Sequence 895311, Application US/10310914A

Publication No. US20060003322A1

Publication No. US2006000332A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Kvuzat

TITLE OF INVENTION: uses thereof

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310, 914A

CURRENT PILING DATE: 2002-112-06

NUMBER OF SEQ ID NOS: 1388402

SEQ ID NO 995311

LENGTH. 20 995311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 14.6; DB 7; Length 26; Pred. No. 2.1e+03;
Score 14.6; DB 7; Length 24; Pred. No. 2.18+03; 2; Mismatches 4; Indels
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; Publication No. US20060003322A1
; GENERAL INFORMATION:
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                                                                                          4 GTCCAGCGTGCGCCATGGGGG 24
                                                                                                                      21 Greeregegegegekingegag 1
      Query Match 60.8%;
Best Local Similarity 71.4%;
Matches 15; Conservative 2
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Best Local Similarity 81.0%;
Matches 17; Conservative
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Best Local Similarity
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US-10-310-914A-721320/c
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US-10-310-914A-895311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: RNA
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Sequence 38276, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
USES THEREFORCE:
USER INFORMATION:
USES THEREFORCE:
USEN 100200. CDUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE:
2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE:
PATENTIN Version 3.3

SEQ ID NO 38276

LENGTH: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 402274, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Uses thereof
                                      APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REPERRNCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT FILING DATE: 2002-12-06
CURRENT FILING DATE: 2002-12-06
SOFTWARE OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 45418
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Pred. No. 2.18+03;
0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 gegecrcaccereccerree 1
                                                                                                                                                                                                                                                                                                                                             Query Match 60.8%;
Best Local Similarity 81.0%;
Matches 17; Conservative
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                      APPLICANT: Bentwich, Isaac
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Best Local Similarity
Matches 15; Conserv
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US-10-310-914A-402274
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US-10-310-914A-38276
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; ORGANISM: Human
US-10-310-914A-38276
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ORGANISM: Human
                                                                                                                                                                                                                                                            TYPE: RNA
ORGANISM: Human
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RESULT 21
US-10-658-947-14
US-10-658-947-14
Sequence 14, Application US/10658947
Fublication No. US20050255153A1
GENERAL INPORMATION:
APPLICANTY: Inex Pharmaceuticals Inc.
APPLICANT: Inex Pharmaceuticals Inc.
Agents in
APPLICANT: Applicant Inc.
Agents in
Applicant Applicant Inc.
Agents in
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                                                                                                                                                                                                                                                                                                                Length 18;
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                                                                                                                                                                                                                                                                                                                Score 14; DB 7; Lo
Pred. No. 3.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 58.3%; Score 14; DB 7; Le
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                              FEATURE:
; OTHER INFORMATION: oligonucleotide-- G3139 Genta
US-10-918-638-24
                                                                                                                                                                                                                                                                                                 58.3%; Scc. 100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/895,480
FILING DATE: 29-Jun-2001
APPLICATION NUMBER: «Unknown»
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: WOLD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/658,947
FILING DATE: 09-5ep-2003
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: Oppedahl & Larson LLP
STREET: PO Box 5068
CITY: Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: other nucleic acid HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                         TYPE: DNA ORGANISM: artificial sequence
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ZIP: 80435
COMPUTER READABLE FORM:
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Best Local Similarity 100.
Matches 14; Conservative
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                                                                                                                                                   SEQ ID NO 24
LENGTH: 18
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us-09-669-187a-8.

"TITLE OF INVENTION: Bloinformatically detectable group of novel regulatory genes and FILE REFERENCE: 06097.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT PILLIG DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 721320
LENGTH: 24
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PUblication No. US2050249663A1
GENERAL INFORMATION:
APPLICANT: Copharos
TITLE OF INVENTION: COBALAMIN MEDIATED DELIVERY OF NUCLEIC ACIDS, ANALOGS
TITLE OF INVENTION: DERIVATIVES THEREOF
FILE REFERENCE: COP1010
CURRENT APPLICATION NUMBER: US/10/918,638
CURRENT PILING DATE: 2004-08-12
PRIOR PILING DATE: 2002-09-17
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: DRUG-CARRIER COMPLEXES AND METHODS OF TITLE OF INVENTION: DRUG-CARRIER COMPLEXES AND METHODS OF TITLE OF INVENTION: USE THEREOF; TITLE OF INVENTION: USE THEREOF; FILE REPERENCE: 0838.1003.001; CURRENT APPLICATION NUMBER: US/10/994,213; CURRENT FILING DATE: 2004-11-19; PRIOR APPLICATION NUMBER: US/09/634,320; PRIOR FILING DATE: 2000-08-09; PRIOR FILING DATE: 2000-08-09; PRIOR FILING DATE: 2000-08-09; PRIOR FILING DATE: 1999-08-09; NUMBER OF SEQ ID NOS: 13; SOFTWARE: FASLSED for Windows Version 4.0; SEQ ID NO 7.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.3%; Score 14; DB 6; Length 18; 100.0%; Pred. No. 3.7e+03; Pred. 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/10994213
Publication No. US20060019911A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 14; Conservative
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Best Local Similarity
Matches 16; Conserv
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CRGANISM: Human
US-10-310-914A-721320
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Matches
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US-10-619-279-45

is Sequence 45, Application US/10619279

sequence 45, Application US/10619279

publication No. US20050267057A1

GENERAL INFORMATION:

it TILE OF INVENTION: Immunostimulatory Nucleic Acid Molecules

TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules

TITLE OF INVENTION: IMMUSER: US/10/619,279

CURRENT FILING DATE: 2003-07-14

PRIOR APPLICATION NUMBER: US 08/960,774

PRIOR APPLICATION NUMBER: US 08/38,652

PRIOR APPLICATION NUMBER: US 08/38,663

PRIOR APPLICATION NUMBER: US 08/386,063

PRIOR APPLICATION NUMBER: US 08/386,063

PRIOR APPLICATION NUMBER: US 08/276,358

NUMBER OF SEQ ID NOS: 123

SEQ ID NO 45:

LENGTH: 18

LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
; OTHER INFORMATION: synthetic immunostimulatory oligonucleotide
US-10-469-561-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.3%; Score 14; DB 7; Length 18; 100.0%; Pred. No. 3.7e+03; rive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Synthetic Oligonucleotide US-10-619-279-45
                                                                        Sequence 6, Application US/10469561
; Sequence 6, Application US/10469561
; Publication No. US20050260216A1
; GENERAL INFORMATION:
; APPLICANT: Claire Ashman
; APPLICANT: James Scott Growe
; APPLICANT: Jonathan Henry Ellis
; APPLICANT: Alan Peter Lewis
; TTTLE OF INVENTION: VACCINE
; FILE REFERENCE: PG4355USW
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.3%; Scc...
100.0%; Pre
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Best Local Similarity
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5 CCAGCGTGCGCCAT 18
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Best Local Similarity 100.
Matches 14; Conservative
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ORGANISM: unknown
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## Sequence 1, Application US/11127654

## Sequence 1, Application US/11127654

## Sequence 1, Application No. US20050250726A1

## Sequence 1, Application No. US20050250726A1

## SPLICANT: Krieg, Arthur M.

## APPLICANT: Krieg, Arthur M.

## APPLICANT: Berg, Daniel J.

## TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC TITLE OF INVENTION: IMPLAMMATORY DISEASES

## TITLE OF INVENTION: INFLAMMATORY DISEASES

## TITLE OF INVENTION: UNMBER: US/11/127,654

## CURRENT FILING DATE: 2005-05-12

## PRIOR PAPLICATION NUMBER: US 60/279,642

## PRIOR APPLICATION NUMBER: US 60/279,642
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                                                                                                                                           APPLICANT: KIINE, JOGEI N.
APPLICANT: KIINE, JOGEI N.
APPLICANT: Klinnen, Dennis
APPLICANT: Steinberg, Alfred D.
TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
FILE REFERENCE: C1039/7048 (Aws)
CURRENT PAPLICATION NUMBER: US/10/435,656
CURRENT FILING DATE: 2003-05-09
FRIOR APPLICATION NUMBER: US 08/276,358
FRIOR APPLICATION NUMBER: US 08/286,063
FRIOR APPLICATION NUMBER: US 08/386,063
FRIOR FILING DATE: 1995-02-07
FRIOR FILING DATE: 1995-10-30
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastESEQ for Windows Version 3.0
SEQ ID NO 55
LENGTH: 18
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ilarity 100.0%; Pred. No. 3.7e+03;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Synthetic oligonucleotide
Seguence 55, Application US/10435656 Publication No. US20050277604A1 GENERAL INFORMATION:
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                                                                                                                    APPLICANT: Krieg, Arthur M.
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Best Local Similarity
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RESULT 26

RESULT 24

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Gaps
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                                                           APPLICANT: Attuct, over, over,
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APPLICANT: Kline, Joel N.
APPLICANT: Kline, Joel N.
APPLICANT: Kline, Joel N.
APPLICANT: Klinean, Dennis
APPLICANT: Klinman, Dennis
APPLICANT: Klinman, Dennis
APPLICANT: Steinberg, Alfred D.
TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
CURRENT APPLICATION NUMBER: US/11/031,460
PRIOR FILING DATE: 2005-01-07
PRIOR PILING DATE: 1995-01-07
PRIOR APPLICATION NUMBER: US 08/276,358
PRIOR APPLICATION NUMBER: US 08/386,063
PRIOR PILING DATE: 1995-02-07
PRIOR FILING DATE: 1995-02-07
PRIOR FILING DATE: 1995-10-30
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.3%; Score 14; DB 11; Length 18; 100.0%; Pred. No. 3.7e+03; tive 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 0;
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Publication No. US20050277609A1
GENERAL INFORMATION:
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APPLICANT: Krieg, Arthur M.
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Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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Sublication No. US20050261225A1

Sublication No. US20050261225A1

GENERAL INFORMATION:

APPLICANT: Stein, CA.

APPLICANT: Stein, CA.

APPLICANT: Benimetskaya, Lyuba

APPLICANT: Benimetskaya, Lyuba

APPLICANT: Guzzo-Pernell, Nancy

TITLE OF INVENTION: PEPTIDES THAT COMPLEX WITH ANTISENSE OLIGONUCLEOTIDES WHICH DOWNR

TITLE OF INVENTION: PEC-PROTEIN EXPRESSION IN CELLS

FILE REPERENCE: 0575/6323

CURRENT PILING DATE: 2005-03-15

PRIOR PILING DATE: 2001-11-02

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin version 3.1

SEQ ID NO 6

LENGTH: 18
         Sequence 85, Application US/11127654

| Sequence 85, Application US/11127654
| Publication No. US20050250726A1
| GENERAL INFORMATION:
| APPLICANT: Berg, Daniel J. |
| TITLE OF INVENTION: INFLAMMATORY DISEASES |
| FILE REFERENCE: C1039.70060US01 |
| CURRENT APPLICATION NUMBER: US/11/127,654 |
| CURRENT FILING DATE: 2005-05-12 |
| PRIOR APPLICATION NUMBER: US 10/112,653 |
| PRIOR PILING DATE: 2002-03-29 |
| PRIOR PILING DATE: 2001-03-29 |
| PRIOR FILING DATE: 2001-03-29 |
| NUMBER OF SEQ ID NOS: 1040 |
| SEQ ID NO 85 |
| LENGTH: 18 |
| LENGTH
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Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels
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US-11-081-140-6
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US-11-134-918-55
; Sequence 55, Application US/11134918
; Publication No. US20050267064A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial sequence
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Best Local Similarity 100.
Matches 14; Conservative
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US-11-127-654-85
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Sequence 132, Application US/11099683
Sequence 132, Application US/11099683
Publication No. US20060019916A1
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur
APPLICANT: Vollmer, Jorg
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS FOR INDUCING IL-10 RESPONSES
FILE REFERENCE: C1037.70047US01
CURRENT APPLICATION NUMBER: US/11/099,683
CURRENT FILING DATE: 2005-04-04
PRIOR FILING DATE: 2004-04-02
NUMBER OF SEQ ID NOS: 143
SOFTWARE: Pacentin version 3.3
SEQ ID NO 132
LENGTH: 18
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APPLICANT: Papisov, Mikhail, I.

TITLE OF INVENTION: DRUG-CARRIER COMPLEXES AND METHODS OF

TITLE OF INVENTION: DRS THEREOF

FILE REFERENCE: 0838.1003-001

CURRENT PAPLICATION NUMBER: US/10/994,213

CURRENT PAPLICATION NUMBER: US/09/634,320

PRIOR PILING DATE: 2004-019

PRIOR FILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FASTESEQ for Windows Version 4.0

SEQ ID NO 8:

LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11; L 3.7e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Synthetic oligonucleotide
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S8.3%; Score 14; DB

Best Local Similarity 100.0%; Pred. No. 3.7

Matches 14; Conservative 0; Mismatches
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; OTHER INFORMATION: c indicates an RNA base US-10-994-213-8
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US-10-994-213-9/c
'Sequence 9, Application US/10994213
'Publication No. US20060019911A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/10994213; Publication No. US20060019911A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial sequence
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RESULT 32
US-11-099-683-132
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US-10-994-213-8
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APPLICANT: Krieg, Arthur
APPLICANT: Vollmer, Jorg
TITLE OF INVENTION: IMMUDATIONITATION NUCLEIC ACIDS FOR INDUCING IL-10 RESPONSES
TITLE OF INVENTION: IMMUDATION OF IL-10 RESPONSES
CURRENT APPLICATION NUMBER: US/11/099,683
CURRENT FILING DATE: 2005-04-04
PRIOR PILING DATE: 2004-04-02
NUMBER OF SEQ ID NOS: 143
SOFTWARE: Patentin version 3.3
SEQ ID NO 131
LENGTH: 18
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                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Krieg, Arthur M.
APPLICANT: Klinman, Dennis
APPLICANT: Klinman, Dennis
APPLICANT: Klinman, Dennis
APPLICANT: Steinberg, Alfred D.
TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
FILE REFERENCE: C1039/7048 (AMS)
CURRENT FILING DATE: 2005-02-25
PRIOR PILING DATE: 2005-02-25
PRIOR PLILING DATE: 1994-07-15
PRIOR PLILING DATE: 1994-07-15
PRIOR FILING DATE: 1995-02-07
PRIOR FILING DATE: 1995-02-07
PRIOR FILING DATE: 1995-02-07
PRIOR PLILING DATE: 1995-02-07
PRIOR PRILING DATE: 1995-02-07
PRIOR PRILING DATE: 1996-10-30
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 55
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100.0%; Pred. No. 3.7e+03;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Synthetic oligonucleotide US-11-067-587-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 131, Application US/11099683 Publication No. US20060019916A1 GENERAL INFORMATION:
                                                          US-11-067-587-55
; Sequence 55, Application US/11067587
; Publication No. US20060003955A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
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Matches 14; Conservative
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Gaps

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Page 11

**ArPLICANT: Shiler, Kvuzat

**TITLE OF INVENTION: Bloinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof;

**TITLE OF INVENTION: uses thereof;

**FILE REFERENCE: 06087.0200.CPUS01

**CURRENT APPLICATION NUMBER: US/10/310,914A

**CURRENT FILING DATE: 2002-12-06

**NUMBER OF SEQ ID NOS: 1388402

**SOFTWARE: PatentIn version 3.3

**SEQ ID NO 100840

**LENGTH: 22

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TITLE OF INVENTION: DRUG-CARRIER COMPLEXES AND METHODS OF
TITLE OF INVENTION: USE THEREOF
FILE REFERENCE: 0838.1003-001
CURRENT APPLICATION NUMBER: US/10/994,213
CURRENT FILING DATE: 2004-11-19
PRIOR APPLICATION NUMBER: US/09/634,320
PRIOR PLICATION NUMBER: US 60/147,919
PRIOR APPLICATION NUMBER: US 60/147,919
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
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; Sequence 2, Application US/10994213
; Publication No. US20060019911A1
; APPLICANT: Papisov, Mikhail, I.
; TITLE OF INVENTION: USE THEREOF
; TITLE OF INVENTION: USE THEREOF
; FILE REFERENCE: 0838.1003-001
; CURRENT APPLICATION NUMBER: US/10/994,213
; CURRENT PILING DATE: 2004-11-19
; PRIOR PILING DATE: 2000-08-09
; PRIOR FILING DATE: 1999-08-09
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 13
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Pred. No. 3.7e+03;
0; Mismatches 5;
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100.0%; Pred. No. 3.7e+03;
iive 0; Mismatches 0;
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milarity 77.3%; E
Conservative 0;
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Best Local Similarity
Then 17; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 38
US-10-994-213-2/c
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LENGTH: 23
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Sequence 81, Application US/11127654

Sequence 81, Application US/11127654

Sequence 81, Application US/11127654

Sequence 81, Application US/20050250126A1

GENERAL INFORMATION:

APPLICANT: Exercible No.

TITLE OF INVENTION: INFLAMMATORY DISEASES

FILE REFERENCE: C1039.70060US01

CURRENT APPLICATION NUMBER: US/11/127,654

CURRENT APPLICATION NUMBER: US/11/127,654

CURRENT FILING DATE: 2005-05-12

PRIOR APPLICATION NUMBER: US 10/112,653

PRIOR APPLICATION NUMBER: US 60/279,642

PRIOR PILING DATE: 2001-03-29

PRIOR PILING DATE: 2001-03-29

NUMBER OF SEQ ID NOS: 1040

SOFTWARE PatentIn version 3.2

SEQ ID NO 81

LENGTH: 20
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                                                                                                                                                                                                                                                  APPLICANT: Papisov, Mikhail, I.
TITLE OF INVENTION: DRUG-CARRIER COMPLEXES AND METHODS OF
TITLE OF INVENTION: URS THEREOF
FILE REFERENCE: 0318.1003-001
CURRENT APPLICATION NUMBER: US/10/994,213
CURRENT APPLICATION NUMBER: US/09/634,320
PRIOR PILING DATE: 2000-08-09
PRIOR FILING DATE: 2000-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1005-13
PRIOR FILING DATE: 1005-08-09
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FASTERO for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Synthetic Oligonucleotide FEATURE:
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US-11-127-654-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: c indicates an RNA base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-310-914A-100840/c
; Sequence 100840, Application US/10310914A
; Publication No. US20060003322A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 14; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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Sequence 46867, Application US/11121849
publication No. US20050272080A1
publication No. US200502
publication Numbers US/11/121,849
publication Numbers 1005-05-03
publication Numbers 60/567,949
publication Priling Date: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 46867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 46870, Application US/11121849
Sequence 46870, Application US/11121849
Sequence 46870, Application US/11121849
Sequence 46870, Application US/11121849
GENERAL INFORMATION:
GENERAL INFORMATION:
FILE REFRENCE: 3684.1
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: MUMBER: US/11/121,849
CURRENT FILING DATE: 2005-03.
SPRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SEQ ID NO 46870
LENGTH: 25
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; APPLICANT: Bentwich, Isaac; APPLICANT: Shiler, Kwuzat; APPLICANT: Shiler, Kwuzat; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                    22 GGGGTCAGGTGTGGGACATGGG 1
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Best Local Similarity 77.3
Matches 17; Conservative
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Best Local Similarity 77.3
Matches 17; Conservative
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CORGANISM: Homo sapien
US-11-121-849-46867
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ORGANISM: Homo sapien
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US-10-310-914A-1042200/c
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US-11-121-849-46870
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Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
FIGURAL SAPPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Kvuzat
TITLE OF INVENTION: USES thereof
FILE REFERENCE: 0600. CPUSO1
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT PILING PATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 903934, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION:
FILE REPRENCE: 06097.0200.CPUS01
TITLE OF INVENTION USES thereof
TITLE OF INVENTION USES TO COUCEUSO1
CURRENT PELICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 903934
LENGTH: 23
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100.0%; Pred. No. 3.7e+03;
tive 0; Mismatches 0;
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Pred. No. 3.7e+03;
                                                                                                              FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide
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  SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                           OTHER INFORMATION: t = amino modified T
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                                                                     TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 77.3
Matches 17; Conservative
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Best Local Similarity
Matches 14; Conservi
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US-10-310-914A-989919/c
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CRGANISM: Human
US-10-310-914A-989919
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; ORGANISM: Human
US-10-310-914A-903934
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LENGTH: 25
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                             SEQ ID NO 2
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Sequence 77551, Application US/10310914A
Publication No. US20060003322A1
Publication No. US2006000332A1
GENERAL INFORMATION:
APPLICANT: Bentwich. Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
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Publication No. US20060003322A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler
APPLI
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                                                                                                                                              Indels
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                                                                           57.5%; Score 13.8; DB 7; 88.2%; Pred. No. 4.5e+03;
                                                                                                                                              0; Mismatches
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; Publication No. US20050272080A1
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                                                                   Query Match
Best Local Similarity 88.2'
Matches 15, Conservative
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Best Local Similarity 88.2
Matches 15; Conservative
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              US-10-310-914A-906465
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APPLICANT: Benewich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: uS/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 906465
LENGTH: 18
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Sequence 19743, Application US/10939294A

Publication No. US20S0266417A1

GENERAL INPORMATION:
APPLICANT: Barany, Francis

APPLICANT: Turner, Daniel

APPLICANT: Pingle, Manesh

CURRENT PILING DATE: 2004-09-10

PRIOR APPLICATION NUMBER: US 60/502/731

PRIOR APPLICATION NUMBER: US 60/502/731

NUMBER OF SEQ ID NOS: 38895

SOFTWARE PATENTIN VERSION 3.3

SEQ ID NO 19743

LENGTH: 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 58.3%; Score 14; DB 7; 3
Best Local Similarity 77.3%; Pred. No. 3.7e+03;
Matches 17; Conservative 0; Mismatches 5
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06097.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 1042200
LENGTH: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: oligonucleotide probe US-10-939-294A-19743
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US-10-310-914A-906465/c
                                                                                                                                                                                                                                                                                                                                                       US-10-310-914A-1042200
                                                                                                                                                                                                                                                                                      TYPE: RNA
ORGANISM: Human
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ORGANISM: Human
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       TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded (TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded (TITLE OF INVENTION: Microarrays
TITLE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR PILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 330122
LENGTH: 25
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APPLICANT: MISSUO SATUCH
APPLICANT: Kazuyasu NAKAMURA
APPLICANT: Kazuyasu NAKAMURA
APPLICANT: Toyohide SUINKAWA
APPLICANT: Toyohide SUINKAWA
APPLICANT: Nobuo HANSAKI
APPLICANT: Nobuo HANAI
TITLE OF INNENTION: AMTIBODY COMPOSITION-PRODUCING CELL
FILE REFERENCE: 249-202
CURRENT FILING ANTE: 2005-05-18
PRIOR PLILING DATE: 2005-05-18
PRIOR PLILING DATE: 2002-08-30
PRIOR FILING DATE: 2002-06-30
PRIOR FILING DATE: 2000-10-06
PRIOR PLILING DATE: 2000-10-06
PRIOR PLILING DATE: 2000-10-06
PRIOR PLILING DATE: 2000-10-06
PRIOR PLILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR PLILING DATE: 2000-10-06
PRIOR PLILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PATENTIN VET: 2.1
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Pred. No. 4.4e+03;
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US-10-310-914A-222305
; Sequence 22305, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 88.2%;
Matches 15; Conservative
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Matches 15, Conservative
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ORGANISM: Homo sapien
US-11-121-849-330122
GENERAL INFORMATION
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US-11-131-212-40/c
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## APPLICANT: Bentwich, Isaac

### APPLICANT: Shiler, Kvuzat

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AX355389 Sequence
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AR05185 Sequence
AR053395 Sequence
AR178131 Sequence
AR178132 Sequence
AR178135 Sequence 43
I66589 Sequence 43
I66590 Sequence 43
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I6836 Sequence 43
                                                                                       February 15, 2006, 17:51:58; Search time 911.686 Seconds (without alignments) 2369.293 Million cell updates/sec
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               GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd
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VERSION AR088703.1 GI:10015467 KEYWORDS COURCE Unknown. ORGANISM Unknown. Unclassified. REFERENCE 1 (Dases 1 to 38) AUTHORS Nabel, G.Jan. TITLE Methods and compositions for treatment of diseases JOURNAL FRATURES Location/Qualifiers 1 .38 //organism="unknown" //mol_type="unassigned DNA"	Query Match 100.0%; Score 38; DB 6; Length 38; Best Local Similarity 100.0%; Pred; No. 2.3e-05; Anatches 38; O; Gaps 0; Qy 1 GGGGACTTTCCGCGGGACTTTCCAGGGGGACTTTCC 38	RESULT 2 AX103956 LOCUS LOCUS DEFINITION Sequence 148 from Patent W00122972. ACCESSION AX103956 VERSION AX103956 KEYWORDS SURCE SYNTHETIC CONSTRUCT	NISM synthetic other sequence other sequence in mannostin E Immunostin MAL Patent: WINVERSITY GmbH (DEI SES I ource	Owicin Query Match Query Match Best Local Similarity 100.0%; Score 38; DB 6; Length 38; Best Local Similarity 100.0%; Pred. No. 2.3e-05; Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy	RESULT 3 AX355389 LOCUS LOCUS AX355389 LOCUS DEFINITION Sequence 417 from Patent W00197843. ACCESSION AX355389. VERSION AX355389.1 GI:18620057 KEYWORDS SOURCE SOUR	ORGANISM Synthetic construct other sequences. REFERENCE 1 AUTHORS Weiner, G. and Hartmann, G. TITLE Methods for enhancing antibody-induced cell lysis and treating cancer JOURNAL Patent: WO 0197843-A 417 27-DEC-2001; UNIVERSITY OF IOWA RESPARCH FOUNDATION (US) FEATURES Location/Qualifiers
AR183803 Sequence AR368186 Sequence B10784 PCR primer I138420 Sequence 5 AR053668 Sequence CQ918211 Sequence AR364432 Sequence AR364432 Sequence AX51394 Sequence AX513945 Sequence AX5139583 Sequence AX5157675 Sequence AR157676 Sequence S69452 TCR V gamma B1268660 Isolation	A43615 Sequence 5 AA288379 Sequence AR289545 Sequence AR214693 Sequence AR214693 Sequence AR2147 Sequence CS120544 Sequence	AA219395 Sequence AX293963 Sequence BD266036 Universal AX289310 Sequence AX289310 Sequence AX279570 Sequence AX198167 Sequence AX198167 Sequence AX260321 Sequence AX260321 Sequence	CQ831062 Sequence 1182400 Sequence 48 AR001104 Sequence AR343272 Sequence AR439958 Sequence AR439958 Sequence AR609191 Sequence AR609191 Sequence AR078082 Sequence AR078082 Sequence AR078082 Sequence AR078082 Sequence AR287028 Sequence AR287028 Sequence	AAK01747 Sequence 132494 Human (clon 182405 Sequence 55 182405 Sequence 56 A83621 Sequence 50 AR206162 Sequence AX51612 Sequence AX516125 Sequence AX517555 Sequence 182396 Sequence	162397 Sequence 44 AX53890 Sequence AX538891 Sequence S80775 gamma delta AX291782 Sequence CQ008373 Sequence CQ008574 Sequence	linear PAT 07-SEP-2000
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RESULT 1
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Unknown...
Unclassified.

1 (bases 1 to 46)

Neininger, A.M.

Sequence-specific detection of nucleic acid hybrids using a Sequence-specific detection of nybrids from non-perfect hybrids
hybrids from non-perfect hybrids

Patent: US 5871902-A 28 16-FEB-1999;

Location/Qualifiers
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Unclassified.
1 (bases 1 to 39)
Frankel.A., Pabo,C., Barsoum,J.G., Fawell,S.E. and Pepinsky,R.Blake.
Tat-derived transport polypeptide conjugates
Patent: US 5747641-A 43 05-MAY-1998;
Location/Qualifiers
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94.1%; Pred. No. 0.028;
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Seguence 28 from patent US 5871902.
AR035456
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/organism="unknown"
/mol_type="unassigned DNA"
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Best Local Similarity 94.1
Matches 32; Conservative
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Weininger,S. and Weininger,A.M.
Weininger,S. and Weininger,A.M.
Sequence-specific detection of nucleic acid hybrids using a
DNA-binding molecule or assembly capable of discriminating perfect
hybrids from non-perfect hybrids
Patent: US 5871902-A 29 16-FEB-1999;
Location/Qualifiers
 1. .38
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide
/inote="Synthetic oligonucleotide
chimeric phosphorcthioate/phosphodiester backbone with
phosphorothioate at 5' and 3' ends"
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Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 38; Conservative 0; Mismatches 0; Indels
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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other sequences; artificial sequences.
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Sequence 148 from Patent WO02053141.
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El (bases 1 to 39)

(S Frankel, A., Pabo,C., Barsoum,J.G., Fawell,S.E. and Pepinsky, R. Blake.

Tat-derived transport polypeptides

Tat-derived transport polypeptides

Location/Qualifiers
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Frankel, A., Pabo, C., Barsoum, J.G., Fawell, S.E. and
Pepinsky, R lalake.
Tat-derived transport polypeptides
Patent: US 6316003-A 44 13-NOV-2001;
Location/Qualifiers
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78.9%; Score 30; DB 6; Length 39;
Best Local Similarity 86.8%; Pred. No. 0.061;
Matches 33; Conservative 0; Mismatches 5; Indels
                                                                                     Score 30; DB 6; Length 39;
Pred. No. 0.061;
0; Mismatches 5; Indels
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    .39
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Sequence 44 from patent US 6316003.
AR178132
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AR178131.1 GI:17921024
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                                                                                             Query Match 78.9%;
Best Local Similarity 86.8%;
Matches 33; Conservative
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Matches 33, Conservative
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Frankel, A., Pabo, C., Barsoum, J.G., Fawell, S.E. and Pepinsky, R. Blake. Tat-derived transport polypeptides and fusion proteins Patent: US 5804604-A 43 08-5EP-1998;
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Frankel, A., Pabo, C., Barsoum, J.G., Fawell, S.E. and
Pepinsky, R. Blake.
Tat-derived transport polypeptides and fusion proteins
Patent: US 8804604-A 44 08-SEP-1998;
Location/Qualifiers
                                                                                     M. Unclassified.

Unclassified.

I (bases 1 to 39)

S Frankel, A., Pabo, C., Barsoum, J.G., Fawell, S.E. and Pepinsky, R. Blake.

Tat-derived transport polypeptide conjugates

AL patent: US 5747641-A 44 05-MAY-1998;

Location/Qualifiers
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Pred. No. 0.061;
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Pred. No. 0.061;
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/mol_type="unassigned DNA"
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Sequence 43 from patent US 5804604.
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Frankel, A., Pabo, C., Barsoum, J.G., Fawell, S.E. and
Pepinsky, R. Blake.
Nucleic acid conjugates of tat-derived transport polypeptides
Patent: US 56706174 43 23-SEP-1997;
Location/Qualifiers
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1 (bases 1 to 39)
Frankel, A., Pabo, C., Barsoum, J.G., Fawell, S.E. and
Pepinsky, R.Blake.
Nucleic acid conjugates of tat-derived transport polypeptides
Patent: US 5670617-A 44 23-SEP-1997;
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Frankel, A., Pabo, C., Barsoum, J.G., Fawell, S.E. and Pepinsky, R.Blake.
Fusion protein comprising tat-derived transport moiety Patent: US 5674980-A 43 07-0CT-1997;
Location/Qualifiers
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Pred. No. 0.061;
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 44 from patent US 5670617.
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Sequence 43 from patent US 5674980.
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/organism="unknown"
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Best Local Similarity 86.8%;
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Nucleic acids encoding and methods of making tat-derived transport polypeptides

Patent: US 5652122-A 44 29-JUL-1997;
                                                                                                                                                               I (Dasses 1 to 39)
Frankel,A., Pabo,C., Barsoum,J.G., Fawell,S.E. and
Pepinsky,R.Blake.
Nuclearids encoding and methods of making tat-derived transport
polypeptides
Patent: US 5652122-A 43 29-JUL-1997;
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Sequence 43 from patent US 5652122.
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Sequence 44 from patent US 5652122.
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Sequence 43 from patent US 5670617.
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/organism="unknown"
/mol_type="unassigned DNA"
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/wol_type="unassigned DNA"
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I66589
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I58472/c
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Arntzen, C.J., Blake, M.E., Gutterman, J.U., Hoffmann, J.J.,
Jayatilake, G.S. and Bailey, D.T.

Triterpene compositions and methods for use thereof
Patent: US 6444233. A 9 03-SEP-2002;
Research Development Foundation; Carson City, NV
Location/Qualifiers
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Haridas,V. and Gutterman,J.U.
Triterpene compositions and methods for use thereof
Patent: US 668939-A 9 10-FEB-2004;
Research Development Foundation; Carson, NV
Location/Qualifiers
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          Score 29.8; DB 6;
Pred. No. 0.076;
0; Mismatches 2;
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AR473523
AR473523.1 GI:42711810
                                                                                                                                                                                      Sequence 9 from patent US 6444233. AR225344

    . .44
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          ch 78.4%;
.1 Similarity 93.9%;
31; Conservative (
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C12N5/04//
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PF 19-MAY-1999 JP 2000549243
PR 19-MAY-1998 US 60/085997,03-SEP-1998 US 60/099066 PI
CHARLES J ARNTZEN,MARY BLAKE TRACEY,JORDAN U GUTTERMAN,JOSEPH
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Arntzen,C.J., Tracey,M.B., Gutterman,J.U., Hoffmann,J.J.,
Bailey,D.T. and Jayatilake,G.S.
Triterpen compositions and methods for use thereof
Patent: JP 2002515430-A 9 28-MAY-2002;
RESEARCH DEVELOPMENT FOUNDATION
ON Artificial Sequence
PN JP 2002515430-A/9
PD 28-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description of Artificial Sequence:SYNTHETIC PRIMER Location/Qualifiers
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Fusion protein comprising tat-derived transport moiety Patent: US 5674980-A 44 07-0CT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism='Artificial Sequence'
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Pred. No. 0.061;
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38
                 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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synthetic construct
other sequences, artificial sequences.
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Sequence 44 from patent US 5674980.
168237
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/mol_type="unassigned DNA"
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BD261195.1 GI:33070965
JP 2002515430-A/9.
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Best Local Similarity 86.8%;
Matches 33; Conservative (
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Weininger, S. and Weininger, A.M.
Sequence-specific detection of nucleic acid hybrids using a
DNA-binding molecule or assembly capable of discriminating perfect
hybrids from non-perfect hybrids
Patent: US 5871902-A 23 16-FEB-1999;
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Weininger, A.M.
Weininger, S. and Weininger, A.M.
Sequence-specific detection of nucleic acid hybrids using a
DNA-binding molecule or assembly capable of discriminating perfect
hybrids from non-perfect hybrids
Patent: US 5871902-A 20 16-FEB-1999;
Location/Qualifiers
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hybrids from non-perfect hybrids
Patent: US 5871902-A 19 16-FEB-1999;
Location/Qualifiers
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    /mol_type="unassigned DNA"

    .45
    /organism="unknown"
    /mol_type="unassigned DNA"

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/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                         Sequence 23 from patent US 5871902.
AR035451
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Sequence 20 from patent US 5871902.
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                PAT 08-OCT-2004
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1 (bases 1 to 45)

weininger, S. and Weininger, A.M.
Sequence-specific detection of nucleic acid hybrids using a
BNA-binding molecule or assembly capable of discriminating perfect
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Aggarwal, B.B. and Darnay, B.G.
Tumor necrosis factor receptor-I-associated protein kinase and methods for its use
Patent: US 5856161-A 12 05-JAN-1999,
Location/Qualifiers
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Arnizen, C.J. and Gutterman, J.U.
Arniterpene compositions and methods for use thereof
Patent: US 6746696-A 9 08-JUN-2004;
Research Development Foundation; Carson City, NV
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                             Length 44;
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Pred. No. 0.076;
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Sequence 12 from patent US 5856161.
AR027239
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Sequence 19 from patent US 5871902.
AR035447
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                AR542759 44 bp
Sequence 9 from patent US 6746696.
AR542759
                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
                                                                                                                                                                                                                                                             /organism="unknown"
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1 Similarity 93.9%;
31; Conservative
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1 (bases 1 to 46)
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Neininger, A.M.
Sequence-specific detection of nucleic acid hybrids using a bNA-binding molecule or assembly capable of discriminating perfect hybrids from non-perfect hybrids
hybrids from non-perfect hybrids
Patent: US 5871902-A 27 16-FEB-1999;
Location/Qualifiers
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Georgopoulos, K.
Ikaros polypeptides
Patent: US 5824770-A 142 20-OCT-1998;
Location/Qualifiers
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AR049839
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Pred. No. 0.2;
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Sequence 142 from patent US 6228611.
AR149733 GI:15114324
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/organism="unknown"
/wol_type="unassigned DNA"
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Matches 30; Conservative 0
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    AR035455.1
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Weininger, S. and Weininger, A.M.
Sequence-specific detection of nucleic acid hybrids using a
Sequence-specific detection of nucleic acid hybrids using a
DNA-binding molecule or assembly capable of discriminating perfect
hybrids from non-perfect hybrids
Patent: US 5871902-A 21 16-FEB-1999;
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1 (bases 1 to 46)
Weininger,S. and Weininger,A.M.
Weininger,S. and weininger,A.M.
Squence-specific detection of nucleic acid hybrids using a
DNA-binding molecule or assembly capable of discriminating perfect
hybrids from non-perfect hybrids
Patent: US 5871902-A 22 16-FEB-1999;
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Sequence 21 from patent US 5871902.
AR035449
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/organism="unknown"
/mol_type="unassigned DNA"
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/mol_type="unassigned DNA"
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Sequence 27 from patent US 5871902.
AR035455
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Sequence 22 from patent US 5871902.
AR035450. GI:5952118
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AR035450
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AR035449
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BD081630 33 bp DNA linear PAT 27-AUG-2002 Inhibition of human immunodeficiency virus (HIV-1) replication. BD081630
           PAT 18-DEC-2003
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Tsichlis P.N.
Tpl2 transgenic knockout mice
Patent: US 6660906-A 11 09-DEC-2003;
Thomas Jefferson University; Philadelphia, PA;
                                                                                                                                                                                              Thomas Jefferson University; Philadelphia, PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     other sequences, artificial sequences.
1 (bases 1 to 33)
Suhadolnik,R.J., Adelson,M.E. and Iacono,K.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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0.44;
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                                                                                                                Unclassified.
1 (bases 1 to 32)
Tsichlis,P.N.
Tpl2 transgenic knockout mice
Patent: US 6660906-A 9 09-DEC-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AR438118 32 bp
Sequence 11 from patent US 6660906.
AR438118 GI:40204580
            AR438116 32 bp
Sequence 9 from patent US 6660906.
AR438116
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    .32
    /organism="unknown"
    /mol_type="genomic DNA"

    .32
    /organism="unknown"
    /mol_type="genomic DNA"

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                                                         AR438116.1 GI:40204578
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synthetic construct
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Unclassified.
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AR438118
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BD081630
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Weininger,S. and Weininger,A.M.
Sequence-specific detection of nucleic acid hybrids using a
Sequence-specific detection of segments of discriminating perfect
hybrids from non-perfect hybrids
Patent: US 5871902-A 38 16-FEB-1999;
Location/Qualifiers
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1 (Dases 1 to 36)
Georgopoulos, K.
Isolated antibody that binds to an Ikaros polypeptide
                          75.8%; Score 28.8; DB 6; Length 36; 93.8%; Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 36;
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The General Hospital Corporation; Boston,
Location/Qualifiers
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                                                                                                        GGGACTTTCCGCTGGGGACTTTCCAGGGAGGC 35
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                                                                                       2 GGGACTTTCCGCTGGGGACTTTCCAGGGGGAC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 75.8%; Score 28.8; Di Similarity 93.8%; Pred. No. 0.2; 30; Conservative 0; Mismatches
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Seguence 142 from patent US 6630141.
AR404853
                                                         0; Mismatches
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/wol_type="unassigned DNA"
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Sequence 38 from patent US 5871902.
AR035466
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                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="unknown"
/mol_type="mRNA"
                                                                                                                                                                                                                                         AR404853.1 GI:40153580
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Best Local Similarity 96.7%;
Matches 29; Conservative
                                          Best Local Similarity 93.8
Matches 30; Conservative
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Best Local S:
Matches 30
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AR404853
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                  Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                 Hominidae; Homo.

1 (bases 1 to 35)
Fujihara,S.M. and Audler,S.G.
Intracellular targeted delivery of compounds by 70 kD heat shock Patent: JP 2002530426-A 1 17-SEP-2002;
BRISTOL WRERS SQUIBE CO
OS Homo sapiens (human)
PN JP 2002530426-A/1
PD 17-SEP-2002
PR 17-NOV-1999 JP 2000583940
PR 24-NOV-1999 US 60/109872
PI SHERI M FUJIHARA,STEVEN G NADLER
                                                                                                                                                                                                                                                                                                 A61P19/02,
pc A61P29/00,A61P29/00,A61P35/00,C12N15/09,A61K37/02,C12N15/00
Intracellular targeted delivery of compounds by 70 kD heat CC shock protein
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Fujihara, S.M. and Nadler, S.G.
Intracellular targeted delivery of compounds by 70 kD heat shock
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/organism='Homo sapiens (human)'.
Location/Qualifiers
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Bristol-Myers Squibb Company; Princeton,
Location/Qualifiers
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Sequence 4 from patent US 6730302.
AR532727
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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    .35
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    /mol_type="genomic DNA"

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Homo sapiens (human)
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Best Local Similarity 100..
Best Local Similarity
Local Similarity
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Intracellular targeted delivery of compounds by 70 kD heat shock
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PC
C12N1/15,C12N1/19,C12N1/21,C12N5/10//A61K35/76,C12N15/00,C12N5/ PC
              Patent: JP 2001520017-A 4 30-OCT-2001;
TEMPLE UNIVERSITY OF THE COMMONWEALTH SYSTEM OF HIGHER EDUCATION OS Artificial Sequence
DN JP 2001520017-A/4
DD 30-OCT-2001
PF 15-OCT-1998 JP 2000516047
PR 16-OCT-1997 US 60/061984
PR 16-OCT-1997 US CURADOLNIK, MARTIN E ADELSON, KATHRYN T IACONO PC CI2N15/09, A61K31/513, A61K45/00, A61K45/06, A61K48/00, A61P31/18, PC
Inhibition of human immunodeficiency virus (HIV-1) replication
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                                                                                                                                                                                                                                                Description of Artificial Sequence: sense probe
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/organism='Artificial Sequence'
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.7%; Score 28; DB 6; Length 33; 100.0%; Pred. No. 0.44; 1ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                  corresponding to NF-kappa beta binding site
Key

    .33
    forganism="synthetic construct"
|mol_type="genomic DNA"
|db_xref="taxon:32630"

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/organism="unknown"
/wol_type="unassigned DNA"
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ACTIVITION OF NF-kB PRECURSOR
Patent: WO 8908147-A 2 08-SEP-1989;
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Sequence 2 from Patent WO 8908147.
109458.1 GI:587836
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BD249738
BD249738.1 GI:33059508
JP 2002530426-A/1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28; Conservative
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CC correspondin
FH Key
FT source
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BD249738
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PAT 29-SEP-1999
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weininger, 8. and weininger, A.M.
Weininger, 6. and weininger, A.M.
Sequence-specific detection of nucleic acid hybrids using a
DNA-binding molecule or assembly capable of discriminating perfect
hybrids from non-perfect hybrids
Patent: US 5871902-A 24 16-FEB-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM Unknown.

Unclassified.

18 (bases 1 to 35)

RS Catania, A.P. and Lipton, J.M.

Antimicrobial and anti-inflammatory peptides for use in human immunodeficiency virus

NAL Patent: US 660344.A 6 12-OCT-2004;

Zengen, Inc.; Woodland Hills, CA

Location/Qualifiers
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                                                                                                                                                                                                                      Gaps
                                                                            1. .35
/organism="synthetic construct"
/organism=unassigned DNA"
/db zref="taxon:32630"
/noTe="Oligonucleotide probe for NF-KB (antisense)"
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Lipton, J. and Catania, A.
A uro-genital condition treatment system
Patent: Ep 1433485-A 10 30-JUN-2004;
Zengen, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                   DNA
                                                                                                                                                                                    Score 27.4; DB Pred. No. 0.8; 0; Mismatches
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Pred. No. 0.8;
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/mol_type="unassigned DNA"
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Sequence 24 from patent US 5871902.
AR035452
                                                                                                                                                                                                                                                                                                                                                            Sequence 6 from patent US 6803044.
                                                                                                                                                                                                                                                     1 GGGGACTITCCGCTGGGGACTITCCAGGG 29
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                                                                                                                                                                                         Query Match 72.1%;
Best Local Similarity 96.6%;
Matches 28; Conservative C
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Best Local Similarity 96.6%;
Matches 28; Conservative
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AR589386/c
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TITLE
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wheninger, S. and Weininger, A.M.
Sequence-specific detection of nucleic acid hybrids using a
BNA-binding molecule or assembly capable of discriminating perfect
hybrids from non-perfect hybrids
Patent: US 5871902-A 26 16-FEB-1999;
Location/Qualifiers
    PAT 08-OCT-2003
                                                                                                                                         van Lint,C., Burny,A., Quivy,V. and Adam,E.
Method for obtaining the elimination of integrated and functional
viruses from infected mammal cells
Patent: WO 03053468-A 2 03-JUL-2003;
UNIVERSITE LIBRE DE BRUXELLES (BE)
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Pred. No. 0.67;
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      linear
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                                                                                                                                                                                                                                                                                                          /note="mutagenic oligonucleotide primer"
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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      DNA
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synthetic construct
other sequences; artificial sequences.
                                                                                                                  other sequences; artificial sequences.
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Sequence 26 from patent US 5871902.
AR035454 GI:5952122
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/mol_type="unassigned DNA"
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Sequence 10 from Patent EP1433485.
CQ846479
    AX798846 42 bp
Agguence 2 from Patent W003053468.
AX798846.1 GI:37604920
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1 Similarity 88.2%;
30; Conservative (
                                                                                    synthetic construct
synthetic construct
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Best Local Similarity
Matches 30; Conservat
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CQ846479/c
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AR035454
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TITLE
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PAT 18-DEC-2003
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Catania, A.P. and Lipton, J.M.
Antimicrobial and anti-inflammatory peptides for use in human immunodeficiency virus
Patent: US 6803044-A 5 12-OCT-2004;
Zengen, Inc.; Woodland Hills, CA
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                                                                                                                                                                                                                                                                                                           Length 35;
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                                                                                                                                            1 (bases 1 to 35)
Lipton,J.M. and Catania,A.P.
Uro-genital condition treatment system
Patent: US 6800291-A 9 05-OCT-2004;
Zengen, Inc.; Woodland Hills, CA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                        / Match 69.5%; Score 26.4; DB Local Similarity 96.4%; Pred. No. 2.1; nes 27; Conservative 0; Mismatches
                        35 bp
Sequence 9 from patent US 6800291.
AR585153
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Sequence 5 from patent US 6803044.
ARS89385.1 GI:56636661
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Sequence 5 from patent US 6617171.
AR397504
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    .35
    /organism="unknown"
    /mol_type="genomic DNA"

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/organism="unknown"
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Faustman, D.L. and Hayashi, T.
                                                                     AR585153.1 GI:56628768
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Unclassified.
                                                                                                                Unknown.
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Best Local Similarity
                                                                                               Unknown.
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AR397504
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                                                                                                                                                                                                                                                                                              1 (bases 1 to 44)
Weininger,S. and Weininger,A.M.
Sequence-specific detection of nucleic acid hybrids using a
Sequence-specific detection of specific acid hybrids molecule or assembly capable of discriminating perfect
hybrids from non-perfect hybrids
Patent: US 5871902-A 25 16-FEB-1999;
                                           Gaps
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/mol type="unassigned DNA"
/mol type="unassigned DNA"
/mole: taxon:38630"
/noFe="Oligonucleotide probe for NP-kB (sense)"
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             Score 27.4; DB 6; Length 44;
Pred. No. 0.81;
0; Mismatches 6; Indels
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                                                                                                                                                                            linear
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Pred. No. 0.99;
0; Mismatches 3;
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A uro-genital condition treatment system
Patent: EP 1433485-A 9 30-JUN-2004;
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synthetic construct
other sequences; artificial sequences.
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/mol_type="unassigned DNA"
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Sequence 25 from patent US 5871902.
AR035453
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Sequence 9 from Patent BP1433485.
CQ846478
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Location/Qualifiers
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90.6%;
               Query Match 72.1%;
Best Local Similarity 83.8%;
Matches 31; Conservative
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Unclassified.
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Matches 29; Conserv
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Matches 27; Conserv
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SM Unknown.

Unclassfied.

SE 1 (bases 1 to 32)

RS Faustman, D.L. and Hayashi, T.

R Faustman, D.L. and Hayashi, T.

Mathods for diagnosing and treating autoimmune disease

NAL Patent: US 6773705-A 1 10-AUG-2004;

General Hospital Corporation; Boston, MA

AES 1.032

/organism="unknown"
/mol_type="genomic DNA"
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Methods for diagnosing and treating autoimmune disease
Patent: US 6617171-A 5 09-SEP-2003;
The General Hospital Corporation; Boston, MA
Location/Qualifiers
1. 32
/organism="unknown"
/mol_type="genomic DNA"
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Sequence 1 from patent US 6773705.
AR575406.1 GI:56576396
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Search completed: February 15, 2006, 18:55:57 Job time : 924.686 secs

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Aad26648 NF-kB wil
Aad30599 Target bi
Aad30603 Target bi
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Aad300136 EMSA prob
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Aad300136 EMSA prob
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Aad30615 Probe nuc
Aad30610 Target bi
Aad3060 HIV enhan
Aad30610 Target bi
Aad4335 NF-kappaB
Aad64353 Human NF
Aad44353 Human NF
Aad64060 Oligonuci
Aad64060 Oligonuci
Abd11310 Nucleocid
Abx15610 NF-kappa
Abx16405 NF-kappa
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Ado40441 NF-kappaB
Aeb34893 Oligonucl
Aaq73476 NF KB tra
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ABX15510
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                   GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 300 summaries
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ABS77664
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ACD99455
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ADB36525
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AAT30609
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AAT88239
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Aat34424 Primer fo Abk64866 Fat regul Adv62240 FeLV pl5E Aat35082 Human int Aac87820 Zymogen a Adx68360 Hymy glyc Adx68360 Hymy glyc Aby75580 Sm protei Aal29909 Human S-H Ac46973 Human S-H Ac469595 Human S-H Ac469595 Human mic Abz43774 Human car Abz43774 Human car Abz43773 Human car Abz43774 Human car Abz43774 Human leu Abz43774 Human leu Abz43774 Human leu Abz4977 Hyman mic Abz65028 Hywan mic Abz65028 Hywan mic Abz65029 Hywan mic Abz65037 Human mic Abz65048 Human mic Abz4207 NoVX olig Abz65048 Human mic Ady83010 Primer #4 Abz4217 Human NDU Abz50114 Human Str Add93717 Human Str Add93717 Human Str Add93717 Human Str Adx63622 Human Str Adx63623 Human Str Adx63623 Human Str Adx63624 Human Str Adx63624 Human Str Adx63622 Human Str Adx63622 Human Str Adx65608 Origonucl Adf18224 DNA-bindi Adf18224 DNA-bindi Adf18224 DNA-bindi Ad44624 GS3A prom Aaz665085 Human HiA	Abg(4752 Oligonuci Abg(1752 Oligonuci Abg(1793 Oligonuci Abg(1786 Oligonuci Abg(12616 Oligonuci Abg(1265 Oligonuci Abg(12657 Oligonuci Adz(159 Human bia Adz(1159 Human bia Adz(1159 Human sin Adz(1159 Human sin Adz(1159 Human sin Adz(1169 Human sin Adz(1169 Human sin Adz(1169 Human sin Adz(1169 Human coly Adz(1169 Human CD2 Adz(1169 Hu
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4.4.3.3.3.3.3.3.3.3.3.3.3.3.3.3.3.3.3.3	

09-FEB-2000 (first entry)

Abba4489 TRIM adap Abs60719 Human DNA Abs43358 Human N-m Abz48698 Human N-m Aaf67676 Chicken i Aaf67676 Chicken i Aaf63534 aveC muta Aas00545 S. avermi Adg3558 Streptomy Abz02656 Human leu Abz02656 Human leu

Human mic Human mic Human mic Human pol Hepatitis TRIM adap Human DNA

Aav06347 Phosphati Aaz36082 Forward P

Ack19133 H Ack19148 H Aci55943 H Abs70875 Add28731 Knock-dow Abd82499 SpoIIB ge Abk87827 Interleuk Ady51614 Transcrip Aaf74484 Clone 179

Adc98706 Double-st Abt08597 Human nov Ado09962 Human NOV

24 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	ABS70875 AAH24489 AABS60719 ABS60719 ABS61358 ABZ48698 AAF61334 AAF61334 AAG08558 AAG00443 AAG00443 AAG00443 AAG02656 AAF74484 AAF74484 AAF74484 AAF78765	10000000000000000000000000000000000000	111083 2011083 2011083 2011083 2011083 2011083 2011083
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ALIGNMENTS

AAZ32919 standard; DNA; 38 BP

AAZ32919

AAZ32919 ID AAZ3 XX AC AAZ3 XX

RESULT 1

Adv07518 Human BAC Aa132219 Human SNP Aa134540 Human SNP Adt01206 Novel mut

Intronic

Aaz25681 Transcrip Adp48377 NF-kappaB

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This sequence represents the kappa-B-PT sequence (SEQ ID 2) which contains three immunoglobulin kappa-B sequences (AAZ12918) which are contains three immunoglobulin kappa-B sequences (AAZ12918) which are bound by activated NF-kappa-B (nuclear factor kappa-B). It can inhibit NF-kappa-B inhibit NF-kappa-B binding to endogenous kappa-B enhancer/promoter elements, thus inhibiting transcription of genes that comprise such elements. NF-kappa-B confiderentiation or activation. For example, the human promyclotic leukaemia cell line (HL-60 cells) can be induced to differentiate into monocytoid cells with concomitant expression of the leukocyte adhesion of the HL-60 cells with this sequence with sportially binds NF-kappa-B. In contrast, use of a mutant kappa-B-PT sequence (AAZ12920) had no effect on differentiation and adhesion. Compositions containing the kappa-B-PT sequence may be used for the treatment of immune and inflammatory diseases, cancer and viral infections. In particular it can be used to treat heumatorid arthritis, ischaemia/intepring noise noise and HIV, crom's disease, ulcerative colitis, psoriasis, transplant rejection, Crohn's disease, ulcerative colitis, psoriasis, element of HIV, entry, respectively on inflammatory and the herpes virus infections and reaction to poison ivy, poison oak and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Composition useful for the treatment of immune and inflammatory diseases,
                                                            Kappa-B-PT sequence, NF-kappa-B; nuclear factor kappa B; adhesion; differentiation; phosphorothioate; treatment; immune disorder; inflammatory disease; cancer; viral infection; immuneglobulin kappa B sequence; rheumatoid arthritis; ischaemia; reperfusion injury; restenosis; transplant rejection; Crohn's disease; ulcarative colitis; psoriasis; glomerulonephritis; leukaemia; malanoma; sarcoma; lymphoma; HIV; HTLV; herpes virus; poison ivy; poison oak;
                                                                                                                                                                                                                                                                                                                     /mod_base= OTHER
/note= "Optionally phosphorothioate linkages"
                                 Kappa-B-PT sequence (SEQ ID 2), used to inhibit NF-kappa-B.
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/bound_moiety= "NF-kappa-B"
29. .38
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/bound_moiety= "NF-kappa-B"
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/bound moiety= "NF-kappa-B"
16. .25
                                                                                                                                                                                                                                                                  Location/Qualifiers
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modified_base
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                                                                                                                                                                                                                                  Synthetic
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Abk89815 Human Kalabk1345 Dry 1993 SI primer Aat51923 Mycobacte Aat61522 Mycobacte Aat6164794 Primer S2 Aat6164794 Primer S2 Aat61657 Proposite Aav18912 Aval PCR Aav18912 Aval PCR Aav18912 Aval PCR Aav2493 Composite Aac6161 Novel Str Aac65184 Novel Str Aac6518694 SDA prime Able4131 Mycobacte Acf67180 M. tuberc Adf11059 Mtb DNA PAG65185 Novel Inc Adn04902 Composite Abb85235 Protein a

RESULT 3

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                                                                                                                                                                                                                                                                                                                                                    Vaccine, cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic; immunostimulatory; tumour; viral infection; bacterial infection; fungal infection; parasitic infection; cancer; asthma; infectious disease; allergy; immune deficiency; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.
                                      Gaps
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DB 3; Length 38;
                                      0; Indels
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                                                                         1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38
                                                                                              GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38
 100.0%; Score 38; DB 3; 100.0%; Pred. No. 2e-05;
                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                     Immunostimulatory nucleic acid #139.
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27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
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                                                                                                                                                                                                       AAF99023 standard; DNA; 38
                                                                                                                                                                                                                                                                              (first entry)
                                      38; Conservative
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Query Match
Best Local Similarity
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Best Local Si
Matches 38,
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                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.
                                                                                                                                        Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth; tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
                                                                                                                                                                           diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound granulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
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100.0%; Pred. No. 2e-05;
trive 0; Mismatches 0
                                                                                                          Angiogenesis inhibitory oligonucleotide #148.
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 BP.
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ABS77664 standard; DNA; 38
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                                   ABS77664;
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Treating and/or preventing allergy or asthma using an immunostimulatory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                            Treating non-allergic inflammatory diseases, such as psoriasis, eczu allergic contact dermatitis, latex dermatitis or inflammatory bowel disease by administering an immunostimulatory nucleic acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ds; allergy; asthma; poly-G nucleic acid; aerosol formulation; hypo-responsive subject; immunostimulatory.
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; Pred. No. 2e-05;
0; Mismatches 0; Indels
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                                                                                 29-MAR-2002; 2002US-00112653
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PETERSEN D
                                                                                                                                                                                                                                   Krieg AM, Berg DJ;
                                                                                                                                                                 KRIE/) KRIEG A M. (BERG/) BERG D J.
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(PETE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOUR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADB36525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of cell surface antigens and antibodies. The methods are useful for treating or preventing cancer auth as basal cell carcinoma, bladder cancer, brain and central nervous system (CNS) cancer, breast cancer, brain and central nervous system (CNS) cancer, breast cancer, cosphageal cancer, colon and rectum cancer, connective tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian cancer, prostete cancer, rhabdomyosarcoma, skin cancer, testicular cancer, rhabdomyosarcoma, skin cancer, testicular cancer, and uterine cancer. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to methods for treating or preventing cancer, involving administering to a subject having or at risk of developing cancer immunostimulatory nucleic acids that induce expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treating or preventing cancer, such as basal cell carcinoma, comprises administering immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies to a subject having or at risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunostimulatory; antiinflammatory; dermatological; antipsoriatic; antiulcer; gene therapy; vaccine; non-allergic inflammatory disease; psoriasis; eczema; allergic contactidermatitis; latex dermatitis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                   Antibody-induced cell lysis; cancer; immunostimulatory; CD20; angiogenesis; metastasis; cytostatic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 38; DB 6; Length 38; 100.0%; Pred. No. 2e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 38 BP; 4 A; 10 C; 14 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GGGGACTITCCGCTGGGGACTITCCAGGGGACTITCC 38
                                         Immunostimulatory nucleic acid SEQ ID NO: 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 201; 312pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunostimulatory nucleic acid #141.
                                                                                                                                                                                                                                                                                                                       22-JUN-2000; 2000US-0213346P
                                                                                                                                                                                                                                                                             22-JUN-2001; 2001WO-US020154
                                                                                                                                                                                                                                                                                                                                                               (IOWA ) UNIV IOWA RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACD99455 standard; DNA; 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
nes 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           Hartmann G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-154611/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               developing cancer.
                                                                                                                                                                                         WO200197843-A2
    16-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-SEP-2003
                                                                                                                                                                                                                                     27-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                           Weiner G,
                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACD99455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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ACD99455
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Gaps

.. 0

Indels

Mismatches

100.0%; S. ilarity 100.0%; P. Conservative 0;

Target binding region #29.

19-FEB-1997

Score 38; DB 13; Length 38; Pred. No. 2e-05;

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Target binding assembly, nucleic acid recognition unit; NF-kappa-B; SP1; ATAR, human papillomavirus; HPV; HPV B2; human immunodeficiency virus; HIV LTR, Tat binding unit; probe; assembly sequence; asymmetry sequence; nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;
         Seguence 38 BP; 4 A; 10 C; 14 G; 10 T; 0 U; 0 Other;
                                                                                                                                                            AAT30609 standard; DNA; 43
                                Query Match
Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                  AAT30609;
                                                                                                                                      RESULT 8
                                                                                                                                                  AAT30609
X S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Suppressing allergies, including asthma, rhinitis, urticaria and atopic dermatitis, in a subject, comprises administering a first and second dose of an immunostimulatory nucleic acid.
                                          The invention relates to a method of treating or preventing allergy or asthma which comprises administering to a subject a poly-G nucleic acid in an aerosol formulation. The methods and compositions of the present invention are useful for diagnosing and/or treating asthma and allergy especially in a hypo-responsive subject. The present sequence represents an immunostimulatory nucleic acid of the invention.
nucleic acid alone or in combination with an asthma/allergy medicament
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                  ss; antiasthmatic; antiallergic; dermatological; antiinflammatory; antibacterial; virucide; immunoglobulin E antagonist; allergy; immunostimulator; asthma; rhinitis; urticaria; dermatitis; bacterial infection; viral infection.
                                                                                                                                                                      .;
0
                                                                                                                                               100.0%; Score 38; DB 9; Length 38; 100.0%; Pred. No. 2e-05; ive 0; Mismatches 0; Indels
                                                                                                                          Sequence 38 BP; 4 A; 10 C; 14 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                             1 GGGGACTITCCGCTGGGGACTITCCAGGGGGACTITCC 38
                                                                                                                                                                                                                    1 GGGGACTITCCGCTGGGGACTITCCAGGGGGACTITCC 38
                                                                                                                                                                                                                                                                                                                                               Allergic response suppressor oligonucleotide #148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 148; 235pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fouron Y;
                     Disclosure; Page 7; 221pp; English
                                                                                                                                                                                                                                                                             ADU89464 standard; DNA; 38 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-APR-2004; 2004US-00831778.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-FEB-2000; 2000US-0179991P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Petersen DM,
                                                                                                                                                                                                                                                                                                                        10-FEB-2005 (first entry)
                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 38, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BETE/) BRATZLER R L. (PETE/) PETERSEN D M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-833006/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PETE/) PETERSEN (FOUR/) FOURON Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2004235774-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bratzler RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-NOV-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                   ADU89464;
                                                                                                                                                                                                                                                     RESULT 7
                                                                                                                                                                                                                                                                  ADU89464
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95WO-US015944. 94US-00353476

07-DEC-1995; 39-DEC-1994;

13-JUN-1996

WO9617956-A2

virus; ss. Synthetic. Weininger S, Weininger AM;

WPI; 1996-287199/29.

(GENE-) GENE POOL INC

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Probe nucleic acids, target binding assemblies, etc - for detection and localisation of specific nucleic acid sequences, esp. HIV and HPV.
                                                                                                                                                                                                                                                                                     HPV, and other nucleic acid containing systems, including bacteria and
                                                                                                                                                                                                                                                                                                                        Seguence 43 BP; 6 A; 12 C; 15 G; 10 T; 0 U; 0 Other;
                                  Disclosure, Page 73; 172pp; English.
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The invention relates to a method of suppressing a symptom of an allergic response in a subject by administering a first and second dose of an immunostimulatory nucleic acid that comprises a nucleotide sequence comprising 5'-cg-3', and where the second dose is administered from 1 day present invention are useful for the treatment or prevention of asthma and allergy, including rhinitis, urricaria and atopic dermatitis, using an immunostimulatory nucleic acid alone or in combination with other medicaments. They can also be used in preventing bacterial and viral infections. This sequence represents an oligonucleotide used in the method of the invention.

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AAT30581-T30614 represent target binding regions (TBR) of a probe of the invention. The probe of the invention contains a TBR, a booster binding convention. The probe of the invention contains a TBR, a booster binding assembly (TBA) recognised by the probe, contains at least one binding assembly (TBA) recognised by the probe, contains at least one conclete acid recognition unit (NAR), and optionally a linker sequence, an assembly sequence (see AAR95999+R95999), an asymmetry sequence (see AAR95999-R96006), a nuclear localisation signal sequence (see AAR95007), and an OSA. The assembly sequence and asymmetry sequence (see AAR95993-R96006), and an OSA. The assembly sequence and asymmetry sequence sare responsible for the folding and association of the NAR9. TATA, human papillomavirus (HPV) E2, HPV LTR, human immunodeficiency virus (HIV) LTR and Tat binding units. The linker sequence is an oligopeptide, which does not interfere with NAR function, but provides stability and control over the spacing of the NAR from the rest of the TBA. The OSA is an attached support or indicator, or other means of localisation of the probe. The probe can be used in a method for detecting or localising a specific target nucleic acid sequence (TNA). The method is highly sensitive, and has a high contein and other nucleic acid containing systems, including bacteria and
                                       ö
                                                                                                                                                                                                                                                                                                                                                            Target binding assembly, nucleic acid recognition unit; NP-kappa-B; SP1; TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus; HIV LTR; that binding unit; probe; assembly sequence; asymmetry sequence; nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probe nucleic acids, target binding assemblies, etc - for detection and localisation of specific nucleic acid sequences, esp. HIV and HPV.
                                       Gaps
                                       ö
81.1%; Score 30.8; DB 2; Length 43; 94.1%; Pred. No. 0.015;
                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 46 BP; 7 A; 10 C; 20 G; 9 T; 0 U; 0 Other;
       3;
0.015;
2;
                                                                             1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACT 34
                   Pred. No. 0.01
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 73; 172pp; English.
                                                                                                                                                                                                             BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95WO-US015944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94US-00353476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Weininger AM;
                                                                                                                                                                                                             AAT30608 standard; DNA; 46
                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                            Target binding region #28.
                                       32, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENE-) GENE POOL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-287199/29.
                 Best Local Similarity
Matches 32, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Weininger S,
                                                                                                                                                                                                                                                                                        19-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9617956-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                virus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                  AAT30608;
   Query Match
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The sequences given in AAQ58049-50 form a double stranded DNA molecule which was used as the cargo moiety in the conjugate of the invention. This oligonuclectide fragment was linked to a peptide fragment of the HIV tat protein which was used as transport moieties. These conjugates are used as cargo molecules for the efficient cytoplasmic and nuclear delivery of biologically active non-tat proteins, nucleic acids and other molecules which are not inherently capable of entering a target cell. The tat basic region amino acid sequence carries cargo molecules by covalent attachment. The reduced size of the transport peptides minimises attachment. The reduced size of the transport peptides minimises with the biological activity of the cargo molecule. By virtue of the absence of the cysteine-rich region (residues 22-36) of the tat protein, problems of genurious trans- activation and disliphide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transport of cargo moieties into cells - using genetic fusions of chemical conjugates comprising a portion of HIV tat protein as transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aggrégation are solved. The reduced transport peptide size also enhances uptake efficiency. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                  HIV; tat; transport; moiety; conjugate; cargo molecule;
cytoplasmic delivery; nuclear delivery; cysteine-rich region;
transactivation; disulphide aggregation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 30; DB 2; Length 39;
Pred. No. 0.03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 39 BP; 4 A; 11 C; 14 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGGGACTITCCGCTGGGGACTITCCAGGGGGACTITCC 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 geogacirriccecreeceaciririccaceeceacriric 38
35
                               6 eeegactrirccecreeegactrirccaeegaeeer 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 21; Page 116; 153pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               93WO-US007833.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 78.9%;
Local Similarity 86.8%;
hes 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ58050 standard; DNA; 39
                                                                                                                        AAQ58049 standard; DNA; 39
                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barsoum JG, Fawell SE,
                                                                                                                                                                                           (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1994-083202/10.
                                                                                                                                                                                                                                                 Oligonucleotide NF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BIOJ ) BIOGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                          WO9404686-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-AUG-1993;
                                                                                                                                                                                           25-MAR-2003
                                                                                                                                                                                                            23-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                              03-MAR-1994.
                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                            AAQ58049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ58050/
ID AAQ5
XX
                                                                                     RESULT 10
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                                                                                                        AAQ58049
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Gaps

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Query Match 79.5%; Score 30.2; DB 2; Length 46; Best Local Similarity 91.4%; Pred. No. 0.026; Matches 32; Conservative 0; Mismatches 3; Indels

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This double-stranded DNA sequence, comprising oligonucleotides NF1 (sense strand) and NF2 (antisense strand), corresponds to the wild-type NF kappa B binding site. It was used in the preparation of transport polypetide. DNA conjugates. Such conjugates, in which modified HIV tat protein is used as transport polypetide, can be used to deliver cargo molecules to cells in vivo or in vitro. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                           New DNA constructs for transporting molecules to cells - encode a fusion protein comprising a modified HIV tat protein and a carboxy-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chemical conjugate; transport polypeptide; tat protein; nucleic acid; delivery; cytoplasm; cell nucleus; therapy; prophylaxis; diagnosis; spurious transactivation; HIV-1; disulphide aggregation; NF-kappaB; transcription; NF2; human immunodeficiency virus type 1; transcriptional activation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.9%; Score 30; DB 2; Length 39; 86.8%; Pred. No. 0.03; 1ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 39 BP; 4 A; 11 C; 14 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NF-kappaB transcriptional activation inhibitor NF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGGACTTTCCGCTGGGGACTTTCCACGGGGGACTTTC 38
                                                                                                                                                                                                                                                                                                                                                      Fawell SE,
                                                                                                                                                                                                                                                                                             (UYJO ) UNIV JOHNS HOPKINS SCHOOL OF MEDICINE (WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                      Pabo C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 17; Col 97; 76pp; English.
                                                                                                                                                                91US-00636662.
92US-00934375.
93WO-US007833.
                                                                                                            95US-00450257
                                                                                                                                              89US-00454450
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                                                                                                                                                                                                                                           94US-00235403
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                                                                                                                                                                                                                                                                                                                                                      Pepinsky RB, Barsoum JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 Similarity 86.8 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-392943/36
                                                                                                                                                                                                                                                                            BIOJ ) BIOGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cargo moiety.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAY-1995;
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                                                                                                            25-MAY-1995;
                                                                                                                                                                  32-JAN-1991;
                                                                                                                                                                                                       19-AUG-1993;
                                                                                                                                                                                                                      24-NOV-1993;
                                                                                                                                                                                                                                           28-APR-1994;
                                  US5652122-A
                                                                                                                                                21-DEC-1989;
                                                                                                                                                                                 21-AUG-1992;
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20-JAN-1998
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                                                                       29-JUL-1997
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Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT88240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT88240/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequences given in AAQS8049-50 form a double stranded DNA molecule which was used as the cargo molety in the conjugate of the invention. This oligonucleotide fragment was linked to a peptide fragment of the HIV tat protein which was used as transport moleties. These conjugates are used as cargo molecules for the efficient cytoplasmic and nuclear delivery of biologically active non-tat proteins, nucleic acids and other molecules which are not inherently capable of entering a target cell. The tat basic region amino acid sequence carries cargo molecules by covalent attachment. The reduced size of the transport peptides minimises interference with the biological activity of the cargo molecule. By virtue of the absence of the cysteine-rich region (residues 22-36) of the aggregation are solved. The reduced transport peptide size also enhances uptake efficiency. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transport of cargo moieties into cells - using genetic fusions of chemical conjugates comprising a portion of HIV tat protein as transport peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                             cargo molecule;
cysteine-rich region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30; DB 2; Length 39; Pred. No. 0.03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 39 BP; 10 A; 14 C; 11 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIV; tat protein; transport protein; cargo delivery; NF-kappa B binding site; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGGACTITCCGCTGGGGACTITCCAGGGGGACTITCC 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 dedeactrirecerrededeactrirecaededeactrire 2
                                                                                                                           HIV; tat; transport; moiety; conjugate; carg
cytoplasmic delivery; nuclear delivery; cyst
transactivation; disulphide aggregation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             Pepinsky RB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 21; Page 116; 153pp; English.
                                                                                                                                                                                                                                                                                                                 93WO-US007833
                                                                                                                                                                                                                                                                                                                                                      92US-00934375
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                                                      (first entry)
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 86.8 es 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NF-kappa B binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                           Barsoum JG, Fawell SE,
                                    (revised)
                                                                                        Oligonucleotide NF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1994-083202/10
                                                                                                                                                                                                                                                                                                                                                                                      (BIOJ ) BIOGEN INC
                                                                                                                                                                                                                                       WO9404686-A1
                                                                                                                                                                                                                                                                                                                                                      21-AUG-1992;
                                25-MAR-2003
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16-DEC-1997
                                                    23-SEP-1994
                                                                                                                                                                                                                                                                            03-MAR-1994
                                                                                                                                                                                                       Synthetic
AAQ58050;
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Frankel A;

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Homo sapiens.
            Synthetic
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(WHED ) I
(UYJO ) I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                 polypeptide moiety consisting of at least residues 49-57 of human immunosed informative interventing of at least residues 49-57 of human immunosed interventy virus (HIV) tat protein, but not residues 22-36 and 73-86, and a cargo moiety comprising a single or double stranded nucleic acid, e.g. the present sequence. The conjugate can be used to deliver cargo moieties into the cytoplasm and nuclei of cells for therapeutic, prophylactic and diagnostic applications. In an example conjugates to inhibit transcriptional activation by NF-kappaB were prepared, the corresponding to the wild type NF-KB binding site, while NF2 for a duplex corresponding to the wild type NF-KB binding site. Traut modified NF1 was annealed with NP2, and Traut modified NF3 annealed with his manaled with bismaleimidohexane activated tat 32-72. The products were tested as in Science 250, 997-1000 (1990) for inhibition of protein is readily taken up into cells and the cell nucleus. The reduced transport polypeptides minimises interference with the protein is readily taken up into cells and the cell nucleus. The reduced belongical activity of the cargo molecule. In addition, by virtue of the benefit of the transport polypeptides minimises interference with the cargo molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                     Conjugate for intracellular delivery - comprising transport moiety having amino acids 49-57 of human immunodeficiency virus tat protein and nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptides solve the potential problems of spurious transactivation and disulphide aggregation. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chemical conjugate; transport polypeptide; tat protein; nucleic acid; delivery; cytoplasm; cell nucleus; therapy; prophylaxis; diagnosis; spurious transactivation; HIV-1; disulphide aggregation; NF-kappaB; thihibition; NR1; human immunodeficiency virus type 1; transcriptional activation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                               Pabo C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 30; DB 2; Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 39 BP; 10 A; 14 C; 11 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NF-kappaB transcriptional activation inhibitor NF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38
                                                                                                                                                                 Frankel A, Pepinsky RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ggggacrirccgcrggggacrirccacggggacrirc 2
                                                                                                                                     (UYJO ) UNIV JOHNS HOPKINS SCHOOL OF MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  iisulphide aggregation. (Updated on 25-MAR-20
(Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 0.03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                       WHITEHEAD INST BIOMEDICAL RES
                                                                                                                                                                                                                                                                             Claim 3; Col 97-98; 77pp; English
           89US-00454450.
91US-00636662.
92US-00934375.
93WO-US007833.
93US-00158015.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT88239 standard; DNA; 39 BP
                                                                                94US-00235403
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                                                                                                                                                               Fawell SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
                                                                                                                                                                                           WPI; 1997-479523/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                   acid cargo moiety.
                                                                                                           BIOGEN
                                                                                                                                                                  Barsoum JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
20-JAN-1998
                                                                                28-APR-1994;
              21-DEC-1989;
02-JAN-1991;
                                                        19-AUG-1993
24-NOV-1993
                                         21-AUG-1992
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                                                                                                          (BIOJ )
(WHED )
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11D AATE
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An onvel covalently linked chemical conjugate, comprises a transport polypeptide moiety consisting of at least residues 49-57 of human conjugated moiety desired that protein, but not residues 22-36 and 73-68, and a cargo moiety comprising a single or double stranded nucleic set the present sequence. The conjugate can be used to deliver cargo moieties into the cytoplasm and nuclei of cells for therapeutic, prophylactic and diagnostic applications. In an example conjugates to inhibit transcriptional activation by NF-kappaB were prepared, the colligonucleotides used were NF1-4 (AAFB8239-42). NF1 and NF2 for a duplex corresponding to the wild type NF-KB binding site, while NF2 and NF4 form a duplex corresponding to a muteant MF-KB binding site, while NF2 and NF4 form a duplex corresponding to a muteant MF-KB binding site. Traut modified NF1 was annealed with NF2, and Traut modified NF3 annealed with NF4. The DNA was the reacted with bismalemidohexane activated tat 32-72. The products were tested as in Science 250, 997-1000 (1990) for inhibition of products were tested as in Science 250, 997-1000 (1990) for inhibition of products were transport polypeptides minimises interference with the correction is readily taken up into cells and the cell nucleus. The reduced size of the transport polypeptides minimises interference with the absence of the cysteine rich region of the HIV tat protein, the virtue of the cargo molecule. In addition, by virtue of the call bid e agreedation of Updated on 25-MRA-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conjugate for intracellular delivery - comprising transport moiety having amino acids 49-57 of human immunodeficiency virus tat protein and nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGGGACTITCCGCTGGGGACTITCCAGGGGGACTITCC 38
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UNIV JOHNS HOPKINS SCHOOL OF MEDICINE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.9%; Score 30; DB 2; 86.8%; Pred. No. 0.03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Col 97-98; 77pp; English.
                                                                                                                                                                                                            89US-00454450.
91US-00636662.
92US-00934375.
93WO-US007833.
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94US-00235403
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hes 33; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acid cargo moiety.
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24-NOV-1993;
28-APR-1994;
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US5670617-A
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                                                                    23-SEP-1997
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This oligonuclectide primer is used with AAR89779 to form a duplex corresponding to the wild type transcription factor NP-kappaB binding site which is used in the construction of a transport polypeptide-DNA conjugate. This conjugate is used in a novel method for delivery of biologically active cargo molecules into the cytoplasm and nuclei of eukaryotic cells. The tat protein from immunodeficiency virus (e.g. HIV-L. SIV) is readily taken up into cells when present e.g. taracellularly and can be modified to covalently link to cargo proteins cryblems of spurious trans-activation and disulphide aggregation. These transport polypeptides also minimise interference with the biological activity of the cargo molecule. This is applicable for therapeutic, prophylactic or diagnostic intracellular delivery of small molecules and macromolecules e.g. proteins, nucleic acids and polysaccharides. (Updated on 25-MAR-2003 to correct
                                                                          Human Immunodeficiency Virus; HIV Type 1; Tat protein; cargo molecule; intracellular delivery; fusion protein; therapeutic; prophylactic; diagnostic; transport polypeptide; E2 repressor protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fusion proteins containing truncated HIV tat sequences - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 30; DB 2; Length 39;
Pred. No. 0.03;
0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                intracellular delivery of viral repressor proteins.
                                         Transcription factor NF-kappaB oligonucleotide NF2
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93US-00158015.
94US-00235403.
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92US-00934375.
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(first entry)
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Matches 33; Conservative
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FAWELL S E.
PEPINSKY R B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BARSOUM J G.
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24-NOV-1993;
28-APR-1994;
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                                                                                                                                                                                                                                                                                           25-MAY-1995;
20-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                            21-AUG-1992
                                                                                                                                                                 Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAN/)
FAWE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BARS/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV56615
    8 X X X E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This oligonucleotide primer is used with AAT89780 to form a duplex corresponding to the wild type transcription factor NP-kappaB binding site which is used in the construction of a transport polypeptide-DNA conjugate. This conjugate is used in a novel method for delivery of biologically active cargo molecules into the cytoplasm and nuclei of eukarypotic cells. The tat protein from immunodeficiency virus (e.g. HIV-1, HIV-2, SIV) is readily taken up into cells when present extracellularly and can be modified to covalently link to cargo proteins cransport polypeptides also minimise interference with the biological cransport polypeptides also minimise interference with the biological activity of the cargo molecule. This is applicable for therapeutic, prophylactic or diagnostic intracellular delivery of small molecules and macromolecules e.g. proteins, nucleic acids and polysaccharides. (Updated on 25-MAR-2003 to correct
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                                                                              Human Immunodeficiency Virus, HIV Type 1, Tat protein, cargo molecule, intracellular delivery; fusion protein; therapeutic; prophylactic; diagnostic; transport polypeptide; E2 repressor protein; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fusion proteins containing truncated HIV tat sequences - useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 39 BP; 4 A; 11 C; 14 G; 10 T; 0 U; 0 Other;
                                         Franscription factor NF-kappaB oligonucleotide NF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGGGACTITCCGCTGGGGACTITCCAGGGGGACTITCC 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   intracellular delivery of viral repressor proteins
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                                                                                                                                                                                                                                                                                                                                                 91US-00636662.
92US-00934375.
93WO-US007833.
93US-00158015.
94US-00235403.
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20-MAR-1998 (first entry)
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es 33; Conservative
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FAWELL S E.
PEPINSKY R B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-502388/46.
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24-NOV-1993;
28-APR-1994;
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21-AUG-1992;
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                                                                                                                                                                 Synthetic.
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(FRAN/) (FAWE/)

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Gaps

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RESULT 16
AAT89780/C
ID AAT89
XX
AC AAT89
XX
DT 25-MA

Matches

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This sequence is a phosphorothioate primer used in a method for the delivery of biologically active cargo molecules into the cytoplasm and mucle of cells, for therapeutic, prophylactic or diagnostic purposes.

This is accomplished by the presence of a small, basic section of the tat transport protein from human immunodeficiency virus (HIV) Type I. This is cused as it is this protein which is observed to cause human cells in culture to take up HIV. The method involves the use of a cargo moiety in combination with a transport moiety usually in the form of a fusion combination with a transport moiety usually in the form of a fusion cretains its biological activity after delivery into a target cell and where the transport moiety is one of following HIV tat protein fragments (a) as 47-58, (b) as 47-72, (c) 38-72, (d) as 38-58, (e) as 37-58, (f) as 37-58, (e) as 37-58, (e) as 38-52. The proteins allow delivery of specific peptides into cells at high concentrations due to use of existing transporters. Previous methods of delivery include bombardment and transforming, which only allow a fraction of the cell population to be infected and can additionally damage cells as they cause physical combination contents of the cell population to be infected and can additionally damage cells as they cause physical contents and transforming of the cell walls/membranes to allow entry. (Updated on 25-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIV tat-derived transport fusion proteins - used to deliver biological active molecules e.g. peptide(s) or nucleic acids, specifically into cytoplasm or nuclei of cells.
                                                                                                              TAT protein; cargo molecule; therapy; diagnosis; transport protein; fusion protein; human papillomavirus E2 repressor; target cell; phosphorothioate; primer; ss.
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                                                                        NF-kappaB binding site phosphorothioate primer NF2.
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Pred. No. 0.03;
0; Mismatches
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93US-00158015.
94US-00235403.
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91US-00636662.
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86.8%;
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                            (first entry)
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les 33; Conservative
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     (revised)
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25-MAR-2003
24-NOV-1998
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                                                                                                                                                                                                                                                                         US5804604-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence is a phosphorothioate primer used in a method for the delivery of biologically active cargo molecules into the cytoplasm and nuclei of cells, for therapeutic, prophylactic or diagnostic purposes. This is accomplished by the presence of a small, basic section of the tat transport protein from human immunodeficiency virus (HIV) Type I. This is used as it is this protein which is observed to cause human cells in culture to take up HIV. The method involves the use of a cargo moiety in combination with a transport moiety usually in the form of a fusion or protein. The cargo moiety is a human papillomavirus B2 repressor that retains its biological activity after delivery into a target cell and where the transport moiety is one of following HIV tat protein fragments of a a 47-58, (b) aa 47-72, (c) 38-72, (d) aa 38-58, (e) aa 37-58, (f) aa 57-58, (c) 38-72, (d) aa 38-58, (e) aa 37-58, (f) acception proteins allow delivery of specific peptides into cells at high concentrations due to use of existing transporters. Previous methods of delivery include bombardment conditionally damage cells as they cause physical cell walls/membranes to allow entry. (Updated on 25-MAR-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIV tat-derived transport fusion proteins - used to deliver biological active molecules e.g. peptide(s) or nucleic acids, specifically into cytoplasm or nuclei of cells.
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                                                                                            TAT protein; cargo molecule; therapy; diagnosis; transport protein; fusion protein; human papillomavirus E2 repressor; target cell; phosphorothioate; primer; ss.
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                                                      NF-kappaB binding site phosphorothioate primer NF1.
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(WHED ) WHITEHEAD INST BIOMEDICAL RES.
(UYJO ) UNIV JOHNS HOPKINS SCHOOL OF MEDICINE.
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94US-00235403
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     24-NOV-1998 (first entry)
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19-AUG-1993;
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Frankel A;

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Gaps

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AAD26647 standard; DNA; 39 BP

AAD26647;

SXS

AAV56616

SXXX

AAV56616/c

RESULT 18

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DB 2; Length 39; 5; Indels

Query Match

Matches

us-09-669-187a-148.szlm50.rng

AAD26648 standard; DNA; 39 BP

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AAD26648/C
            The invention relates to a method for delivering a biologically active cargo molecule of interest into a cell. The method comprises presenting to the cell an extracellular fusion protein or a covalently linked conjugate consisting of a cargo moiety and a transport moiety having amino acids 49-57 of human immunodeficiency virus (HIV) transactivator (tat) protein and lacking amino acids 22-36 and 73-86 of HIV tat protein. The method is useful for delivering a molecule of interest such as polypeptides, antigen, monoclonal antibody, single- or double-stranded conclet acid, a therapeutic, prophylactic and diagnostic molecule to a cell in vitro or in vivo. The method delivers proteins or peptides, including regulatory factors, enzymes, drugs or toxins into the cytoplasm and cell nucleus. The method is useful for diagnostic, prophylactic or therapeutic intracellular delivery of small and macro molecules. The present sequence is a phosphorothiate oligonucleotide used for generating nuclear factor kappa B (NFRB) wild type binding site used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                         Delivering biologically active cargo molecules such as polypeptides, nucleic acids into cells by using transport polypeptides which comprise human immunodeficiency virus transactivator protein linked to cargo
                                                       Human immunodeficiency virus, HIV-1; tat; therapeutic; toxin; enzyme; regulatory factor; prophylactic; extracellular fusion protein; drug; NFkB; nuclear factor kappa B; phosphorothioate backbone; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                NF-kB wild type binding site generating NF1 phosphorothioate oligo.
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                                                                                                                                                                             /note= "Phosphorothioate backbone"
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(UYJO ) UNIV JOHNS HOPKINS SCHOOL MED]
(BIOJ ) BIOGEN INC.
                                                                                                                           Location/Qualifiers
1. .39
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                                                                                                                                                                  OTHER
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92US-00934375.
93WO-US007833.
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            26-MAR-2002 (first entry)
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modified_base
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21-AUG-1992;
19-AUG-1993;
                                                                                                      Unidentified
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The invention relates to a method for delivering a biologically active cargo molecule of interest into a cell. The method comprises presenting to the cell an extracellular fusion protein or a covalently linked conjugate consisting of a cargo molety and a transport molety having amino acids 49-57 of human immunodeficiency virus (HIV) transactivator (tat) protein and lacking amino acids 22-36 and 73-86 of HIV tat protein. The method is useful for delivering a molecule of interest such as polypeptides, antigen, monoclonal antibody, single- or double-stranded cucleic acid, a therapeutic, prophylactic and diagnostic molecule to a cell in vitro or in vivo. The method delivers proteins or peptides, including regulatory factors, enzymes, drugs or toxins into the cytoplasm and cell nucleus. The method is useful for diagnostic, prophylactic or therapeutic intracellular delivery of small and macro molecules. The therapeutic intracellular delivery of small and macro molecules. The present sequence is a phosphorothiate oligonucleotide used for generating nuclear factor kappa B (NFRB) wild type binding site used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            which comprise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                            Human immunodeficiency virus; HIV-1; tat; therapeutic; toxin; enzyme regulatory factor; prophylactic; extracellular fusion protein; drug; NFkB; nuclear factor kappa B; phosphorothioate backbone; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Delivering biologically active cargo molecules such as polypeptides, nucleic acids into cells by using transport polypeptides which comprhuman immunodeficiency virus transactivator protein linked to cargo
                                                                                                                             NF-kB wild type binding site generating NF2 phosphorothioate oligo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 30; DB 6; Length 39;
Pred. No. 0.03;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 39 BP; 10 A; 14 C; 11 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GGGGACTITCCGCTGGGGACTITCCAGGGGGACTITCC 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fawell SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (WHED ) WHITEHEAD INST BIOMEDICAL RES. (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE. (BIOJ ) BIOGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 17; Col 97; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barsoum JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .39
/*tag= a
/mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91US-00636662.
92US-00934375.
93WO-US007833.
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Best Local Similarity 86.8%;
Matches 33; Conservative
                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-088872/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 modified base
                                                                                                                                                                                                                                                                                                                                   Unidentified
                                                              26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US6316003-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-APR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Frankel A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               molecules.
AAD26648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
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상 음 셤

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NFkappaB; antiinflammatory; antiarteriosclerotic; antirheumatic; antiarthritic; osteopathic; antiparkinsonian; nootropic; monoterpene; neuroprotective; antiparkinsonian. Barrette seophagitis; osteoarthritis; inflammatory bowel disease; chronic pancreatitis; chronic prostatitis; familial polyposis; actinic keracosis; rheumatoid arthritis; multiple sclerosis; Parkinson's disease; Alzheimer's disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inhibiting inflammation used for treating e.g. osteoarthritis and multiple sclerosis comprises administering monoterpene composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 28; Page 349; 349pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inhibiting nuclear factor kappaB.
                                                      ABL61552 standard; DNA; 44 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-NOV-2000; 2000US-0249710P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-NOV-2001; 2001WO-US043286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (RERE-) RES DEV FOUND.
                                                                                                                                                                                                                              HIV-LTR NFkappaB DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-557793/59.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified base
                                                                                                                                                                       20-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JUL-2002
                                                                                                                    ABL61552;
RESULT 22
                              ABL61552
                                                             8XCCCCCCCCCCCCX8XX1111X8X1X8X11X8X1X8X111111X8X8XXX11111X8X8X8X8X1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a mixture comprising one or more triterpene glycosides isolated from Acacia victoriae. The composition is used for the treatment of cancer, inhibiting the initiation and promotion of mammalian epithelial cells (such as skin, colon, uterine, ovarian, pancreatic, prostate, renal, lung, bladder or breast cells), for preventing the abnormal profileration of mammalian epithelial cells (such as crypt or colon cells), and/or regulating angiogenesis. The triterpene glycosides may also be used as solvent, an antioxidant, antifungal or antiviral agent, piscicide, molluscicides, contraceptive, antihelmintic, angiogenesis regulator, UV-protectant, expectorant, diuretic, anti-inflammatory agent, regulator of cholesterol metabolism, cardiovascular effecter, anti-ulcer agent, analgesic, sedative, immunomodulator, combating the effects of aging, increasing skin collagen, enhancing penile function and improving cognition and memory. The present sequence represents an integral and int
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mixture containing triterpene glycosides, useful for treating variety of
                                                                                                                                                                                                                                                                                                                                                                                                         Triterpene glycoside; antitumor; cytotoxic; antioxidant; contraceptive; antihelmintic; expectorant; diuretic; anti-inflammatory; cardiant; anti-inflammatory; cardiant; anti-inflammatory; cardiant; vantiuleer; analgesic; sedative; immunomodulator; antipyretic; cancer; vasotropic; Acacia victoriae; angiogenesis; antifungal; cholesterol; cardiovascular effecter; HIV; NF-kappaB; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and improving cognition and memory. The present sequence repre
32P-labelled NP-kappaB oligo from HIV long terminal repeat use
electrophoretic mobility shift assay. (Updated on 15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bailey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 29.8; DB 3; Length 44; Pred. No. 0.037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gutterman JU, Hoffmann JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 44 BP; 7 A; 9 C; 16 G; 12 T; 0 U; 0 Other;
      39 GGGGACTTTCCGCTGGGGACTTTCCACGGGGGACTTTC 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 27; Page 199; 312pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                     HIV LTR NF-kB oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US011041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0085997P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0099066P
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                                                                                                                                                  AAZ48474 standard; DNA; 44
                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tracey MB,
                                                                                                                                                                                                                                                                   (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (RERE-) RES DEV FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-105567/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arntzen CJ, T
Jayatilake GS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09959578-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-SEP-1998;
                                                                                                                                                                                                                                                                                                  28-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumor cells.
                                                                                                                                                                                                                                                                15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-NOV-1999
                                                                                                                                                                                                         AAZ48474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                           RESULT 21
                                                                                                                    AAZ4847
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/mod_base= OTHER /note= "32P labelled"

/*tag= a /mod_base= OTHER

Location/Qualifiers

(first entry)

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This sequence represents a novel method for inhibiting inflammation which comprises administering a monoterpene composition that inhibits NFKappaB. The products of the invention have antiinflammatory,
                                                                                           antiparkingolerotic, antirhemmatic, antiarthrilic, osteopathic, antiparkingonian, nootropic, neuroprotective and antiparkingonian activity. The method described can be used for treating inflammatory diseases, particularly premalignant inflammatory disease (e.g. Barretts esophagitis, inflammatory bowel disease, chronic pancreatitis, chronic prostatitis, familial polyposis and actinic keratosis), artherosclerosis, rheumatoid arthritis, osteoarthritis, multiple sclerosis, Parkinson's disease and Alzheimer's disease. This sequence represents a 32P-labelled NFkappaB Oligonicleotide used in an electrophoretic mobility shift assay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                   detect the biological characteristics of active triterpenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 6; Length 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 44 BP; 7 A; 9 C; 16 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GGGACTTTCCGCTGGGGACTTTCCAGGGGGACT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 gegactriccecregegactriccaegeaeger 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.4%; Score 29.8;
93.9%; Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 93.9%;
les 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 23
AAT30599
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Gaps ö

Indels

5

0; Mismatches

ilarity 93.9%; Conservative

Local Similarity see 31; Conserv

Best Loca Matches

34

GGGACTTTCCGCTGGGGACTTTCCAGGGAGGCT 42

GGGACTTTCCGCTGGGGACTTTCCAGGGGGACT

Target binding assembly, nucleic acid recognition unit; NF-kappa-B; SPl; ATAR; human papillomavirus; HPV; HPV E2; human immunodeficiency virus; HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence; nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;

19-FEB-1997 (first entry)

Farget binding region #23.

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AAT30581-T30614 represent target binding regions (TBR) of a probe of the invention. The probe of the invention contains a TBR, a booster binding region (BBR), and an optional support or attachment (OSA). The target binding assembly (TBA) recognised by the probe, contains at least one nucleic acid recognition unit (NAR) and optionally a linker sequence, an assembly sequence (see AAR$95994-R$998), an asymmetry sequence (see AAR$95994-R$989), an asymmetry sequence (see AAR$95994-R$9893) are association of the NARs. The NARS (see AAR$96007), and an OSA. The assembly sequence and asymmetry sequence (see Cor the folding and association of the NARs. The NARS (see AAR$96007).

Cor the folding and association of the NARs. The NARS (see AAR$96007).

Cor the folding and association of the NARs. The NARS (see AAR$96007).

Cor the Linker sequence is an oligopetide, which does not interfere with NAR function, but provides stability and control over the spacing of the TBA. The OSA is an attached support or indicator, or other means of localisation of the probe. The probe can be used in a method for detecting or localising a specific target nucleic acid sequences, including those found in human calls, in HIV, HIV, and other nucleic acid containing systems, including bacteria and
                                                                                                                                                     Target binding assembly, nucleic acid recognition unit; NF-kappa-B; SPI; TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus; HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence; nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe nucleic acids, target binding assemblies, etc - for detection and localisation of specific nucleic acid sequences, esp. HIV and HPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 45 BP; 7 A; 12 C; 16 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 70; 172pp; English.
BP
                                                                                                                                                                                                                                                                                                                                                                                               95WO-US015944.
                                                                                                                                                                                                                                                                                                                                                                                                                                      94US-00353476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Weininger AM;
AAT30599 standard; DNA; 45
                                                                            (first entry)
                                                                                                                 Target binding region #19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENE-) GENE POOL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-287199/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Weininger S,
                                                                                                                                                                                                                                                                                                                  WO9617956-A2
                                                                                                                                                                                                                                                                                                                                                                                             07-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                      09-DEC-1994;
                                                                          19-FEB-1997
                                                                                                                                                                                                                                                                                                                                                     13-JUN-1996
                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                        virus; ss
                                     AAT30599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  viruses
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Probe nucleic acids, target binding assemblies, etc - for detection and localisation of specific nucleic acid sequences, esp. HIV and HPV.

95WO-US015944. 94US-00353476.

WO9617956-A2

Synthetic. virus; ss.

13-JUN-1996

Weininger S, Weininger AM;

WPI; 1996-287199/29.

GENE-) GENE POOL INC.

09-DEC-1994; 07-DEC-1995;

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ANTIOSBI-T30614 represent target binding regions (TBR) of a probe of the invention. The probe of the invention contains a TBR, a booster binding cregion (BBR), and an optional support or attachment (OSA). The target binding assembly (TBA) recognised by the probe, contains at least one nucleic acid recognition unit (NAR), and optionally a linker sequence, an assembly sequence (see AARS95994-R95998), an asymmetry sequence (see AARS9599-R96006), a nuclear localisation signal sequence (see AARS96007), and an OSA. The assembly sequence and asymmetry sequence (see AARS9599-R96006), an association of the NARS. The NARS (see AARS96007), and an OSA. The association of the NARS. The NARS (see AARS9605-CR95993) are selected from NF-Kappa B, SPI, TATA, human papillomavirus (HPV) E2, HPV LTR, human immunodeficiency virus (HIV) LTR and Tat binding cuits. The linker sequence is an oligopeptide, which does not interfere with NAR function, but provides stability and control over the spacing of the NAR from the rest of the TBA. The OSA is an attached support or indiactor, or other means of localisation of the probe. The probe can be used in a method for detecting or localisation a specific target nucleic acid sequence (TNA). The method is highly sensitive, and has a high edgree of specificity. The method can be used for detecting and edgree of specificity. The method can be used for detecting and edgree of specificity. The method can be used for detecting and edgree of specificity. The method can be used for detecting and edgree of specificity. The method can be used for detecting and edgree of specificity. The method can be used for detecting and edgree of specificity. The method can be used for detecting and edgree of specificity in HIV, and other nucleic acid containing systems, including bacteria and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 76.8%; Score 29.2; DB 2; Length 45; 1. Similarity 91.2%; Pred. No. 0.064; 31; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 45 BP; 8 A; 11 C; 16 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGACTTTCCGCTGGGGACTTTCCAGGGAGGCGT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GGGACTITCCGCTGGGGACTITCCAGGGGGACTT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Page 71, 172pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX28079 standard; DNA; 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
(first entry)
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Matches 31; Conserv
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10-JUN-1999
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SAXARE
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Gaps

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Score 29.2; DB 2 Pred. No. 0.064; 0; Mismatches

76.8%; 91.2%;

31; Conservative

Local Similarity

Best Loca Matches

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Query Match

2 GGGACTITCCGCTGGGGACTITCCAGGGGGACTT 35 GGGACTTTCCGCTGGGGACTTTCCAGGGAGGCGT 40

AAT30603 standard; DNA; 45 BP

RESULT 24
AAT30603
ID AAT30
XX
AC AAT30

AAT30603

DB 2; Length 45; Indels

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The invention relates to a method for inhibiting the proliferation of, and inducing apoptosis in multiple myeloma cells comprising and inducing apoptosis in multiple myeloma cells comprising cadministration of curcumin (diferuloylmethane). The invention also relates to a method for increasing the cytotoxic effects of a chemotherapeutic agent (e.g., vincristine, bichloroethylnitrosourea, chemotherapeutic agent (e.g., vincristine, prediisone or dexamethasone) against multiple myeloma cells (preferably CD138+ plasma cells) comprises administration of the chemotherapeutic agent against increases the cytotoxic effects of the chemotherapeutic agent against increases the cytotoxic effects of the chemotherapeutic agent against cultiple myeloma cells. It suppresses constitutive I-kappa-B-alpha phosphorylation through inhibition of I-kappa-B kinase activity, and compression of proliferation and arrest of cells at the GI/S phase of the call cycle. The methods of the invention are used for the treatment of multiple myeloma. The present sequence represents an NF-kappa-B binding call cycle. The methods of the invention are used for the treatment of multiple myeloma. The present sequence represents an NF-kappa-B binding call an example of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 osteopathic; osteogenesis; nuclear factor kappa B; cancer; breast tumor; myeloma; osteoporosis; Paget's disease; rheumatoid arthritis; head and neck tumor; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMSA probe for detecting NF-kappaB activation in curcumin treated cells.
                                                                                                                                                                                                                                            Inhibiting proliferation of multiple myeloma cells comprises administering curcumin and optionally with vincristine, bichloroethylnitrosourea, melphalan, cyclophosphamide, adriamycin, predmisone or dexamethasone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 45 BP; 7 A; 9 C; 17 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.8%; Score 29.2; DB 12; 91.2%; Pred. No. 0.064; ive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 gegacirirceecreegaacirirceagagagaa 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GGGACTTTCCGCTGGGGACTTTCCAGGGGGACTT
                                                                                                                                                                                                                                                                                                                                                                          Example 3; SEQ ID NO 4; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADZ00136 standard; DNA; 45 BP
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24-JUN-2003; 2003WO-US019837
                                               24-JUN-2002; 2002US-0390926P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-AUG-2004; 2004US-00925608
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les 31; Conservative
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                                                                                                 (RERE-) RES DEV FOUND
                                                                                                                                                                                                  WPI; 2004-156362/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AGGA/) AGGARWAL B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2005080023-A1.
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                                                                                                                                                Aggarwal B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADZ00136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a HIV-LTR oligonuclectide used to test the method of the invention. The method is for inhibition of activation of the NF-kappaB transcription factor (A), for treatment of toxic or septic shock or graft versus host reactions in humans, comprises administration of curcumin (I, diferuloylmethane). (I) is used to treat toxic or septic shock and graft versus host reactions in humans. (I) may be used to inhibit activation of (A) e.g. in cases of radiation damage, atherosclerosis, cancer and human immune deficiency virus (HIV) infection. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Multiple myeloma, proliferation inhibition; apoptosis induction, curcumin, diferulcylmethane, chemotherapy potentiator; I-kappa-B kinase inhibitor; I-kappa-B-alpha phosphorylation suppressor; NF-kappa-B suppressor; I-kappa-B-alpha, Bcl-2; Bcl-XL; cyclin D1; interleukin-6; IL-6; cell cycle arrest; cytostatic; NF-kappa-B; HIV-1 LTR; long terminal repeat; electrophoretic mobility shift assay;
                                                                      Inhibitor; activator; NF-kappaB transcription factor; toxic shock; septic shock; graft versus host disease; curcumin; diferuloylmethane; radiation damage; atherosclerosis; cancer; HIV infection; HIV-LTR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inhibiting activation of NFkappaB with curcumin used for treatment of e.g. septic shock or guest versus host reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 45 BP; 7 A; 9 C; 17 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIV-1 LTR NF-kappa-B sequence used as EMSA probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGACTTTCCGCTGGGGACTTTCCAGGGGGACTT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGACTTTCCGCTGGGGACTTTCCAGGGAGGCGT 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Col 5; 21pp; English.
                                                                                                                                                                          Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                           96US-00712932.
                                                                                                                                                                                                                                                                                                                                                                             96US-00712932.
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                          HIV-LTR oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                               (RERE-) RES DEV FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-253918/21
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                                                                                                                                                                                                                                                                                                                              26-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                             26-SEP-1996;
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                                                                                                                                                                                                                                                                              06-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aggarwal BB
                                                                                                                                                                                                                            US5891924-A
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Best Local Si
Matches 31;
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EMSA;

RESULT 26 ADH1217

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Gaps

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35

Length 45; Indels

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Weininger S,
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                                                                                                                            The invention relates to a method of reducing or inhibiting osteoclast development induced by the receptor for activation of nuclear factor Kappa B ligand (RANKL) by contacting the osteoclast or its precursor with acetoxychavicol or their analogues. (I) is useful for reducing or inhibiting osteoclast development induced by RANKL, inhibiting the formation of osteoclasts in an individual and reducing osteoclasts in an individual and reducing osteolytic activity and bone loss in an individual having breast cancer, multiple myeloma, post-menopausal osteoporosis, Paget's disease, rheumatoid arthritis or head and neck squamous cell carcinoma. The diferuloylmethane (curcumin) is safe to humans. This sequence corresponds to an electromobility shift assay (EMSA) probe used to analyze NF-kappaB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligo from HIV long terminal repeat containing NF-kappaB binding site.
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nuclear factor-kappa B; NF-kappaB; NF-kappaB inhibitor; apoptosis stimulation; cancer; cytostatic; HIV long terminal repeat;
                                              Use of compounds comprising diferuloylmethane, guggulsterone, 1'-acecoxychavicol or their analogues to e.g. reduce/inhibit osteoclast development induced by the receptor for activation of nuclear factor kappa B ligand.
                                                                                                                                                                                                                                                                   activation in curcumin-treated or untreated cells. The sequence is derived from the human immunoeficiency virus 1 long terminal repeat.
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                                                                                                                                                                                                                                                                                                                        Score 29.2; DB 14; Length 45; Pred. No. 0.064; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                    Sequence 45 BP; 7 A; 9 C; 17 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                     2 GGGACTTTCCGCTGGGGACTTTCCAGGGGGACTT 35
                                                                                                                                                                                                                                                                                                                                                                                  10 GGGACTTTCCGCTGGGGACTTTCCAGGGAGGCGT 43
                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /bound_moiety= "NF-kappaB"
24. 32
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                                                                                                          Example 7; SEQ ID NO 1; 43pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                     91.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                31; Conservative
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                               WPI; 2005-295074/30.
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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And The present invention relates to cell permeable nuclear factor (NF)-
kappaB, and specifically to polypeptides that selectively inhibit NF-
kappaB, and specifically to polypeptides that selectively inhibit NF-
cappaB, and specifically NF-kappaB mediated gene expression and
chibitor comprises (i) a peptide fragment of the p65 submit of NF-
cappaB, where the peptide comprises phosphorylation site(8) of the p65
submit and (ii) a protein transduction domain which is able to transport
the polypeptide across cell membrane. The protein transduction domain is
cerived from a protein of domain selected from third helix of the
antennapedia homeodomain (SEQ ID NO:3), herpes virus structural protein,
or HIV tat protein. Also disclosed is an isolated DNA encoding the
inhibitor. Provided is a method of inhibiting the DNA binding activity of
NF-kappaB; a method of increasing the level of apoptosis; and a method of
treating cancer. Inhibiting the DNA binding activity of NF-kappaB in a
cell comprises contecting a cell with the inhibitor above, where the
inhibitor suppresses NF-kappaB binding to DNA. Activity is induced by an
agent, e.g. TNF, LPS, IL-1, okadaic acid, phorbol myristate acetate
ceptor-associated death domain (TRADD), TNF receptor-associated factor-
ceptor-associated death domain (TRADD), TNF receptor-associated factor
ceptor-associated death domain (TRADD), TNF receptor-associated factor
ceptor-associated death domain (TRADD), TNF receptor-associated from the
central complex to examine the specificity of binding of NF-kappaB
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                                                                                    New cell permeable nuclear factor kappaB inhibitor comprising a peptide fragment and a protein transduction domain, useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 0.064;
0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 45 BP; 7 A; 9 C; 17 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GGGACTITCCGCTGGGGACTITCCAGGGGGACTT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 gegacitricceriegeacitriccaegeaegeer 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                Example 2; SEQ ID NO 1; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95WO-US015944
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Best Local Similarity 91.2%;
Matches 31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-FEB-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Target binding region #27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POOL INC.
WPI; 2005-372280/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9617956-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to the DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           virus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
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Weininger AM;

invention. The probe of the invention contains a TBR, a booster binding region (BBR), and an optional support or attachment (OSA). The target binding assembly (TBA) recognised by the probe, contains at least one nucleic acid recognition unit (NAR), and optionally a linker sequence, assembly sequence (see AAR95994-R95998), an asymmetry sequence (see AAR96007), and an OSA. The assembly sequence and asymmetry sequence (see AAR96007), and an OSA. The assembly sequence and asymmetry sequence are responsible for the folding and association of the NARS. The NARS (see AAR95965-COMPS), and an OSA. The assembly sequence and asymmetry sequence are responsible for the folding and association of the NARS. The NARS (see AAR95965-COMPS), and an OSA. The assembly sequence is an oligopeptide, which does not interfere with NAR function, but provides stability and control over the spacing of the NAR from the rest of the TBA. The OSA is an attached support or indicator, or other means of localisation of the probe. The probe can be used in a method for detecting or localising a specific target nucleic acid sequence (TNA). The method is highly sensitive, and has a high chart of the control of the mean of the capter of indicator, and has a high chart of the control of the method of the highly sensitive, and has a high chart of the control of the capter indicator, and sequence for specific the control of the capter indicator, and has a high chart of the control of the capter indicator, and has a high chart of the capter indicator in human calls, in HIV, the method is highly sensitive, and has a high capter of specificatry. The method can be used for detecting specific and sequences including those found in human calls, in HIV, in the method can be used for detecting specific and sequences including those found in human calls, in HIV, in the method can be used for detecting the capter of specificator. AAT30581-T30614 represent target binding regions (TBR) of a probe of the Probe nucleic acids, target binding assemblies, etc - for detection and localisation of specific nucleic acid sequences, esp. HIV and HPV. and other nucleic acid containing systems, including bacteria and Disclosure; Page 72; 172pp; English. WPI; 1996-287199/29 Probe

Sequence 46 BP; 8 A; 11 C; 17 G; 10 T; 0 U; 0 Other;

76.3%; Score 29; DB 2; Length 46; 100.0%; Pred. No. 0.077; ive 0; Mismatches 0; Indels 2 GGGACTITCCGCTGGGGACTITCCAGGGG 30 7 degacirircecirededacirirceaeded 35 29; Conservative Query Match Best Local Similarity Matches 29; Conserva 셤

AAT30602 standard; DNA; 46 BP RESULT 30

AAT30602;

(first entry) 19-FEB-1997 Target binding region #22.

Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SP1, TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus; HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence; nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria; virus; ss AAT30602

AAT30602

AAC30602

AAC306

Synthetic.

WO9617956-A2

13-JUN-1996

95WO-US015944 07-DEC-1995; 94US-00353476 09-DEC-1994;

(GENE-) GENE POOL INC.

Weininger AM;

Weininger S,

WPI; 1996-287199/29.

Probe nucleic acids, target binding assemblies, etc - for detection and

AAT30581-T30614 represent target binding regions (TBR) of a probe of the invention. The probe of the invention contains a TBR, a booster binding convention. The probe of the invention contains a TBR, a booster binding assembly (TBA) recognised by the probe, contains at least one binding assembly (TBA) recognised by the probe, contains at least one concleic acid recognition unit (NAR), and optionally a linker sequence, an assembly sequence (see AAR95094-R95999), an asymmetry sequence (see AAR95097), and an OSA. The assembly sequence and asymmetry sequence (see AR95097), and an OSA. The assembly sequence and asymmetry sequence (see AAR95093) are selected from NF-Kappa-B, SPI, TATP, human papillomavirus (HPV) E2, HPV LTR, human immunodeficiency virus (HIV) LTR and Tat binding contints. The linker sequence is an oligopeptide, which does not interfere with NAR function, but provides stability and control over the spacing of the NAR from the rest of the TBA. The OSA is an attached support or indicator, or other means of localisation of the probe. The probe can be used in a method for detecting or localisation as pecific target nucleic acid sequence (TNA). The method is highly sensitive, and has a high conteic acid sequences, including those found in human calls, in HIV, HPV, and other nucleic acid containing systems, including bacteria and localisation of specific nucleic acid sequences, esp. HIV and HPV. Disclosure, Page 71; 172pp; English.

Sequence 46 BP; 8 A; 11 C; 17 G; 10 T; 0 U; 0 Other;

Gaps ö 'Match 76.3%; Score 29; DB 2; Length 46; Local Similarity 100.0%; Pred. No. 0.077; les 29; Conservative 0; Mismatches 0; Indels Query Match Best Loc Matches

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2 GGGACTITCCGCTGGGGACTITCCAGGGG 30

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Gaps .; 0

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RESULT 31

AAT30601 standard; DNA; 46

AAT30601;

(first entry) 19-FEB-1997

Target binding region #21.

Target binding assembly, nucleic acid recognition unit; NF-kappa-B; SP1; TATA; human papillomavitus; HPV; HPV E2; human immunodeficiency virus; HIV LTR; human jamillomavitus; Arbeb; assembly sequence; asymmetry sequence; HIV LTR; HIV LTR; HIV; bacteria; nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria; virus; ss.

Synthetic.

WO9617956-A2

13-JUN-1996.

95WO-US015944 07-DEC-1995; 94US-00353476 09-DEC-1994;

(GENE-) GENE POOL INC.

Weininger AM; Weininger S,

WPI; 1996-287199/29.

Probe nucleic acids, target binding assemblies, etc - for detection and localisation of specific nucleic acid sequences, esp. HIV and HPV.

Disclosure; Page 70; 172pp; English.

AAT30581-T30614 represent target binding regions (TBR) of a probe of the invention. The probe of the invention contains a TBR, a booster binding region (BBR), and an optional support or attachment (OSA). The target binding assembly (TBA) recognised by the probe, contains at least one nucleic acid recognition unit (NAR) and optionally a linker sequence, an assembly sequence (see AAR5994-R5999), an asymmetry sequence (see AAR5999-R96006), an unclear localisation signal sequence (see AAR9509).

AAR9599-R96006), a nuclear localisation signal sequence (see AAR96007), and an OSA. The assembly sequence and asymmetry sequence (see AAR95993) are selected from NF-kappa-B, SPI, TATA, human papillomavirus (HFV) E2, HPV LTR, human immunodeficiency virus (HIV) LTR and Tat binding units. The linker sequence is an oligopeptide, which does not interfere with NAR function, but provides stability and control over the spacing of the NAR from the rest of the TBA. The OSA is an attached support or indiactor, or other means of localisation of the probe. The probe can be used in a method for detecting or localising a specific target nucleic acid sequences (TNA). The method is highly sensitive, and has a high edgree of specificity. The method can be used for detecting and edgree of sequences, including those found in human calls, in HIV, HIV, and other nucleic acid containing systems, including bacteria and viruses

Sequence 46 BP; 7 A; 11 C; 17 G; 11 T; 0 U; 0 Other;

Gaps ö ch 76.3%; Score 29; DB 2; Length 46; I Similarity 100.0%; Pred. No. 0.077; 29; Conservative 0; Mismatches 0; Indels Length 46; GGGACTITCCGCTGGGGACTITCCAGGGG 30 7 eggacrirccecreeggacrirccaegge 35 Query Match Best Local Similarity ద

AAT30600 standard; DNA; 46 RESULT 32

19-FEB-1997 (first entry) AAT30600;

Target binding region #20

Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SP1; TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus; HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence; nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria; virus; ss.

Synthetic.

WO9617956-A2

13-JUN-1996.

95WO-US015944

07-DEC-1995;

94US-00353476 09-DEC-1994;

(GENE-) GENE POOL INC.

Weininger S, Weininger AM;

WPI; 1996-287199/29.

Probe nucleic acids, target binding assemblies, etc - for detection and localisation of specific nucleic acid sequences, esp. HIV and HPV.

Disclosure; Page 70; 172pp; English.

AAT30581-T30614 represent target binding regions (TBR) of a probe of the invention. The probe of the invention contains a TBR, a booster binding

region (BBR), and an optional support or attachment (OSA). The target binding assembly (TBA) recognised by the probe contains at least one nucleic acid recognition unit (NAR), and optionally a linker sequence, an assembly sequence (see AAR95994-R95998), an asymmetry sequence (see AAR95999-R96006), a nuclear localisation signal sequence (see AAR96007), and an OSA. The assembly sequence and asymmetry sequence (see AAR96007), company of the NARS. The NARS (see AAR95965-Company and association of the NARS. The NARS (see AAR95965-Company of TRA) numan immunodeficiency virus (HIV) ITR and Tat binding units. The linker sequence is an oligopoptide, which does not interfered with NAR from the rest of the TBA. The OSA is an attached support or indicator, or other means of localisation of the probe. The probe can be used in a method for detecting or localising a specific target nucleic acid sequence (TNA). The method is highly sensitive, and has a high degree of specificity. The method can be used for detecting specific carget nucleic acid sequences, including those found in human calls, in HIV, HIV, and other nucleic acid containing systems, including bacteria and

Sequence 46 BP; 7 A; 11 C; 18 G; 10 T; 0 U; 0 Other;

Gaps ő 76.3%; Score 29; DB 2; Length 46; 100.0%; Pred. No. 0.077; 0; Indels 100.0%; Pred. ... 29; Conservative Best Local Similarity Query Match Matches

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RESULT 33 AAV67098

AAV67098 standard; cDNA; 36 BP AAV67098;

(first entry)

14-JAN-1999

HIV LTR #2

CD3-delta gene; Ikaros gene; T cell; progenitor stem cell; leukaemia; differentiation marker; immune system; corpus striatum; AIDS; Alzheimer's disease; ss.

Human immunodeficiency virus 1. US5824770-A Synthetic.

95US-00465590. 05-JUN-1995; 20-OCT-1998.

92US-00946233. 93US-00121438. 94US-00238212. 14-SEP-1992; 14-SEP-1993; 02-MAY-1994;

(GEHO) GEN HOSPITAL CORP.

Georgopoulos K;

WPI; 1998-582621/49

Ikaros poly:peptide(s) - useful for treating disorders of immune system or corpus striatum

Disclosure; Col 27; 111pp; English.

The present invention describes a purified peptide having at least one of the following properties: (a) it stimulates transcription of a DNA sequence under the control of a delta A element, an NFKB element or an Ikaros binding oligonucleotide consensus sequence; (b) it binds to any of

a delta A element, an NFKB element or an Ikaros binding oligonucleotide consensus sequence; (c) it competitively inhibits the binding of a naturally occurring Ikaros isoform to amy of a delta A element, an NFKB element or an Ikaros binding oligonucleotide consensus sequence; (d) it competitively inhibits Ikaros binding to Ikaros responsive elements; or (e) it inhibite protein-protein interactions of transcriptional complexes formed with naturally occurring ikaros isoforms. The proteins, provided that they stimulate gene transcription under the control of delta A elements, NFKB elements and/or Ikaros-binding oligonucleotides, competitively inhibit binding of naturally occurring Ikaros isoforms to delta A elements, NFKB elements and/or Ikaros-binding oligonucleotides, competitively inhibit Ikaros binding to Ikaros-binding oligonucleotides, competitively inhibit Ikaros binding to Ikaros-binding oligonucleotides, competitively inhibit Ikaros binding to Ikaros-responsive elements and/or intubit protein-protein interactions of transcriptional complexes with alternating control of the present invention or ADDS, or corpus striatum disorders, e.g. leukaemia or ADDS, or corpus striatum disorders, e.g. given in the present invention

Sequence 36 BP; 6 A; 9 C; 14 G; 7 T; 0 U; 0 Other;

Gaps .; 0 75.8%; Score 28.8; DB 2; Length 36; 2; Indels Pred. No. 0.088; 0; Mismatches GGGACTTTCCGCTGGGGACTTTCCAGGGAGGC 35 2 GGGACTITCCGCTGGGGACTITCCAGGGGGAC 33 93.8%; 30; Conservative Best Local Similarity Matches 30; Conserv Query Match a

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AAQ61543 standard; cDNA; 37

AAQ61543;

(first entry) (revised) 25-MAR-2003 21-OCT-1994 HIV long terminal repeat sequence comprising Ikaros binding site.

Ikaros; zinc finger; protein; immune disorder; therapy; treatment; corpus striatum; regulatory gene; enhancer; regulatory element; gene expression; HIV; human immunodeficiency virus; ss.

Human immunodeficiency virus.

WO9406814-A1

31-MAR-1994

93WO-US008743. 14-SEP-1993; 92US-00946233. 14-SEP-1992;

(GEHO) GEN HOSPITAL CORP.

Georgopoulos K;

WPI; 1994-118387/14.

I-cell pathway regulatory gene, Ikaros - encodes family of unique zinc finger proteins, useful for treating immune system disorders. Disclosure; Page 29; 112pp; English.

The Ikaros gene encodes a zinc finger protein which can be used in a therapeutic composition to treat animals with an immune system disorder. It may also be used for assessing whether a subject is at risk for an immune disorder. It is of particular use in treating a disorder of the corpus striatum. Heterologous genes may be expressed by placing them under the control of an Ikaros responsive control element and contacting the element with an Ikaros protein. Potential high affinity binding sites

AAT30615-T30634 represent probe nucleic acids of the invention. The probe of the invention contains a target binding region (TBR), a booster binding region (BRR), and an optional support or attendment (GSA). The target binding assembly (TBA) recognised by the TBR (see AAT30581-T30614) of the probe, contains at least one nucleic acid recognition unit (NAR), or optionally a linker sequence, an assembly sequence (see AAR9599-R96006), a nuclear reguence (see AAR96007), and an OSA. The assembly sequence and asymmetry sequence (see AAR96007), and an OSA. The assembly sequence and asymmetry sequences are responsible for the folding and sequence and asymmetry sequences are responsible for the folding and sequence and asymmetry sequences are responsible for the folding and immunodeficiency virus (HIV) LTR and Tat binding units. The linker immunodeficiency virus (HIV) LTR and Tat binding units. The linker count of the NAR function, but provides stability and control over the spacing of the NAR function, but provides stability and control over the spacing of the NAR function, cost the TBA. The OSA is an attached support or indicator, or other means of localisation of the probe. The probe can be used in a method for ö for the Ikaros proteins were found in the enhancer and promoter regions of the TCR-alpha, -beta and -delta, the CD3-delta, -epsilon and -gamma genes, the SL3 and HIV long terminal repeat and in the regulatory domains of other T cell restricted antigens. Related sequences to the Ikaros motif were also found in the purine boxes of the IL2 gene in the in the HIV long terminal repeat. See also AAQ61504-Q61543. (Updated on 25-MAR-2003 to correct PN field.) Target binding assembly, nucleic acid recognition unit; NF-kappa-B; SP1; TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus; HIV LTR; human papillomavirus; HIV LTR; acquence; asymmetry sequence; nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria; Probe nucleic acids, target binding assemblies, etc - for detection and localisation of specific nucleic acid sequences, esp. HIV and HPV. Gaps . 0 2; Length 37; 1; Indels Sequence 37 BP; 6 A; 9 C; 15 G; 7 T; 0 U; 0 Other; Score 28.4; DB Pred. No. 0.13; 0; Mismatches 4 GGGACTTTCCGCTGGGGACTTTCCAGGGAG 33 31 2 GGGACTITCCGCTGGGGACTITCCAGGGGG Disclosure; Page 76; 172pp; English BP. 95WO-US015944. 94US-00353476 74.7**%**; 96.7**%**; AAT30615 standard; cDNA; 37 Query Match
Best Local Similarity 96....
Best 29; Conservative Weininger S, Weininger AM; 21-FEB-1997 (first entry) Probe nucleic acid PNA1. (GENE-) GENE POOL INC. WPI; 1996-287199/29. WO9617956-A2 07-DEC-1995; 09-DEC-1994; 13-JUN-1996 virus; ss. Synthetic. AAT30615; RESULT 35 AAT30615 8888888888888 ð

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detecting or localising a specific target nucleic acid sequence (TNA). The method is highly sensitive, and has a high degree of specificity. The method can be used for detecting specific nucleic acid sequences, including those found in human cells, in HIV, HPV, and other nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and AAV42840) and polypeptides, vectors and host cells. These are used to treat T and B cell diseases, to control expression of heterologous genes placed under control of an Imaros-responsive element, to treat nervous system diseases and to modulate cell division, amplification or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      τo
                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                              Length 37;
                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ikaros, mIK; transcription factor; mouse; lymphocyte;
cell differentiation; T cell; cancer; immunodeficiency;
Alzheimer's disease; therapy; diagnosis; HIV; ss.
                                                                                                                                          containing systems, including bacteria and viruses
                                                                                                                                                                                                            Sequence 37 BP; 7 A; 9 C; 13 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                              Score 28.4; DB
Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         2 GGGACTTTCCGCTGGGGACTTTCCAGGGGG 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGACTTTCCGCTGGGGACTTTCCAGGGAG 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIV LTR binding site for Ikaros.
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                                                                                                                                                                                                                                                                                                                                                   29; Conservative
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                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JAN-1997;
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                                                                                                                                                                                                                                                                                  Query Match
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AAV46402

AAV66402

AAV664
   88888888
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DB 2; Length 37;

74.7%; Score 28.4;

Query Match

differentiation, especially in haematopoietic cells

Sequence 37 BP; 6 A; 9 C; 15 G; 7 T; 0 U; 0 Other;

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The invention relates to an animal with a structurally intact Tp12 gene but functionally disrupted endogenous Tp12 (a protooncogene which encodes a cytoplasmic serime threoning kinase). The animal has increased resistance to lipopolysaccharide-induced endotcoxin shock or tumour resistance to lipopolysaccharide-induced endotcoxin shock or tumour and DNA are useful for identifying compounds that agonise or inhibit the function of Tp12 protein. Tp12 is useful for treating rheumatoid arthritis. Th7alpha-mediated inflammatory diseases or inhibit the function of Tp12 protein. Tp12 is useful for treating she marrow derived cells arthritis. Th7alpha-mediated by transfecting bone marrow derived cells invitro with a DNA construct which encodes sequences that interferes with the expression of function of the endogenous Tp12 in the cells and administering the cells to an animal. The knock out animals and the constructs used to generate the animals are useful in the development of compositions and methods of treating inflammation. Tp12 agonist and constructs useful in taraction of the mechanistic action of the novel cantagonist are useful as targets for the development of novel the alutidation of the mechanistic action of the novel cantagonist and protein interactions involved in inflammatory disorders. Tp12 endotoxin shock and/or antiinflammatory component sequence and protein interactions involved in inflammatory disorders. Tp12 endotoxin shock and/or antiinflammatory component sequence and protein interactions involved in Inflammatory disorders. Tp12 endotoxin shock and/or antiinflammatory component sequence and protein interactions involved in the present sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                  Tpl2; serine threonine kinase; tumour necrosis factor; TNFalpha; NF-kB; inflammatory disease; therapy; rheumatoid arthritis; endotoxin shock; research tool; LPS; lipopolysaccharide; nuclear factor kappa B; HIV;
                                                                                                                                                                                                                                                                                                                                                           Human immunodeficiency virus LTR NF-kB-specific double-stranded oligo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is human immunodeficiency virus LTR NF kB-specific (nuclear factor ka
B) double-stranded oligonucleotide used in the exemplification of the
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                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 32 BP; 6 A; 8 C; 11 G; 7 T; 0 U; 0 Other;
                         1;
  0.13;
                         0; Mismatches
                                                                 2 GGGACTTTCCGCTGGGGACTTTCCAGGGGG 31
                                                                                               4 GGGACTTTCCGCTGGGGACTTTCCAGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 28;
Pred. No.
  No.
  Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus; ds
                                                                                                                                                                                                                          ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.7%; S
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-MAR-2001; 2001WO-US007588.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAR-2000; 2000US-00522775.
96.78;
                                                                                                                                                                                                                          AAD17457 standard; DNA; 32
                                                                                                                                                                                                                                                                                                              (first entry)
                         29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-582266/65.
  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200166559-A1.
                                                                                                                                                                                                                                                                                                              10-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rsichlis PN;
                                                                                                                                                                                                                                                                    AAD17457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
    Best Local
                         Matches
                                                                                                                                                                              RESULT 37
                                                                                                                                                                                                   AAD17457
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요
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an animal with a structurally intact Tp12 gene but functionally disrupted endogenous Tp12 (a protooncogene which encodes a cytoplasmic serine threomine protein kinase). The animal has increased resistance to lipopolysaccharide-induced endotoxin shock or tumour and DNA are useful for identifying compounds that agoinse or inhibit the cumour of Tp12 is useful for treating rheumatoid arthritis. TNFalpha-mediated inflammatory diseases. Tp12 protein arthritis. TNFalpha-mediated inflammatory diseases or LPS induced arthritis. TNFalpha-mediated inflammatory diseases or LPS induced conductorin shock, may be treated by transfecting bone marrow derived cells invitro with a DNA construct which encodes sequences that interferes with the expression of function of the endogenous Tp12 in the cells and constructs used to generate the animals are useful in the development of compositions and methods of treating inflammation. Tp12 agonist and an encodensist are useful as targets for the development of novel therapeutic antagonist are useful in the development of antagonist are useful as targets for the development of novel therapeutic agents which eliminate the functional role of Tp12 and as research tools to facilitate the elucidation of the mechanistic action of the novel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polynucleotide sequences facilitate the discovery and development of antiendetoxin shock and/or antinflammatory compounds. The present sequence is an oligonucleotide used for generating nulcear factor kappa B (NF-kB) DNA binding site probe used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Knock-out animal resistant to lipopolysaccharide-induced endotoxin shock and tumor necrosis factor alpha-mediated inflammatory disease, comprises a functionally disrupted endogenous Tpl2 gene.
                                                                                                                                                                                                                                                                     Tpl2; serine threonine kinase; tumour necrosis factor; TNFalpha; NF-kB; inflammatory disease; therapy; rheumatoid arthritis; endotoxin shock; research tool; LPS; lipopolysaccharide; nuclear factor kappa B; ss.
 Gaps
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                                                                                                                                                                                                                                        Nuclear factor kappa B binding site probe generating oligo #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.7%; Score 28; DB 5; Length 32; 100.0%; Pred. No. 0.18; ive 0; Mismatches 0; Indels
 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 32 BP; 6 A; 8 C; 11 G; 7 T; 0 U; 0 Other;
Mismatches
                               29
                                                          GGGACTTTCCGCTGGGGACTTTCCAGGG 32
                               GGGACTITCCGCTGGGGACTITCCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 8; Page 50; 98pp; English
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                                                                                                                                             BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAR-2000; 2000US-00522775.
                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAR-2001; 2001WO-US007588
                                                                                                                                           AAD17455 standard; DNA; 32
                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 28; Conservative
 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-582266/65.
                                                                                                                                                                                                                                                                                                                                                                     WO200166559-A1
                                                                                                                                                                                                         10-DEC-2001
                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                   13-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rsichlis PN
                                                                                                                                                                           AAD17455;
                               N
 Matches
                                                                                                          RESULT 38
                                                                                                                              AAD17455
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new
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nuclear factor kappa B inhibitor complex; HIV enhancer; immunoglobulin kappa light chain enhaner; transcription factor; ds.
                                                                                                                                                                                                                                                                                                                          88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                 Primer, PCR, amplification; HIV-1; genome, vector; inhibition, replication; gene expression; infection; probe; hybridisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   replication and the subsequent infection of neighbouring cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.7%; Score 28; DB 2; Length 33; 100.0%; Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 33 BP; 7 A; 8 C; 11 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                       HIV probe corrsponding to NF-kappaB binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New vectors for inhibiting HIV replication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ilarity 100.0%; Pred. No. 0.1
Conservative 0; Mismatches
5 GGGACTTTCCGCTGGGGACTTTCCAGGG 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GGGACTTTCCGCTGGGGACTTTCCAGGG 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Part of the kappa light chain enhancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Iacono KT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 25; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus 1.
                                                                                                                                ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-US021880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0061984P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Suhadolnik RJ, Adelson ME,
                                                                                                                                AAX34336 standard; DNA; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAN90922 standard; DNA; 34
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                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UTEM ) UNIV TEMPLE
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Les 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9919496-A1
                                                                                                                                                                                                                    06-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-SEP-2004
25-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                          AAX34336;
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Matches
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                                                                                        RESULT 39
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                                                                                                                                                                        The present invention provides assays for identifying compounds which modulate NF-kappaB. NF-kappaB, along with IgNF-A, IgNF-B and IgNF-B, i lymphoid cell nuclear factor which regulates the transcription of the immunoglobulin genes. The modulators are useful in the control of activation of host cells
                                                                            DNA
                                                                         Identifying an NF-kappa B modulator, useful for analyzing protein DNA interactions in cells or in identifying transcriptional regulatory factors by detecting NF-kappa B or IKB DNA binding activity level or cytoplasmic localization.
                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               necrosis factor kappa B; NF-kappaB;
transcriptional regulatory DNA element; immunoglobulin;
transcription enhancer; immunoassay; IgNF-B; HIV enhancer; ds.
   Lenardo MJ;
                                                                                                                                                                                                                                                                                                73.7%; Score 28; DB 4; Length 34; 100.0%; Pred. No. 0.18; O; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                      Sequence 34 BP; 7 A; 8 C; 11 G; 8 T; 0 U; 0 Other;
   Baeuerle PA, Lebowitz JH,
                                                                                                                                                                                                                                                                                                                                                           2 GGGACTTTCCGCTGGGGACTTTCCAGGG 29
                                                                                                                                                                                                                                                                                                                                                                              6 GGGACTTTCCGCTGGGGACTTTCCAGGG 33
                                                                                                                                                  Disclosure; Fig 14; 66pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIV enhancer NF-KB binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВР.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86US-00817441.
86US-00946365.
88US-00162607.
88US-00180173.
89US-00341436.
91US-00791898.
95US-00418266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-JAN-2002; 2002US-00037341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADT77252 standard; DNA; 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                             Local Similarity 100.
 Fan C, Maniatis TP,
Corcoran LM, Staudt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORCORAN L M.
BAEUERLE P A.
LENARDO M J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEBOWITZ J H.
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CLERC R G.
                                             WPI; 2001-060011/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BALTIMORE D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHARP P A.
SINGH H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2004214757-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-NOV-1991;
06-APR-1995;
05-JUN-1995;
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24-DEC-1986;
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21-APR-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-OCT-2004
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                                                                                                                                                                                                                                                                                                   Query Match
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(LEBO/)
(BALD/)
(CLER/)
(CORC/)
(BAEU/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BALT/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SENR/
                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lymphoid cell nuclear factor; immunoglobulin gene transcription; Ig gene; IgNF-A; IgNF-E; IgNF-E; IgNF-E; IgNF-E; IgNF-B; IgNF-A; IgNF-B; Ss.
                                                                                                                                                                                                                       Altering gene expression in a cell - by controlling dissociation of nuclear factor kappa B inhibitor complex to prevent or cause binding to an enhancer, e.g. HIV-dna.
                                                                                                                                                                                                                                                                                                           The sequence is part of the HIV LTR enhancer. Tag a and tag b represent binding sites for NF-kB. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                          Revised record issued on 09-SEP-2004 : Correction to Feature Table Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Singh H, Sen R, Baldwin AS, Clerc RG, Baltimore D;
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0
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                                                                                                                                                                                                                                                                                                                                                                                      Sequence 34 BP; 7 A; 8 C; 11 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lymphoid cell nuclear factor related sequence #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GGGACTITCCGCTGGGGACTITCCAGGG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGACTTTCCGCTGGGGACTTTCCAGGG 33
                                                                                                                                                             (WHED ) WHITEHEAD INST BIOMEDICAL RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HARD ) HARVARD COLLEGE.
(MASI ) MASSACHUSETTS INST TECHNOLOGY.
(WHED ) WHITEHEAD INST.
                                                                                                                                                                                                                                                                                  Disclosure, Fig 1, 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86US-00946365.
88US-00155207.
88US-00165260.
88US-0016269.
89US-00318901.
89US-0031898.
95US-0041836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC66959 standard; DNA; 34 BP
                                                                                                     89WO-US000820
                                                                                                                                 88US-00162680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                28; Conservative
                                                                                                                                                                                            WPI; 1989-278306/38
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Homo sapiens
Unidentified
                                                                                                     01-MAR-1989;
                                                                                                                                 01-MAR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                          WO8908147-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-MAR-2001
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05-DEC-1988;
                                                                         08-SEP-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JAN-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-DEC-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-MAR-1989,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-APR-1989,
13-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sharp PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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Sequence 34 BP; 7 A; 8 C; 11 G; 8 T; 0 U; 0 Other;
                                                           Disclosure; SEQ ID NO 53; 126pp; English.
            Sen R, S
Clerc RG,
(FANC/) FAN C.
(MANI/) MANIATIS T P.
                             WPI; 2004-774818/76
            Baltimore D,
                     Maniatis TP;
                                                   interest
                 Baldwin AS,
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Gaps
                              ö
73.7%; Score 28; DB 13; Length 34; 100.0%; Pred. No. 0.18;
                            0; Indels
            100.0%; Prec. ...
                                                      2 GGGACTTTCCGCTGGGGACTTTCCAGGG 29
                                                                       6 GGGACTTTCCGCTGGGGACTTTCCAGGG 33
                              28; Conservative
                  Best Local Similarity
    Query Match
                              Matches
                                                         8
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Electrophoretic mobility shift assay protein concentration primer #1
                                                                              Heat shock protein 70; Hsp70; NF-kappaB; transplant rejection; autoimmune disease; inflammatory disease; cancer; vascular disease; primer; ss.
                AAA61055 standard; DNA; 35 BP.
                                                 (first entry)
                                                 06-NOV-2000
                                                                                                                  Synthetic
                                 AAA61055;
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(BRIM) BRISTOL-MYERS SQUIBB CO.

99WO-US027244. 98US-0109872P

17-NOV-1999; 24-NOV-1998;

02-JUN-2000

WO200031113-A1

The present seguence is that of a primer corresponding to nucleotides 344 Use of deacetylase inhibitor combined with one or more compounds used in viral treatment, for manufacturing medicament for obtaining elimination of integrated, functional and pathogenic virus e.g. HIV-1 in mammal cell. Adam E; Disclosure; Page 10; 56pp; English Quivy V, Burny A, WPI; 2003-569183/53. Van Lint C,

shock protein, useful in the treatment of transplant rejection, autoimmune diseases and cancer. The present sequence is a primer which was used to determine the concentration of a fusion protein in an electrophoretic mobility shift assay. The fusion protein comprised the Cterminuus of the 70kD heat shock protein (HBP70), and the p50 subunit of transcription factor NF-kappaB. The fusion protein was created in order to determine the ability of the HBP70 sequence to direct other proteins into the cell, a feature which can be used in the treatment of transplant rejection, autoimmune diseases guch as rheumatoid arthritis, multiple sclerosis, diabetes, asthma, inflammatory bowel disease, psoriasis, hepatitis, Graves disease and viteligo, inflammatory distress including osteoarthritis, pancreatitis and adult respiratory distress syndrome, cancer, vascular diseases (such as restenosis and atherosclerosis) and DNA and RNA viral replication diseases (including herpes) Sequence 35 BP; 5 A; 9 C; 13 G; 8 T; 0 U; 0 Other; Example 6; Page 21; 37pp; English. Fujihara SM, Nadler SG; WPI; 2000-400029/34 Best Loca Matches RESULT 44 셤 ò The invention describes an isolated nuclear protein NF-kappaB (I) which binds: in a sequence specific manner, to a transcriptional regulatory DNA clement of an immunoglobulin light or heavy chain genes, or both; in a sequence specific manner, to enhancer DNA sequences of the kappa light chain gene; or to DNA sequences in the upstream region of both mouse cheavy and kappa light chain gene promoters, and to DNA sequences of mouse cheavy chain gene enhancer. (I) is useful for enhancing the transcription of the gene of interest, and for screening for expression of sequence specific binding protein. A polyclonal or monoclonal antibody (II) specific binding protein. A polyclonal or monoclonal antibody (II) specific manner, to a transcriptional regulatory DNA element of an immunoglobulin light or heavy chain gene, or both is useful in an immunoglobulin light or heavy chain gene, or both is useful in an immunoglobulin light or heavy chain gene, or both is useful in a biological fluid, where (II) is specifically reacts with lower be not a transcription of the section of a transcription of the sequence comprising (III) linked to DNA encoding an activator of the RNA comprising (III) linked to DNA encoding the construct into the cell. Novel isolated nuclear protein NF-kappaB that binds in sequence specific manner to transcriptional regulatory DNA element of immunoglobulin light or heavy chain genes, or both, useful for enhancing transcription of gene Sharp PA, Singh H, Staudt L, Lebowitz JH; , Corcoran LM, Baeuerle PA, Lenardo MJ, Fan C;

Gaps .. 0 y Match 73.7%; Score 28; DB 3; Length 35; Local Similarity 100.0%; Pred. No. 0.18; nes 28; Conservative 0; Mismatches 0; Indels 1 GGGGACTITCCGCTGGGGACTITCCAGG 28 8 deceaerircecreceaecrirceaec 35 Query Match

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HIV-1; long terminal repeat; virus elimination; PCR; primer; ss. HIV-1 LAI long terminal repeat 5' PCR primer. BP ACF05495 standard; DNA; 42 (first entry) 06-NOV-2003 ACF05495; ACF05495

Human immunodeficiency virus type 1. 23-DEC-2002; 2002WO-BE000197. 21-DEC-2001; 2001EP-00870289 WO2003053468-A1. 03-JUL-2003 Synthetic.

(ULBR) UNIV LIBRE BRUXELLES

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to 377 of the coding strand sequence of the HIV-1 LAI 5' long terminal repeat (LTR), and including an added KpnI restriction site. This was used as 5' primer, with the 3' primer given in ACF05496, to amplify a 186 bp fragment of the 5' LTR (nuclectides 345-531) for use in the plasmid construct pLTR(345-531)-luc. This plasmid was used to demonstrate the trichostatin-A (TSA) inducibility of HIV-1 LTRs and also to show that inteat kappaB sites are required for maximal TSA inducibility of the HIV-1 LTRs and also to show that inteat kappaB sites are required for maximal TSA inducibility of the HIV-1 LTRS and also to show that concer. The invention relates to the use of a deacetylase inhibitor and the manufacture of a medicament for obtaining elimination of integrated, functional and pathogenic viruses, e.g. HIV-1, in a mammal cell, including a human cell. This allows significant elimination and possible suppression of the presence of virus in a patient and therefore improves long-term control of viral infections in patient and therefore highly active antiretroviral therapy (HAART) treatment
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Sequence 42 BP; 7 A; 11 C; 15 G; 9 T; 0 U; 0 Other;

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Gaps
                                     ;
73.7%; Score 28; DB 9; Length 42; 100.0%; Pred. No. 0.19; ive 0; Mismatches 0; Indels
                                                                        2 GGGACTTTCCGCTGGGGACTTTCCAGGG 29
                                                                                                         15 GGGACTTTCCGCTGGGGACTTTCCAGGG 42
                                   28; Conservative
                    Best Local Similarity
 Query Match
                                   Matches
                                                                                                         g
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AAT30606 standard; DNA; 45 BP. (first entry) Target binding region #26. 19-FEB-1997 AAT30606;

Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SP1; TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus; HIV LTR; Tat binding unit; probe assembly sequence; asymmetry sequence; nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria; virus; ss.

Synthetic.

WO9617956-A2

13-JUN-1996.

95WO-US015944. 07-DEC-1995; 94US-00353476 09-DEC-1994;

(GENE-) GENE POOL INC.

WPI; 1996-287199/29.

Weininger AM;

Weininger S,

Disclosure; Page 72; 172pp; English.

Probe nucleic acids, target binding assemblies, etc - for detection and localisation of specific nucleic acid sequences, esp. HIV and HPV.

AAT30581-T30614 represent target binding regions (TBR) of a probe of the invention. The probe of the invention contains a TBR, a booster binding region (BBR), and an optional support or attachment (OSA). The target binding assembly (TBA) recognised by the probe, contains at least on nucleic acid recognition unit (NAR), and optionally a linker sequence, an assembly sequence (see AAR95994-R95998), an asymmetry sequence (see AAR95994-R95998), an asymmetry sequence (see AAR96007), and an OSA. The assembly sequence and asymmetry sequence ser responsible for the folding and association of the NARS. The NARS (see AAR95965-

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R95993) are selected from NF-kappa-B, SP1, TATA, human papillomavirus (HPV) E2, HPV LTR, human immunodeficiency virus (HIV) LTR and Tat binding units. The linker sequence is an oligopeptide, which does not interfere with NAR function, but provides stability and control over the spacing of the NAR from the rest of the TBA. The OSA is an attached support or indicator, or other means of localisation of the probe. The probe can be used in a method for detecting or localising a specific target nucleic acid sequence (TNA). The method is highly sensitive, and has a high andleic acid sequences, including those found in human cells, in HIV, HPV, and other nucleic acid containing systems, including bacteria and
                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                          72.6%; Score 27.6; DB 2; Length 45; 88.2%; Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                Sequence 45 BP; 9 A; 11 C; 15 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                    4,
                                                                                                                                                                                                                                                                                                                                                                                                                                     35
                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 GGGACTTTCCGCTGGGGACTTTCCAGAGAGGCT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GGGACTTTCCGCTGGGGACTTTCCAGGGGGACTT
                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         30; Conservative
                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                          viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 46
AAA99616/c
                                                                                                                                                                                                                                                                                                                                                                                      Matches
         8888888888888888
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NF-kB; alpha-melanocyte stimulating hormone; alpha-MSH; antibacterial; fungicide; virucide; antiinflammatory; vaginitis; cystitis; urethritis; balanoposthitis; toxic shock syndrome; sexually transmitted disease; AAA99616 standard; DNA; 35 (first entry) NF-kB oligonucleotide #2. 22-JAN-2001 probe; ss. AAA99616;

Homo sapiens.

WO200056353-A2

28-SEP-2000.

23-MAR-2000; 2000WO-US007846.

24-MAR-1999; 99US-0126233P.

(ZENG-) ZENGEN INC.

Catania A; Lipton J,

WPI; 2000-628219/60.

Treating uro-genital conditions, such as vaginitis, cystitis, urethritis, or balanoposthitis comprises using alpha-melanocyte stimulating hormone or a derivative of it.

Example 9; Page 15; 37pp; English.

The present sequence is an oligonucleotide used to determine the level of NF-kB activity in human UI cells treated with alpha-melanocyte stimulating hormone (alpha-MSH). Alpha-MSH and its derivatives were shown to inhibit TNF-alpha induced NF-kB activation and binding. Alpha-MSH and its derivatives have potent antipyretic and antinflammatory properties, yet they have extremely low toxicity. A uro-genital condition treatment system has been developed that comprises a carrier and a polypeptide including a sequence derived from alpha-MSH. The system may be used to treat a uro-genital condition such as vaginitis, cystitis, urethritis, or balanoposthitis. It may also be used to prevent toxic shock syndrome and infection from sexually transmitted diseases, and to treat an antibiotic resistant microorganism. The polypeptides used in the treatment system

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RESULT 48
             AAT30604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to the use of alpha-melanocyte stimulating hormone (MSH), its derivative, or both, to combat cancer and in inhibiting cancer cell proliferation by administering the above alpha-MSH to a patient with cancer. The alpha-MSH is useful for combating cancer and for inhibiting cancer cell proliferation, where the cancer is mesothelioma, and is selected from Hodgkin lymphoma, non-Hodgkin lymphoma, squamous cell carcinoma, breast cancer and colorectal cancer. Sequences ACC47365-366 represent positive and negative strands of NF-kappaB DNA binding site, used in DNA binding assays for determining alpha-MSH inhibition of NF-kappaB in cancer cells
can reduce the viability of microbes, reduce the germination of yeast, kill microbes, treat inflammation associated with microbial infection, increase the accumulation of CAMP in microbes and inhibit replication and
                                                                                                                                                                                                                                                                                                MSH, alpha-melanocyte stimulating hormone; alpha-MSH; cancer; cytostatic;
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of alpha-melanocyte stimulating hormone to combat cancer and in
                                                                                                     ö
                                                                              72.1%; Score 27.4; DB 3; Length 35; 96.6%; Pred. No. 0.32;
                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 35 BP; 9 A; 11 C; 9 G; 6 T; 0 U; 0 Other;
                                                       Sequence 35 BP; 9 A; 11 C; 9 G; 6 T; 0 U; 0 Other;
                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                          NF-kappaB DNA binding site negative strand
                                                                                                                           1 GGGGACTTTCCGCTGGGGACTTTCCAGGG 29
                                                                                                                                         GGGGACTTTCCGCTGGGGACTTTCCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inhibiting cancer cell proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; Page 14; 27pp; English.
                                   expression of viral pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                          05-SEP-2001; 2001US-0317514P.
                                                                                                                                                                                                                                                                                                                                                                                                    05-SEP-2002; 2002WO-US028257
                                                                                                                                                                                                        ACC47366 standard; DNA; 35
                                                                                                                                                                                                                                                     (first entry)
                                                                                                     28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Catania AP
                                                                                                                                                                                                                                                                                                                                                                                                                                               (LIPT/) LIPTON J.
(CATA/) CATANIA A P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-290144/28.
                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                        WO2003020223-A2
                                                                                                                                                                                                                                                                                                             NF-kappaB; ss.
                                                                                                                                                                                                                                                     11-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                               13-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lipton J,
                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                              ACC47366;
                                                                               Query Match
                                                                                                     Matches
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AAT30581-T30614 represent target binding regions (TBR) of a probe of the invention. The probe of the invention contains a TBR, a booster binding region (BBR), and an optional support or attachment (OSA). The target binding assembly (TBA) recognised by the probe, contains at least one nucleic acid recognition unit (NAR), and optionally a linker sequence, an assembly sequence (see AAR95994-R85998), an asymmetry sequence (see AAR95994-R85998), an asymmetry sequence (see AAR95007), and an OSA. The assembly sequence and asymmetry sequence see AAR96007), and an OSA. The assembly sequence and asymmetry sequence see AAR95007), and an OSA. The assembly sequence in an asymmetry sequence (see AAR95965-CC for the folding and association of the NARs. The NARs (see AAR95965-CC in the Innker sequence is an Oligopeptide, which does not interfere with NAR function, but provides stability and control over the spacing of the NAR from the rest of the TBA. The OSA is an attached support or indicator, or other means of localisation of the probe. The probe can be used in a method for detecting or localisation of the probe. The probe can be degree of sepecificity. The method is highly sensitive, and has a high degree of specificity. The method can be used for detecting specific nucleic acid sequences, including those found in human cells, in HIV, HIV, and other nucleic acid containing systems, including bacteria and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                           Target binding assembly, nucleic acid recognition unit; NF-kappa-B, SP1, TATA, human papillomavirus, HPV E2, human immunodeficiency virus; HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence; nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probe nucleic acids, target binding assemblies, etc - for detection and localisation of specific nucleic acid sequences, esp. HIV and HPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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72.1%; Score 27.4; DB 2; Length 44;
Best Local Similarity 83.8%; Pred. No. 0.33;
Matches 31; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 44 BP; 6 A; 12 C; 16 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GGGACTITCCGCTGGGGACTITCCAGGGGGACTITCC 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eccacrircecricecacrirecececeaecerece 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 71; 172pp; English
BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94US-00353476.
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AAT30604 standard; DNA; 44
                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                         Target binding region #24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POOL INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-287199/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Weininger S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9617956-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENE-) GENE
                                                                                                                                                              19-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          virus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                               AAT30604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                viruses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT30605
ID AAT3
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Gaps

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72.1%; Score 27.4; DB 10; Length 35; 96.6%; Pred. No. 0.32; ive 0; Mismatches 1; Indels

29

1 GGGGACTTTCCGCTGGGGACTTTCCAGGG gegeactricecreegeactriceares

Conservative

Local Similarity tes 28; Conserv

Best Loc Matches

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Query Match

NF-kB; alpha-melanocyte stimulating hormone; alpha-MSH; antibacterial; fungicide; virucide; antiinflammatory; vaginitis; cystitis; urethritis; balanoposthitis; toxic shock syndrome; sexually transmitted disease;

22-JAN-2001 (first entry) NF-kB oligonucleotide #1. 23-MAR-2000; 2000WO-US007846

WO200056353-A2.

28-SEP-2000.

Homo sapiens.

probe; ss.

99US-0126233P

24-MAR-1999;

Catania A;

Lipton J,

(ZENG-) ZENGEN

WPI; 2000-628219/60.

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Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SP1; ATAR; human papillomavirus; HPV; HPV E2; human immunodeficiancy virus; HIV LTR; human papillomavirus; HPV LTR; par binding unit; probe; assembly sequence; asymmetry sequence; nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;
                                                                                                                                                                                                                                                                               Probe nucleic acids, target binding assemblies, etc - for detection and localisation of specific nucleic acid sequences, esp. HIV and HPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 44 BP; 6 A; 12 C; 17 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                           Disclosure, Page 72; 172pp; English.
                                                                                                                                                                                                    94US-00353476
                                                                                                                                                                                                                                           Weininger AM;
                           (first entry)
                                             Target binding region #25.
                                                                                                                                                                                                                       GENE-) GENE POOL INC.
                                                                                                                                                                                                                                                             WPI; 1996-287199/29.
                                                                                                                                            WO9617956-A2
                                                                                                                                                                                 07-DEC-1995;
                                                                                                                                                                                                   09-DEC-1994;
                                                                                                                                                                                                                                           Weininger S,
                           19-FEB-1997
                                                                                                                                                              13-JUN-1996
                                                                                                        virus; ss.
                                                                                                                          Synthetic.
         AAT30605;
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invention. The probe of the invention contains a TBR, a booster binding invention. The probe of the invention contains a TBR, a booster binding invention. The probe of the invention contains a TBR, a booster binding assembly, and an optional support or attachment (OSA). The target binding assembly (TBA) recognition unit (NAR), and optionally a linker sequence, an assembly sequence (see AAR95994-R95998), an asymmetry sequence (see AAR95066), a nuclear localisation signal sequence (see AAR95067), and an OSA. The assembly sequence and asymmetry sequence see AR86007), and an OSA. The assembly sequence and asymmetry sequence see AR895965. Cfor the folding and association of the NARS. The NARS (see AAR95965-CC For the folding and association of the NARS. The NARS (see AAR95965-CC For HV) E2, HPV LTR, human immunodeficiency virus (HIV) LTR and Tat binding units. The linker sequence is an olisopopebide, which does not interfere with NAR from the rest of the TBA. The GSA is an attached support or indicator, or other means of localisation of the probe. The probe can be used in a method for detecting or localisation of the probe. The probe can be caid sequence (TNA). The method can be used for detecting specific cucles and sequences, including those found in human cells, in HIV, and other nucleic acid sequences, including those found in human cells, in HIV, and other nucleic acid sequences, including systems, including bacteria and
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The present sequence is an oligonucleotide used to determine the level of NF-KB activity in human UI cells treated with alpha-melanocyte trimulating hormone (alpha-MSH). Alpha-MSH and its derivatives were shown to inhibit TMF-alpha induced NF-KB activation and binding. Alpha-MSH and its derivatives have potent antipyretic and antiinflammatory properties; yet they have extremely low toxicity. A uro-genital condition treatment system has been developed that comprises a carrier and a polypeptide including a sequence derived from alpha-MSH. The system may be used to treat a uro-genital condition such as vaginitis, cystitis, urethritis, or balanoposthitis. It may also be used to prevent toxic shock syndrome and infection from sexually transmitted diseases, and to treat an antibiotic resistant microorganism. The polypeptides used in the treatment system can reduce the viability of microbes, treat inflammation associated with microbial infection, increase the accumulation of cAMP in microbes and inhibit replication and

Treating uro-genital conditions, such as vaginitis, cystitis, urethritis, or balanoposthitis comprises using alpha-melanocyte stimulating hormone or a derivative of it.

Example 9; Page 15; 37pp; English.

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3.7 47 3 US-U3-841-638-11046 Sequence 104. 3.2 38 2 US-08-120-607A-12 Sequence 12, 3.2 38 2 US-08-453-848-27 Sequence 27, 3.2 38 3 US-09-169-027-27 Sequence 27,	2.6 40 2 US-08-682-218-23 Sequence 23,	1.6 47 3 US-09-386-642-36 Sequence 36,	0.5 25 3 US-09-388-349-4 Sequence 4, 4	0.5 25 3 US-09-396-196G-110222 Sequence 110222,	0.0 23 3 US-07-808-452-9 Sequence 9,	0.0 23 6 PCT-US92-10//0-9 Sequence 9, 4	9.5 15 2 US-08-353-476-4 Sequence 4, 7	9.5 33 2 US-08-435-350-30 Sequence 30,	9.5 45 2 US-08-528-057-17 Sequence 17,	8.9 31 2 US-08-390-850-254 Sequence 254,	8.9 31 2 US-08-390-850-255 Sequence 255,	8.9 31 2 US-08-390-850-256 Sequence 256,	6.9 31 2 US-08-435-634-254 Sequence 255, 8.9 31 2 US-08-435-634-255 Sequence 255,	8.9 31 2 IIS-08-435-634-256 Semience 256.	8.4 25 3 US-09-396-196G-50814 Sequence 5081	8.4 25 3 US-09-396-196G-89802 Sequence	8.4 25 3 US-09-396-196G-124375 Sequence	8.4 47 3 US-09-671-317-664 Sequence	8.4 50 3 US-US-852-5/1-5 Seguence	7.9 25 3 US-09-396-196G-50815 Sequence	7.9 37 2 US-08-426-236-8 Sequence	7.9 38 3 US-09-770-158-11 Sequence	7.9 46 3 US-U9-3/Z-934-Z5 Sequence Z5,	7.9 46 3 US-09-766-898-25 Sequence 25,	7.9 46 3 US-09-637-040C-25 Sequence 25,	7.9 46 3 US-10-306-249-25 Sequence 25,	7.9 50 3 US-10-131-827-434 Sequence 434,	7.4 25 3 US-09-396-196G-2950 Sequence 2950	7.4 25 3 US-09-396-196G-67905 Sequence 679	7.4 40 2 US-08-503-964-3 Sequence 3,	7.4 40 2 US-08-766-014-19 Sequence 19	7.4 40 2 US-08-679-522D-8 Sequence 8,	7.4 40 2 US-08-664-863B-12 Sequence 12	7.4 40 3 US-09-141-401-8 Sequence 8,	7.4 40 3 US-09-290-5/7-40 Sequence 40.7.4 40 3 US-09-061-757B-7 Sequence 7.	7.4 40 3 US-09-290-452-40 Sequence 40	7.4 40 3 US-09-290-338-40 Sequence 40	7.4 40 3 US-09-686-I/9A-7 Sequence 7,	7.4 40 3 US-09-954-594A-40 Sequence 40,	7.4 40 3 US-09-981-621-7 Sequence 7,	7.4 40 3 US-09-705-043A-8 Sequence 8,	7.4 40 3 US-U9-865-80/-40 Sequence 40.	7.4 44 3 US-09-339-913B-100 Sequence 100	7.4 44 3 US-09-339-904A-100 Sequence 100	7.4 44 3 US-08-769-062B-100 Sequence 10	7.4 44 3 US-U9-344-UUZB-IUU Sequence IU 7.4 44 3 US-09-559-565C-IUO Sequence IO	7.4 44 3 US-09-693-350-100 Sequence 100	7.4 44 3 US-09-693-389-100 Sequence 100	7.4 44 3 US-09-559-671A-100 Sequence 10	7.4 44 3 US-09-333-326A-100 Sequence 10:	7.4 47 3 US-09-422-978-1819 Sequence 18:	7.4 50 2 US-08-832-468-5 Sequence 5,	6.8 21 3 US-09-021-247-6 Sequence 6, 6, 8 21 3 US-09-810-863-6
3.7 47 3 US-U3-641-653-11046 Sequence 104 3.2 38 2 US-08-120-607A-12 Sequence 12, 3.2 38 2 US-08-453-848-27 Sequence 27, 3.2 38 3 US-09-169-027-27 Sequence 27,	.2 42.6 40 2 US-08-682-218-23 Sequence 23,	.8 41.6 47 3 US-09-386-642-36 Sequence 36,	.4 40.5 25 3 US-U9-388-349-4 Sequence 4, .	.4 40.5 25 3 US-09-396-196G-110222 Sequence 110222,	.2 40.0 23 3 US-07-808-452-9 Sequence 9,	.2 40.0 23 6 PCT-US92-10770-9 Sequence 9, 4	15 39.5 15 2 US-08-353-476-4 Sequence 4, 7	5 39.5 33 2 US-08-435-350-30 Sequence 30,	15 39.5 45 2 US-08-528-057-17 Sequence 17,	.8 38.9 31 2 US-08-390-850-254 Sequence 254,	.8 38.9 31 2 US-08-390-850-255 Sequence 255,	.8 38.9 31 2 US-08-390-850-256 Sequence 256,	.8 38.9 31 2 US-08-435-634-254 Sequence 255.	.8 38.9 31 2 IIS-08-435-634-256 Semience 256.	6 38.4 25 3 US-09-396-196G-50814 Sequence 5081	.6 38.4 25 3 US-09-396-196G-89802 Sequence	.6 38.4 25 3 US-09-396-196G-124375 Sequence	.6 38.4 47 3 US-09-671-317-664 Sequence	.6 .58.4 50 3 US-US-852-5/1-5 Sequence	.4 37.9 25 3 US-09-396-196G-50815 Sequence	.4 37.9 37 2 US-08-426-236-8 Sequence	.4 37.9 38 3 US-09-770-158-11 Sequence	.4 37.9 46 3 US-US-3/2-334-29 SEQUENCE 25,	.4 37.9 46 3 US-09-766-898-25 Sequence 25,	.4 37.9 46 3 US-09-637-040C-25 Sequence 25,	.4 37.9 46 3 US-10-306-249-25 Sequence 25,	.4 37.9 50 3 US-10-131-827-434 Sequence 434,	.4 57.9 50 5 05-IO-ISI-627-2647 Sequence 2950	.2 37.4 25 3 US-09-396-196G-67905 Sequence 67.	.2 37.4 40 2 US-08-503-964-3 Sequence 3,	.2 37.4 40 2 US-08-766-014-19 Sequence 19	.2 37.4 40 2 US-08-679-522D-8 Sequence 8,	.2 37.4 40 2 US-08-664-863B-12 Sequence 12	.2 37.4 40 3 US-09-141-401-8 Sequence 8,	.2 37.4 40 3 US-09-290-577-40 Sequence 40, 2 37.4 40 3 US-09-061-757B-7 Sequence 7.	.2 37.4 40 3 US-09-290-452-40 Sequence 40	.2 37.4 40 3 US-09-290-338-40 Sequence 40	.2 37.4 40 3 US-09-686-179A-7 Sequence 7,	.2 37.4 40 3 US-09-954-594A-40 Sequence 40	.2 37.4 40 3 US-09-981-621-7 Sequence 7,	.2 37.4 40 3 US-09-705-043A-8 Sequence 8,	.2 3/.4 40 3 US-09-865-80/-40 Seguence 40, 2 37 4 40 3 US-09-865-80/-40	7.4 44 3 US-09-339-913B-100 Sequence 100	.2 37.4 44 3 US-09-339-904A-100 Sequence 100	.2 37.4 44 3 US-08-769-062B-100 Sequence 10	.2 37.4 44 3 US-09-344-0028-100 Sequence 10:	.2 37.4 44 3 US-09-693-350-100 Sequence 10	.2 37.4 44 3 US-09-693-389-100 Sequence 100	.2 37.4 44 3 US-09-559-671A-100 Sequence 10	.2 37.4 44 3 US-09-339-926A-100 Sequence to	37.4 47 3 US-09-422-978-1819 Sequence 18:	.2 37.4 50 2 US-08-832-468-5 Sequence 5,	36.8 21 3 US-09-021-247-6 Sequence 6,

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| LOCATION: replace(1..38, "")
| OTHER INFORMATION: /noce= "ANY OF THE PHOSPHATE GROUPS
| OTHER INFORMATION: LINKING ANY OF THE NUCLEOSIDES MAY BE REPLACED
| OTHER INFORMATION: WITH PHOSPHOROTHIOATE GROUPS, METHYL ESTER
| US-08-607-519-2
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Patent No. 587190

Sequence 29, Application US/08353476

Sequence 29, Application US/08353476

Sequence 29, Application US/08353476

Patent No. 5871902

APPLICANT: Weininger, Susan

APPLICANT: Weininger, Arthur M

TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION

NUMBER OF SEQUENCES:

ADDRESSEE: Saliwanchik & Saliwanchik

STREET: 2421 N.W. 41st St., Sulte A-1

CITY: Cainesville

STATE: Florida

CONTYR: USA

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Florida

COMPUTER READABLE FORM:

MEDIUM TYPE: Florida

COMPUTER READABLE FORM:

MEDIUM TYPE: Plorida

COMPUTER PREADABLE FORM:

MEDIUM 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 38;
  : P.C.
1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                   OPERATION SYSTEM:
OPERATION SYSTEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/607,519
FILING DATE: 27-FEB-1996
CLASSIFICATION: 514
PRIOR APPLICATION S14
PRIOR APPLICATION NUMBER: US 08/123,188
FILING DATE: 20-SEP-1993
ATTONNEY/AGENT INPORMATION:
NAME: Oblon, No. 5990090man F.
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFRA: (703) 413-3220
TELETRY: (703) 413-2220
TELETRY: (703) 413-2220
TELETRY: 248855 OPAT UR
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38
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Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 38; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: SYNTHETIC DNA
                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATITE SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                       ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: both
                             STREET: 1755 S. CITY: Arlington STATE: Virginia COUNTRY: U.S.A.
     ADDRESSEE:
Sequence 82, Appl
Sequence 82, Appl
Sequence 82, Appl
Sequence 82, Appl
Sequence 3363, Ap
Sequence 4564, Ap
Sequence 63468, A
Sequence 90869, A
Sequence 90869, A
Sequence 90860, A
Sequence 90860, A
Sequence 106418, Sequence 16418, Sequence 16418, Sequence 16418, Sequence 112751, Sequence 112751, Sequence 118, Appl
Sequence 19, Appl
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Sequence 33, Appl
Sequence 18, Appl
Sequence 36, Appl
Sequence 5, Appli
Sequence 96047, A
Sequence 96049, A
Sequence 96049, A
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5171670
7, Appli
1, Appli
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Sequence 119899,
Sequence 119900,
Sequence 119901,
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Patent No. 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7,
Sequence 4,
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Sequence 1
Sequence 1
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Sequence
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Patent No. 5990090
GENERAL INFORMATION:
APPLICANT: NAME OF INVENTION: METHODS AND COMPOSITIONS FOR TREATMENT
TITLE OF INVENTION: OF DISEASES
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
US-10-015-671A-82
US-10-015-393A-82
US-10-016-33A-82
US-10-016-041A-82
US-10-016-041A-82
US-10-118-127-3363
US-09-396-1966-4564
US-09-396-1966-90869
US-09-396-1966-90899
US-09-396-1966-90899
US-09-423-423-59
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US-08-963-946-18
US-08-963-946-33
US-08-963-946-18
US-09-425-804-18
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US-09-396-196G-96047
US-09-396-196G-96048
US-09-396-196G-96049
US-09-396-196G-106466
US-09-396-196G-119899
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US-09-205-928-924
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US-08-607-519-2
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Gaps

Gaps

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                                                        79.5%; Score 30.2; DB 2; Length 46; 91.4%; Pred. No. 0.0045;
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                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: BARSOUM, Stephen E.
APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENTS ADDRESS:
ADDRESSEE: FISH & NEAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,257
FILNG DATE: 25-May-1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,403
APPLICATION NUMBER: US 07/934,375
FILING DATE: 28-APR-1992
APPLICATION NUMBER: US 07/934,375
FILING DATE: 28-APR-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 12-AUG-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 24-DEC-1999
APPLICATION NUMBER: US 07/454,450
FILING DATE: 24-NOV-1993
APPLICATION NUMBER: US 07/454,650
FILING DATE: 24-NOV-1993
APPLICATION NUMBER: US 07/636,662
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,744
REGISTRATION NUMBER: 27,744
                                                                                                                                                         1 GGGGACTITCCGCTGGGGACTITCCAGGGGGACTT 35
                                                                                                                                                                                                       6 GGGACTTTCCGCTGGGGACTTTCCAGGGAGGCGT 40
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Pred. No. 0.0052;
                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B170 CIP 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                           Sequence 43, Application US/08450257
Patent No. 5652122
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.9%;
86.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
                                                                                                         32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 14-8367
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
EDNESS: single
                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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          US-08-353-476-28
                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

81.1%; Score 30.8; DB 2; Length 43;
Best Local Similarity 94.1%; Pred. No. 0.0025;
Matches 32; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 28, Application US/08353476

Setent No. 5871902.
GENERAL INFORMATION:
APPLICANT: Weininger, Susan
APPLICANT: Weininger, Arthur
TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 32606
CMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 GGGGACTTTCCGCTGGGGACTTTCCAGGGAGGCT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st St., Suite A-1 CITY: Gainesville
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,476
FILING DATE:
CLASSIFTCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bencen, Gerard H
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100
TELECOMMUNICATION INFORMATION:
TELEFAX: (904) 375-810
TELEFAX: (904) 375-810
TELEFAX: (904) 372-580
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bencen, Gerard H
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100
TELEPHONE: (904) 375-8100
TELEPHONE: (904) 372-5800
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STANDEDIESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear,
TOPOLOGY: linear,
MOLECULE TYPE: CDN,
HYPOTHETICAL: NO
SANTI-SENSE: NO
US-08-353-476-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Florida
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
US-08-353-476-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: BARSOUM, Stephen E.
APPLICANT: FAWELL, Stephen E.
APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
UNDMER OF SEQUENCES: 69
CORRESPONDENCES: 69
ADDRESSEE: FISH & NEAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                               CUUNTEY: USA

ZIP: 10020

COMPUTER READABLE FORM:
MEDIUM TYPE: DOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,246
FILING DATE: 23-AMY-1995
CLASSIFICATION NUMBER: US 08/235,403
FILING DATE: 28-AR-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 28-AR-1993
APPLICATION NUMBER: US 07/934,375
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: PCT/US93/07833
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/656
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
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39 GGGGACTTTCCGCTGGGGACTTTCCACGGGGACTTTC 2
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llarity 86.8%; Pred. No. 0.0052;
Conservative 0; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                      1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B170 CIP
                                                                                                        Sequence 43, Application US/08450246 Patent No. 5670617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Haley Jr., James F. REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 14-8367
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                  RESULT 6
US-08-450-246-43
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  Gaps
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5; Indels
                                                                                                                                                                                                                                                                                                       APFLICANT:
APPLICANT: BARSOUM, COME.
APPLICANT: FAWELL, Stephen E.
APPLICANT: PERINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
CTREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTR:

ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,257
TILING DATE: 25-MAY-1995
TILING DATE: 25-MAY-1995
                                             GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38
                                                                         1 GGGGACTITCCGCTGGGGACTITCCAGGGGGACTITCC 38
  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PILING DATE: 25-MX-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,403
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/934,375
FILING DATE: 28-UJU-1993
APPLICATION NUMBER: US 07/098,766
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
RESTRENCE/DOCKET NUMBER: 27,794
                                                                                                                                                      RESULT 5
US-08-450-257-44/c
US-08-450-257-44/c
; Sequence 44, Application US/08450257
; Patent No. 5652122
; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: FRANKEL, Alan
                                                                                                                                                                                                                                                                                             PABO, Carl
BARSOUM, James G.
FAWELL, Stephen E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9000
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-450-257-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION TELEPHONE: (212) 596-9000
  33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDAL
STREET: 122.
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS
                                                                                                                                                                                                                                                                                                APPLICANT:
  Matches
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Gaps
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0
Indels
                                1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38
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Length 39;

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Query Match 78.9%; Score 30; DB 2; Length 39; Best Local Similarity 86.8%; Pred. No. 0.0052; Matches 33; Conservative 0; Mismatches 5; Indels
                     APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: PAWELL, Stephen E.
APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,098
FILING DATE: 25-MAY-1995
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1993
APPLICATION NUMBER: US 07/934,450
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/436,662
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/436,662
FILING DATE: 20-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 08/158,015
FILING DATE: 27-MAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION NUMBER: B170 CIP 2
TELECOMMUNICATION NUMBER: B170 CIP 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GGGACTITCCGCTGGGGACTITCCACGGGGGACTITC 38
                                                                                                                                                                                                  ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 44, Application US/08450098
Patent No. 5674980
GENERAL INFORMATION:
APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: PABO, Carl
APPLICANT: FAWELL, Stephen E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-450-098-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
     FRANKEL, Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212) 596-909
TELEX: 14-81367
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                  CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-450-098-44/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
                                                                                         APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: BARSOUM, James G.
APPLICANT: PEBINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                           COUNTER: NEW JOIR COUNTER: NEW JOIR COUNTER: USA COUNTER READELE FORM:
MEDIUW TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PAtentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,246 FILING DATE: 25-MAY-1995
CLASSIFICATION DATA: US/08/450,246 FILING DATE: 25-MAY-1995
FILING DATE: 21-MG-1995
APPLICATION NUMBER: US 07/934,375
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: US 07/934,375
FILING DATE: 12-MG-1993
APPLICATION NUMBER: US 07/098,766
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/098,766
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/654,450
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/656,662
FILING DATE: 12-DC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 12-DC-1989
APPLICATION NUMBER: US 08/158,015
FILING DATE: 12-AUG-1993
APPLICATION NUMBER: US 08/158,015
FILING DATE: 12-DC-1989
ATTONEY/AGENT INFORMATION: NAME: HALBY JT: JAMES F. REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 dedeactricecrededactriceacededeactric 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 30; DB 2;
Pred. No. 0.0052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELECOMMUNE: (212) 596-9000
TELERX: (122) 596-9000
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
US-08-450-098-43
Sequence 43, Application US/08450098
Patent No. 5674980
GENERAL INFORMATION:
                     Sequence 44, Application US/08450246
Patent No. 5670617
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.9%;
86.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                   CITY: New York
STATE: New York
US-08-450-246-44/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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APPLICANT: PRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: PAWELL, Stephen B.
APPLICANT: PRANKEL, Stephen B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOGTWARE: Patentin Release #1.0, Version #1.25

SURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/451,233

FILING DATE: 25-MAY-1995

CLASSIFICATION NUMBER: US 08/235,403

FILING DATE: 28-APR-1994

APPLICATION NUMBER: US 07/934,375

FILING DATE: 28-APR-1992

APPLICATION NUMBER: US 07/934,75

FILING DATE: 28-JUL-1993

APPLICATION NUMBER: US 07/098,766

FILING DATE: 28-JUL-1993

APPLICATION NUMBER: US 07/454,450

FILING DATE: 19-AUG-1993

APPLICATION NUMBER: US 07/636,662

FILING DATE: 21-DEC-1989

APPLICATION NUMBER: US 07/636,662

FILING DATE: 21-DEC-1989

APPLICATION NUMBER: US 07/636,662

FILING DATE: 19-AUG-1993

APPLICATION NUMBER: US 07/636,662

FILING DATE: 21-DEC-1989

APPLICATION NUMBER: US 08/158,015

FILING DATE: 21-DEC-1989

ATTORNEY/AGENT INFORMATION:
NAME: Haley JT., James F.

RESTERANION NUMBER: B170 CIP 2

TELECOMMUNICATION NUMBER: B170 CIP 2

TELECOMMUNICATION NUMBER: B170 CIP 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38
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Pred. No. 0.0052;
0; Mismatches
                                                          Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 44, Application US/08451233
Patent No. 5747641
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic) US-08-451-233-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 86.8%;
Matches 33; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPAONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELER: 14-8367
INFORMATION FOR SEQ ID NO: 43
SEQUENCE CHARACTERISTICS:
         ADDRESSEE: FISH & NEAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 base pairs
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STRANDEDNESS: single
                                                                                                                                                                                                                        ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                 STREET: 1251 AVCCITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-451-233-44/c
                                                                                                                                       STATE: Ne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
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APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
NUMBER OF SEQUENCES: ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: FAWELL, Stephen E.
APPLICANT: FPRISKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,098
FILING DATE: 25-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/235,403
FILING DATE: 28-MAY-1995
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1993
APPLICATION NUMBER: US 07/934,450
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1999
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DR-1999
APPLICATION NUMBER: US 07/454,650
FILING DATE: 21-DR-1999
APPLICATION NUMBER: US 07/454,450
FILING DATE: 24-NOV-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 24-NOV-1993
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
APPLICATION NUMBER: US 08/158,015
FILING DATE: 21-DR-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
APPLICATION NUMBER: US 08/158,015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39 GGGGACTITCCGCTGGGGACTITCCACGGGGGACTITC 2
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Pred. No. 0.0052;
0; Mismatches
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REGISTRATION NUMBER: 27,794
REPERBNEK/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELECHONE: (212) 596-9000
TELERAX: (212) 596-9000
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
LENGTH: 39 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 43, Application US/08451233 Patent No. 5747641 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.9%;
ilarity 86.8%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: FRANKEL, Alan
APPLICANT: PABC, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: FRWELL, Stephen E.
APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
OPERATING SYSTEM: PC-LOUS/MS-DUS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,236
FILING DATE: 25-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,403
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/934,375
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/98,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 08/158,015
FILING DATE: 22-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATCORNEY/AGENT INFORMATION:
NAME: Haley JT., James F.
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
BEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 44, Application US/08450236 Patent No. 5804604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: DNA (genomic) US-08-450-236-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212) 596-900
TELERAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -08-450-236-44/C
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Patent No. 5804604

GENERAL INFORMATION:

APPLICANT: FRANKEL, Alan

APPLICANT: FAMELL, Stephen E.

CORRESPONDENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: FISH & NEAVE

STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.9%; Score 30; DB 2; Length 39; 86.8%; Pred. No. 0.0052;
              COMPUTER READABLE FORM:
MEDIUM TYRE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,233
FILING DATE: 25-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/934,375
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/098,766
FILING DATE: 21-MG-1993
APPLICATION NUMBER: US 07/098,766
FILING DATE: 29-MG-1993
APPLICATION NUMBER: US 07/65,662
FILING DATE: 19-MG-1993
APPLICATION NUMBER: US 07/65,662
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/65,662
FILING DATE: 24-NOV-1991
APPLICATION NUMBER: US 07/636,662
FILING DATE: 24-NOV-1991
APPLICATION NUMBER: US 07/636,662
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 21-DEC-1989
ATTORNEY/AGRAT INFORMATION:
FILING DATE: 21-DEC-1989
ATTORNEY/AGRAT INFORMATION:
TELEPONE: (212) 596-9000
TELEPRAN: (212) 596-9000
TELEPAN: (212) 596-9000
TELEPAN: (212) 596-9000
TELEPAN: (212) 596-9000
TELEPAN: TENERALTERISTICS:
TENEX: 14-8367
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACATERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 39 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 86.8
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucle:
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-451-233-44
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US-08-450-236-43
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Gaps
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APPLICANT: PRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: BARSOOM, James G.
APPLICANT: PRELICANT: Stephen E.
APPLICANT: PERINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 geceacrircecreceacrircaceceeeeacrirc 38
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 30; DB 3;
Pred. No. 0.0052;
0; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1251 Avenue of the Americas CITY: New York STATE: New York COUNTRY: USA ZIP: 10020 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IRM PC COMPATER: IRM PC COMPATER: IRM PC COMPATER: PATENTING SYSTEM: Pc-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Versi
                    FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: W 07/098,766
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: PCT/US93/07833
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
RECISTRATION NUMBER: 27,794
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/934,375
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833
FILING DATE: 19-AUG-1993
FILING DATE: 19-AUG-1993
  US 07/934,375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 44, Application US/08235403
Patent No. 6316003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic) US-08-235-403-43
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Best Local Similarity 86.8%;
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 14-8367
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS-08-235-403-44/c
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TELEX: 14
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Patent No. 6316003
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MANAL: HALLEY J., JOHNS F. P., PARALES F., PEGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INPORMATION:
TELECHONE: (212) 596-9000
TELERAX: (212) 596-9000
TELERAX: 14-8367
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
                                                                         PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/235,403
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/936,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: US 07/536,662
FILING DATE: 21-DEC-1999
APPLICATION NUMBER: US 07/636,662
FILING DATE: 24-NOV-1993
ATTORNEY,AGENT INFORMATION:
NAMME: HALBY JT., JAMES F.
REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.9%; Score 30;
86.8%; Pred. No. 0
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STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
US/08/450,236
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                          25-MAY-1995
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
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US-08-235-403-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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APPLICANT: BLAKE, MARY E.

APPLICANT: BLAKE, MARY E.

APPLICANT: GUTTERMAN, JORDAN U.

APPLICANT: HOFPWANN, JOSEPH J.

APPLICANT: BAILEY, DAVID T.

APPLICANT: JAYATILAKE, GAMINI S.

TITLE OF INVENTION: TRITERPENE COMPOSITIONS AND METHODS FOR USE THEREOF

TILE REFERENCE: CLFR.09/999,495

CURRENT FILING DATE: 2001-11-30

PRIOR APPLICATION NUMBER: 09/314,691

PRIOR PLLING DATE: 1999-05-19

PRIOR PLLING DATE: 1999-05-19

PRIOR FILING DATE: 1998-05-19

PRIOR FILING DATE: 1998-05-19

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PALENTIN VEY: 2.0

SOFTWARE: PALENTIN VEY: 2.0

SOFTWARE: PALENTIN VEY: 2.0
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| GENERAL INFORMATION:
| APPLICANT: BLAKE, MARY E. |
| APPLICANT: BLAKE, MARY E. |
| APPLICANT: GUTTERMAN, JOSEPH J. |
| APPLICANT: BAILEY, DAVID T. |
| APPLICANT: JAYATILAKE, GAMINI S. |
| APPLICANT: JAYATILAKE, 1000 |
| FILE REFERENCE: CLFR.006 |
| CURRENT PRILING DATE: 2001-11-16 |
| PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/314,691 |
| PRIOR PPLING DATE: BARLIER FILING DATE: 1999-05-19 |
| PRIOR FILING DATE: BARLIER PILING DATE: 1998-05-19 |
| PRIOR FILING DATE: BARLIER PILING DATE: BARLIER DATE: BARLIER PILING DATE: BARLIER PILING DATE: BARLIER DATE: BARLIER PILING DATE: BARLIER PILING DATE: BARLIER PILI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic: US-09-992-837-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.4%; Score 29.8; DB 3; Length 44; 93.9%; Pred. No. 0.0065; ive 0; Mismatches 2; Indels
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               Sequence 9, Application US/0999495
Patent No. 6889389
GENERAL INFORMATION:
APPLICANT: ARNIZEN, CHARLES J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/09992837
Patent No. 6746696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Matches 31; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-999-495-9
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Matches
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US-09-114-691-9

Sequence 9, Application US/09314691

Patent No. 6444233

GENERAL INFORMATION:
APPLICANT: BLAKE, MARY E.
APPLICANT: HOFFMANN, JORDAN U.
APPLICANT: HOFFMANN, JORDAN U.
APPLICANT: HOFFMANN, JORDAN U.
APPLICANT: PALAES, DAVID T.
APPLICANT: PALAES, DAVID T.
APPLICANT: APPLICANT: DAVID T.
APPLICANT: BAILEY, DAVID T.
APPLICANT STRING DATE: 1998-09-19
EARLIER FILING DATE: 1998-09-03

EARLIER FILING DATE: 1998-09-19

EARLIER FILING DATE: 1998-05-19

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PALENTIN VEY: 2.0

SEQ ID NO 9

LENGTH: 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

78.9%; Score 30; DB 3; Length 39;
Best Local Similarity 86.8%; Pred. No. 0.0052;
Matches 33; Conservative 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 GGGGACTTTCCGCTGGGGACTTTCCACGGGGGACTTTC 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GGGACTTTCCGCTGGGGACTTTCCAGGGGGACT 34
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APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-4M-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTONENY,AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTAATION NUMBER: 27,794
REFERENCE,DOCKET NUMBER: B170 CIP 2
REGISTAATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEPHONE: (212) 596-9000
TELEPAX: (212) 596-9000
TELEPAX: (213) 596-9000
TELEPAX: (213) 596-9000
TELEPAX: (213) 596-9000
TELEPAX: (213) 596-9000
TELEPAX: (212) 596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic) US-08-235-403-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 93.9
Matches 31; Conservative
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US-09-999-495-9
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FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENGEN, Gerard H
REGISTRATION NUMBER: 35,746
TELECOMMUNICATION INFORMATION:
TELEPRANCE (904) 375-8100
TELEPRAN: (904) 372-8800
INFORMATION: (904) 372-8800
INFORMATION: (904) 372-8800
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 76.8%;
Best Local Similarity 91.2%;
Matches 31; Conservative
                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 45 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: both
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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ORIGINAL SOURCE:
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GENERAL INFORMATION:

APPLICANT: ARNYZEN, CHARLES J.

APPLICANT: BLAKE, MARY E.

APPLICANT: BLAKE, MARY E.

APPLICANT: BALLEY, DAVID T.

APPLICANT: BALLEY BA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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US-08-580-988A-12
US-08-580-988A-12
; Sequence 12, Application US/08580988A
; Patent No. 5856161
; GENERAL INFORMATION:
APPLICANT: Aggarwal et al.
TITLE OF INVENTION: Tumor Necrosis Factor
TITLE OF INVENTION: Por Its Use
TITLE OF INVENTION: For Its Use
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. Benjamin A. Adler
STREET: 8011 Candle Lane
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic ; OTHER INFORMATION: Primer US-10-000-720-9
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Pred. No. 0.0065;
0; Mismatches 2; Indel8
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   2 GGGACTTTCCGCTGGGGACTTTCCAGGGGGACT 34
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MEDIUM TYPE: 1.44 Mb floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/580,988A
FILING DATE: January 3, 1996
CLASSIFICATION: 424
                                                                     GGGACTTTCCGCTGGGGACTTTCCAGGGAGGCT
                                                                                                                                                                                                                              ; Sequence 9, Application US/10000720
; Patent No. 6962720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 78.4%;
1 Similarity 93.9%;
31; Conservative
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                   RESULT 19
US-10-000-720-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 9
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; Sequence 19, Application US/08353476
; Patent No. 587190;
; GENERAL INFORMATION:
; APPLICANT: Weininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; TORRESPONDENCE 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik STREET: 2421 N.W. 41st St., Suite A-1
CITY: Gainewille
; CITY: Gainewille
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 29.2; DB 2;
Pred. No. 0.011;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 GGGACTTTCCGCTGGGGACTTTCCAGGGAGGCGT 43
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5721CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
TELEPHONE: 713-777-6908
INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
LENGTH: 45 bp
TYPE: nucleic acid
STRANDEDNESS: double
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Patent No. 5871902

GENERAL INFORMATION:
APPLICANT: Weininger, Susan
APPLICANT: Weininger, Arthur M
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
NUMBER OF SEQUENCES: 117

CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st St., Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 29; DB 2; Length 46; Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/353,476
                                                                                                                                                                                                                       OPERATING SYSTEM: PC_DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 76.3%; Score 29; DB Best Local Similarity 100.0%; Pred. No. 0.C Matches 29; Conservative 0; Mismatches
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                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st St., Suite A-1 CITY: Gainesville STRATE: Ploxida COUNTRY: USA ZIP: 32606
                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PatentIn Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bencen, Gerard H
REGISTRATION NUMBER: 35,746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: both
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA UVDOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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US-08-353-476-20
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0
                                    76.8%; Score 29.2; DB 2; Length 45; 91.2%; Pred. No. 0.011; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 76.8%; Score 29.2; DB 2; Length 45; Best Local Similarity 91.2%; Pred. No. 0.011; Matches 31; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                            Sequence 23, Application US/08353476
| Patent No. 5871902
| GENERAL INFORMATION:
| APPLICANT: Weininger, Susan
| APPLICANT: Weininger, Arthur M
| TILLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
| TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: 2421 N.W. 41st St., Suite A-1
| CITY: Gainesville
| STATE: Florida
| COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20, Application US/08353476

BAPERAL NO. 5871902.
GENERAL INFORMATION:
APPLICANT: Weininger, Susan
APPLICANT: Weininger, Arthur
ITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
ITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 32606

ZIP: 32606

CMEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,476
                                                                                                                        2 GGGACTITCCGCTGGGGACTITCCAGGGGGACTI 35
                                                                                                                                                           7 GGGACTTTCCGCTGGGGACTTTCCAGGGAGGCGT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GGGACTITCCGCTGGGGACTITCCAGGGGGACTI 35
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                                                 91.2%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bencen, Gerard H
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100
TELEPHONE: (904) 375-8100
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
                                                        Best Local Similarity 91.2
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA
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US-08-353-476-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
                                                                                                                                                                                                                          RESULT 22
US-08-353-476-23
US-08-353-476-19
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US-08-353-476-20
                                         Query Match
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Gaps

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Weininger, Susan
APPLICANT: Weininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st St., Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 76.3%; Score 29; DB 2; Length 46; Best Local Similarity 100.0%; Pred. No. 0.014; Matches 29; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/353,476

FILING DATE:

CLASSIFICATION: 435

ATTONERY/AGBNT INFORMATION:

NAME: Bencen, Gerard H

REGISTRATION NUMBER: 35,746

REPRENCE/DOCKFY NUMBER: 35,746

TELECOMMUNICATION NUMBER: 35,746

TELECOMMUNICATION 1NFORMATION:

TELECOMMUNICATION 1NFORMATION:

TELEPAX: (904) 372-5800

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE (TARAACTERISTICS:

LENGTH: 46 base pairs
7 GGGACTTTCCGCTGGGGACTTTCCAGGGG 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 GGGACTTTCCGCTGGGGACTTTCCAGGGG 35
                                                                                                                                                                                                                                                                                 STREET: 2421 N.W. 41st St., Suite A-1 CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
CITY: BOSTON
STATE: MASSACHUCETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY.

MOLECULE TYPE: CD
                                                                                                                                                                                                                                                                                                                                                                                       Florida
: USA
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US-08-353-476-27
                                                                                                                                                                                                                                                                                                                                                                                                                             32606
                                                                                      RESULT 26
US-08-353-476-27
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                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                         Query Match 76.3%; Score 29; DB 2; Length 46; Best Local Similarity 100.0%; Pred. No. 0.014; Matches 29; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 22, Application US/08353476
Fatent No. 5871902
GENERAL INFORMATION:
APPLICANT: Weininger, Susan
APPLICANT: Weininger, Arthur M
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 32606

ZIP: 32606

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st St., Suite A-1 CITY: Gainesville STATE: Florida COUNTRY: USA ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                               2 GGGACTTTCCGCTGGGGACTTTCCAGGGG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGACTTTCCGCTGGGGACTTTCCAGGGG 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Bencen, Gerard H
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEPAX: (904) 375-8100
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
        REFERENCE/DOCKET NUMBER: GP-100
                        TELECOMMUNICATION INFORMATION:
TELEPRONE: (904) 375-8100
TELEPRONE: (904) 372-5800
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARATERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ANTI-SENSE: NO
US-08-353-476-22
                                                                                                                                                                                                                                            HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 25
US-08-353-476-22
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Sequence 142, Application US/08465590
Factor No. 2014770
GENERAL INFORMATION:
APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION:
TUTLE OF INVENTION:
NUMBER OF SEQUENCES: 164
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02109
COMPUTER READABLE FORM:
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2 GGGACTTTCCGCTGGGGACTTTCCAGGGG 30

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Sequence 142, Application US/09723909
Patent No. 6630141
GENERAL INPORMATION:
APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IXAROS: A T CELL PATHWAY REGULATORY GENE NUMBER OF SEQUENCES: 202
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 75.8%; Score 28.8; DB 3; Length 36; Best Local Similarity 93.8%; Pred. No. 0.016; Matches 30; Conservative 0; Mismatches 2; Indels
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COUNTRY: USA
ZIP: O2110-2804
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPatible
COMPUTER: IBM COMPatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEO for Windows Version 2.0b
CURRENT APPLICATION DATA: US/09/723,909
FILING DATE: 28-No. 6630141-2000
PRIOR APPLICATION DATA: US/08/711,417
APPLICATION NUMBER: US/08/711,417
FILING DATE: 02-SEP-1996
APPLICATION NUMBER: 08/238,212
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 07/946,233
RIGISTRATION NUMBER: 07/946,233
RESERRACE OF OTHER OF OTHER OT
                                      REFERENCE DOCKET NUMBER: 10287/007001
TELECOMMUNICATION INFORMATION:
TELEPRAN: 617/542-8070
TELEPRAN: 617/542-806
TELEX: 200154
INFORMATION FOR SEQ ID NO: 142:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDEDNESS: single
TOPLOGY: 1inear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 142:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GGGACTTTCCGCTGGGGACTTTCCAGGGGGAC 33
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MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 142:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 200154
INFORMATION FOR SEQ ID NO: 142:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-711-417C-142
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TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 202
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE Fish & Richardson P.C.
STRET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
COMPUTER: READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/711,417C
FILING DATE:

APPLICATION NUMBER: 08/28,212
FILING DATE:

APPLICATION NUMBER: 08/238,212
FILING DATE: 02-MA-1994
APPLICATION NUMBER: 08/121,438
FILING DATE: 14-SEP-1993
APPLICATION NUMBER: 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEY,AGENT INFORMATION:
NAME: Myers, Louis P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GGGACTITCCGCTGGGGACTITCCAGGGGGAC 33
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Ascil (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,590
FILING DATE: 05-UNN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/238,212
FILING DATE: 02-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: MYSTER PAUL L.
REGISTRATION NUMBER: 35,695
REFERENCE/DOCKET NUMBER: 35,695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 142, Application US/08711417C; Patent No. 6228611; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 142:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 75.8
Best Local Similarity 93.8
Matches 30; Conservative
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US-08-711-417C-142
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US-09-522-775A-11

Sequence 11, Application US/09522775A

Fatent No. 6660906

GENERAL INFORMATION:

APPLICANT: Taichlis, Philip N.

TITLE OF INVENTION: Inhibition of Tpl2 To Treat inflammatory Diseases

FILE REFERENCE: OTT-3202

CURRENT APPLICATION NUMBER: US/09/522,775A

CURRENT FILING DATE: 2000-03-08

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 28.4; DB 2; Length 37; Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.7%; Score 28; DB 3; Length 32; 100.0%; Pred. No. 0.032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 73.7%; Score 28; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 28; Conservative 0; Mismatches
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             CLASSIFICATION: 435
ATTORNEY/AGENT INFRMATION:
NAME: Bencen, Gerard H
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100
TELEPHONE: (904) 375-8100
TELEPHONE: (904) 372-5800
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                               74.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 96.7 Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Probe US-09-522-775A-9
                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                   TOPOLOGY: lin
MOLECULE TYPE: O
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO
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US-09-522-775A-9
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LENGTH: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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0
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TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 152
COMPUTER READMALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                        75.8%; Score 28.8; DB 3; Length 36; 93.8%; Pred. No. 0.016; 2; Indels ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 28.8; DB 6; Length 36;
Pred. No. 0.016;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 38, Application US/08353476
Patent No. 5871902
GENERAL INFORMATION:
PAPLICANT: Weininger, Susan
APPLICANT: Weininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,476
                                                                                                                              2 GGGACTITCCGCTGGGGACTITCCAGGGGGAC 33
                                                                                                                                                                       4 edeactriccecreeseactriccasesasec 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCII.
SOFTWARE: ASCII.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08743
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 946,233
FILING DATE: 14-SEP-1992
TELECOMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7410
TELEPHONE: (617)227-7410
TELEPHONE: (617)227-7410
TELEPHONE: (617)227-7410
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
LENGTH: 36 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSEE: Saliwanchik & Saliwanchik
7: 2421 N.W. 41st St., Suite A-1
Gainesville
                                                                                                                                                                                                                                                        TT-US93-08743-142
Sequence 142, Application PC/TUS9308743
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GGGACTTTCCGCTGGGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 75.8%;
Best Local Similarity 93.8%;
Matches 30; Conservative
                                      Query Match 75.8
Best Local Similarity 93.8
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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STATE: Florida
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US-09-723-909-142
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US-08-353-476-38
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 Gaps
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Patent No. 6660906
GENERAL INFORMATION:
TITLE OF INVENTION: Inhibition of Tpl2 To Treat inflammatory Diseases
FILE REFERENCE: OTT-3202
CURRENT APPLICATION NUMBER: US/09/522,775A
CURRENT FILING DATE: 2000-03-08
NUMBER OF SEQ ID NOS: 13
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us-09-669-187a-148.szlm50.rni

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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide US-09-533-341-6
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APPLICANT: Lipton, James M.
APPLICANT: Catania, Anna P.
TITLE CATANIAN: CATANIAN CATANIAN PRINTINFLAMMATORY PEPTIDES FOR USE IN HUMAN TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS
FILER REFERENCE: 54275.8004.US00
CURRENT APPLICATION NUMBER: US/09/533,341
CURRENT FILING DATE: 2000-03-23
PRIOR FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 35
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Pred. No. 0.05;
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APPLICANT: Weininger, Susan
APPLICANT: Weininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 GGGACTTTCCGCTGGGGACTTTCCAGAGGGGT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GGGACTTTCCGCTGGGGACTTTCCAGGGGGACTT 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Patent No. 5871902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/09533341
Patent No. 6803044
TELECOMMUNICATION INFORMATION
                            TELEPHONE: (904) 375-8100
TELEPAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 26:
SEGUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                     72.6%;
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Best Local Similarity 96.6'
Matches 28; Conservative
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MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

NATI-SENSE: NO

US-08-353-476-26
                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: both
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APPLICANT: Zengen, Inc.
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Best Local Similarity
Matches 30; Conserv
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Pred. No. 0.032;
0; Mismatches 0; Indels
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100.0%; Pred. No. 0.033;
cive 0; Mismatches 0; Indels
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Patent No. 5871902
GENERAL INFORMATION:
APPLICANT: Weininger, Susan
APPLICANT: Weininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,476
                                                                                                                                                          Query Match 73.7%; Score 28; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 28; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                    2 GGGACTTTCCGCTGGGGACTTTCCAGGG 29
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STREET: 2421 N.W. 41st St., Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Bencen, Gerard H
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100
      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 100.0
---hes 28; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                             CTHER INFORMATION: Probe US-09-522-775A-11
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US-08-353-476-26
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US-09-440-967-4
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nucleic acid
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                                            MOLECULE TYPE:
             STRANDEDNESS:
TOPOLOGY: li
                                                           HYPOTHETICAL:
                                                                           ANTI-SENSE:
                                                                                          US-08-353-476-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,476
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/ARBNT INFORMATION:
NAME: Bencen, Gerard H
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: 35,746
TELECOMMUNICATION INFORMATION:
TELEFONE: (904) 372-5800
TELEFONE: (904) 372-5800
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LANGTH: 44 base pairs
        COMPUTER READABLE FORM:
MEDTUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/353,476
FILING DATE:
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                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Bencen, Gerard H
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                      CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                linear
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Matches 31; Conserv
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MOLECULE TYPE:
HYPOTHETICAL: N
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US-08-353-476-25
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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APPLICANT: Zengen, Inc.
APPLICANT: Lipton, James M.
APPLICANT: Lipton, James M.
APPLICANT: Catania, Anna P.
TITLE OF INVENTION: ANTIMICROBIAL AND ANTI-INFLAMMATORY PEPTIDES FOR USE IN HUMAN
TITLE OF INVENTION: IMMONOBERICIENCY VIRUS
FILE REPERRACE: 54275.8004.US90
CURRENT APPLICATION NUMBER: US/09/533,341
CURRENT PILING DATE: 2000-03-23
PRIOR PPLICATION NUMBER: US 60/126,233
PRIOR FILING DATE: 1999-03-24
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APPLICANT: Lipton, M.J.
APPLICANT: Lipton, M.J.
APPLICANT: Lipton, M.J.
TILLE CALAILA, A.J.
TILLE OF LIPTONION A LYS-PRO-VAL DIMER, FORMULATIONS AND APPLICATIONS
FILE REFERENCE: 54275.8005.US00
CURRENT APPLICATION NUMBER: US/09/535,066F
CURRENT PILING DATE: 2000-03-23
PRIOR APPLICATION NUMBER: US 60/126,233
PRIOR FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 35
                                                             Gaps
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69.5%; Score 26.4; DB 3; Length 35;
Best Local Similarity 96.4%; Pred. No. 0.14;
Matches 27; Conservative 0; Mismatches 1; Indels
                                                          Indels
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Score 27.2; DB 2;
Pred. No. 0.072;
0; Mismatches 3;
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Patent No. 6800291
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Patent No. 6803044
GENERAL INFORMATION:
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SOFWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
  Query Match 71.6%;
Best Local Similarity 90.6%;
Matches 29; Conservative
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Query Match
Best Local Similarity 100.
Matches 26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 44
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Patent No. 6773705
GENERAL INFORMATION:
APPLICANT: Faustman et al., Denise L.
TITLE OF INVENTION: Mthods for disagnosing and treating autoimmune disease FILE REFERENCE: 1763-1120 Kethleen M. Williams
CURRENT APPLICATION NUMBER: US/09/258,682
CURRENT APPLICATION NOWBER: US/09/258,682
SUMMER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                       Gaps
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                                                                        69.5%; Score 26.4; DB 3; Length 35; 96.4%; Pred. No. 0.14; 1ve 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                    1 GGGGACTTTCCGCTGGGGACTTTCCAGG 28
                                                                                                                                                                                                                                                                                                       8 GGGGACTTTCCGCTGGGGACTTTCCATG 35
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US-08-484-397A-25
; Sequence 25, Application US/08484397A
; Patent No. 5869055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
                                      Query Match
Best Local Similarity 96.4.
These 27; Conservative
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US-09-031-629A-5
JS-09-533-341-5
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US-09-258-682-1
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LENGTH: 32
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APPLICANT: Juan Shao-Chieh
APPLICANT: Lichenstein, Henri S.
APPLICANT: Wright, Samuel D.
TITLE OF INVENTION: ANTI-INFLAMMATORY CD14 POLYPEPTIDES
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSE: AMGEN INC
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 33;
GENERAL INFORMATION:
APPLICANT: Juan, Shao-Chieh
APPLICANT: Lichenstein, Henri S.
APPLICANT: Lichenstein, Henri S.
APPLICANT: Lichenstein, Henri S.
APPLICANT: APPLICANT: STICH D.
TITLE OF INVENTION: ANTI-INFLAMMATORY CD14 POLYPEPTIDES
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC
STREET: Lade Declavilland Drive
CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                      CITY: Thousand Oaks
CITY: Thousand Oaks
CITY: US
COUNTRY: US
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDTUM TYPE: CIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,397A
FILLING DATE: O7-JUM-1995
CLASSIFICATION: 424
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,397A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.4%; Score 26; DB 100.0%; Pred. No. 0.2 ive 0; Mismatches
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; Sequence 26, Application US/08484397A
; Patent No. 5869055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A-324A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: CURTY, DAILEL R.
REGISTRATION NUMBER: 32,727
REFERENCE/DOCKET NUMBER: A-33
TELECOMMUNICATION INFORMATION:
TELECHONE: 805/447-1000
TELEFAX: 805/447-1090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS: LENGTH: 33 base pairs TYPE: nucleic acid STRANDEDNESS: single
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Batent No. 5871902

GENERAL INFORMATION:
APPLICANT: Weininger, Susan
TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: BM PC Compatible
COMPUTER: BM PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CUMSTRIATION NUMBER: US/08/353,476
FILING DATE:
CLASSIFICATION: 435.3,746
REGISTRATION NUMBER: 35,746
REGISTRATION NUMBER: 35,746
REGISTRATION NUMBER: 35,746
REGISTRATION NUMBER: 35,746
REGISTRATION NUMBER: GP-100
TELECOMMUNICATION INFORMATION:
TELEFHONE: (904) 375-8100
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Bencen, Gerard H
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100
TELECOMMUNICATION INFORMATION:
TELEPRONE: (904) 375-5800
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 CTTTCCGCTGGGGACT
                     ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: both
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US-08-353-476-30
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COUNTRY:
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APPLICANT: Lipton, M.J.
APPLICANT: Catania, A.P.
TITLE OP INVENTION: A LP.
TITLE OP INVENTION: A LP.
FILE REFERENCE: 54275.6005.US00
CURRENT APPLICATION NUMBER: US/09/535,066F
CURRENT FILING DATE: 2000-03-23
PRIOR APPLICATION NUMBER: US 60/126,233
PRIOR PILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 10
SSCTWARES: Patentin version 3.1
SSCTWARES: Patentin version 3.1
SEQ ID NO 10
LENGTH: 35
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Patent No. 5871902

GENERAL INFORMATION:

APPLICANT: Weininger, Susan

APPLICANT: Weininger, Arthur M

TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION

NUMBER OF SEQUENCES: 117

CORRESPONDENCE ADDRESS:

ADDRESSE: Saliwanchik & Saliwanchik

STREET: 2421 N W. 41st St., Suite A-1

CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                          Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Oligonuclectide probes for NF-kB.
US-09-535-066F-10
                                                                                                                                                                                                                                                                                                                                                         68.4%; bccc. No. c. 100.0%; Pred. No. c. 0; Mismatches
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US-09-535-066F-10/c
; Sequence 10, Application US/09535066F
; Patent No. 6806291
                                                                      A-324A
                 REGISTRATION NUMBER: 32,727
REFERENCE/DOCKET NUMBER: 32,727
REFERENCE/DOCKET NUMBER: 32,727
REFERENCE/DOCKET NUMBER: 32,727
TELECOMMUNICATION INFORMATION:
TELEPAN: 805/47-1000
TELEFAX: 805/47-1000
INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
LENGTH: 33 base pairs
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
MOLECTUE TYPE: CDNA
US-08-484-397A-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: ZENGEN, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Florida
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US-08-353-476-30
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                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 44, Application US/08479852
Sequence 44, Application US/08479852
Patent No. 5712385
GENERAL INFORMATION:
APPLICANT: Sherrol H. McDonough, Thomas B. Ryder,
APPLICANT: Yeasing Yang
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION
TITLE OF INVENTION: OLIGONUCLEOTIDES AND PROBES
TITLE OF INVENTION: TO HUMAN IMMUNDEFICIENCY VIRUS TYPE 1
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 27;
                                                                                                                                          DB 3; Length 25; 1.2;
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: 1BM P.2 Model 50Z or 55SX
OPERATING SYSTEM: 1BM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA: US/08/479,852
FILING DATE:
CLASSIFICATION 135
PRIOR APPLICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/040,745
                                               ; FEATURE:
; OTHER INFORMATION: Synthesized nucleotide sequence
US-09-844-915-2
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Pred. No. 1.3;
                                                                                                                                        Query Match 63.2%; Score 24; DB Best Local Similarity 100.0%; Pred. No. 1.2 Matches 24; Conservative 0; Mismatches
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100.0%; Pre
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STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
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  TYPE: DNA ORGANISM: Artificial Sequence
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morrePAX: (213) 955-0440
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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Patent No. 6936468

GENERAL INFORMATION:
APPLICANT: Robbins, Paul D.
APPLICANT: Lu, Lina
APPLICANT: Glannoukakis, Nick
TITLE OF INVENTION: TOR ENHANCING TOLEROGENICITY IN A HOST AND METHODS FOR TITLE OF INVENTION: TOR BHANCING TOLEROGENICITY IN A HOST AND TITLE OF INVENTION: MAKING THE SAME
CURRENT APPLICATION NUMBER: US/09/844,915
CURRENT APPLICATION NUMBER: 60/200,479
PRIOR APPLICATION NUMBER: 60/200,479
PRIOR PILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 1
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; Sequence 2, Application US/09844915
; Patent No. 6936468
; GENERAL INPORMATION:
APPLICANT: Robbins, Paul D.
APPLICANT: Lu, Lina
APPLICANT: Gamnoukakis, Nick
TITLE OF INVENTION: FOR ENHANCING TOLEROGENICITY IN A HOST AND METHODS FOR
TITLE OF INVENTION: MAKING THE SAME
FILE REFERENCE: AP12.717 0.7236.0225
; CURRENT APPLICATION NUMBER: 05.200.479
; PRIOR APPLICATION NUMBER: 60.200.479
; PRIOR PILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 2
; SEQ ID NO 2
; LENGTH: 25
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; OTHER INFORMATION: Synthesized nucleotide sequence
US-09-844-915-1
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ORGANISM: Artificial Sequence
27 base pairs
                 TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
MANTI-SENSE: NO
US-08-353-476-7
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US-09-844-915-1
LENGTH:
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Search completed: February 15, 2006, 21:14:22 Job time : 89.4215 secs

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US-10-235-682-9

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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: chimeric phosphorothioate/phosphodiester backbone
OTHER INFORMATION: with phosphorothioate at 5' and 3' ends
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Publication No. US20030087848A1

GENERAL INFORMATION:

APPLICANT: Bratzler, Robert L.

APPLICANT: Bratzler, Deanna M.

TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Lacatment of Asthma and Allergy FILE REFERENCE: C1037/7013 (HCL/MAT)

CURRENT APPLICATION NUMBER: US/09/776,479

FRIOR APPLICATION NUMBER: US 60/179,991

PRIOR PILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 1093

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 38
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Matches 38; Conservative 0; Mismatches 0;
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100.0%; Score 38; DB 3; I
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 38; Conservative 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/09/888,326
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: US 60/213,346
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 848
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO
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US-11-036-317-784869
US-11-036-317-934251
 US-10-681-773-71139
US-10-719-956-136286
US-10-719-956-520851
US-10-719-956-520851
US-10-719-956-589484
US-10-719-956-589485
US-10-719-900-727474
US-10-719-900-727474
US-10-719-900-87398
US-10-719-900-87398
US-10-719-900-87398
US-10-719-900-87398
US-10-809-188-88802
US-10-809-188-88802
US-10-809-189-124375
US-10-956-157-112549
US-10-956-157-11257
US-10-956-157-11257
US-10-956-157-11257
US-10-956-157-11257
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US-10-956-157-11257
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US-10-098-263B-119129
US-10-681-773-82622
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US-10-669-841-10683
US-10-601-610-5
US-10-098-263B-9124
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US-10-719-956-398069
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US-10-294-934-664
US-09-864-785-3351
US-09-877-478-5792
US-09-770-478-5792
US-10-156-336-7511
US-10-156-336-7511
US-10-342-902-5792
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Gaps

RESULT 3
US-09-776-479-148
US-09-776-479-148
Squence 148, Application US/09776479
Fublication No. US20040067902A9
GENERAL INFORMATION:
APPLICANT: Bratzler, Robert L.
APPLICANT: Pouron, Yves
TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Treatment of Asthma and Allergy
TITLE OF INVENTION: Treatment of Asthma and Allergy
FILE REPERENCE: C1037/7013 (HCL/MAT); CURRENT APPLICATION NUMBER: US/09/776,479

Sequence 417, Application US/0988326;
Publication No. US20030026801A1;
GENERAL INFORMATION:
APPLICANT: Weiner, George;
APPLICANT: Hartmann, Gunther;
TITLE OF INVENTION: Methods for Enhancing Antibody-Induced;
TITLE OF INVENTION: Cell Lysis and Treating Cancer;
FILE REFERENCE: C1039/7052 (AWS)

US-09-888-326-417

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Gaps

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Sequence 141, Application US/10112653

Publication No. US2003005268A1

GENERAL INFORMATION:

APPLICANT: Krieg, Arthur M.

APPLICANT: Berg, Daniel J.

TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR

TITLE OF INVENTION: TRADMENT OF NON-ALLERGIC INFLAMMATORY DISBASES

FILE REFERENCE: C01039/70060(AMS)

CURRENT APPLICATION NUMBER: US 60/2/9,642

PRIOR FILING DATE: 2002-03-29

PRIOR FILING DATE: 2001-03-29

NUMBER OF SEQ ID NOS: 1040

SEQ ID NO 141

LENGTH: 38
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US-10-017-995-148

US-10-017-995-148

Sequence 148, Application US/10017995

Publication No. US20030055014A1

GENERAL INFORMATION:

APPLICANT: Bratzler, Robert L.

TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids

FILE REFERENCE: C1037/7025 (HCL/MAT)

CURRENT FILING DATE: 2001-12-18

PRIOR APPLICATION NUMBER: US 60/255,534

PRIOR FILING DATE: 2000-12-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 38; DB 5; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 38; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                           Length 38;
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100.0%; Score 38; DB 3; I
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 38; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Synthetic Oligonucleotide US-10-112-653-141
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: US 60/179,991
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 148
LENGTH: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 148
LENCTH: 38
                                                                                                                                                                                                                                               OTHER INFORMATION: Synthetic Sequence
                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                           US-09-776-479-148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
US-10-112-653-141
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                                                                                                                                                                                                                          FEATURE:
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Sequence 148, Application US/10831778

Sequence 148, Application US/10831778

Publication No. US20040235774A1

GENERAL INFORMATION:

APPLICANT: Bratzler, Robert L.

APPLICANT: Petersen, Deanna M.

APPLICANT: Petersen, Deanna M.

TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION UNUBER: US/10/831,778

CURRENT FILING DATE: 2000-02-03

PRIOR FILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 1093

SOFTWARE: FastSEQ for Windows Version 3.0

LENGHAL: 38

***CHARL SECTION UNIBER OF SEQ ID NO 148

***LENGHAL: 38

***CHARL SECTION UNIBER OF SEQ ID NO 148

***LENGHAL: 38
                                                                                                                                                                    Length 38;
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                                                                                                                                                                                                                                                        0; Indels
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US-10-314-578-148

Sequence 148, Application US/10314578

Publication No. US20030212026A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Vollmer, Uncy timunostimulatory Nucleic Acids
FILE REFERENCE: C1039/7035 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/10/314,578
CURRENT APPLICATION NUMBER: US 60/156,113
PRIOR PELING DATE: 1999-09-25
PRIOR APPLICATION NUMBER: US 60/156,135
PRIOR APPLICATION NUMBER: US 60/156,135
PRIOR APPLICATION NUMBER: US 60/156,135
PRIOR APPLICATION NUMBER: US 60/156,136

PRIOR APPLICATION NUMBER: US 60/156,136
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100.0%; Pred. No. 2.7e-05;
tive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 38; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INPORMATION: Synthetic Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                        Query Match
Best Local Similarity 100.0
Matches 38; Conservative
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APPLICANT: Weininger, Susan
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US-08-860-844-29

is Sequence 29, Application US/08860844

is Sequence 29, Application US/08860844

is Publication No. US20030104361A1

is GENERAL INFORMATION:

APPLICANT: Weininger, Arthur M

TITLE OF INVENTION: RETHOD OF DETECTION OF NUCLEIC ACIDS WITH A

TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION

NUMBER OF SEQUENCES: 118

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik & Saliwanchik

STREF: 2421 N.W. 41st St., Sulte A-1

CITY: Gainesville

STATE: Florida

CONNTRY: USA
                                                                                                      Gaps
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                                            Query Match
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 38; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: EN PC Compatible

COMPUTER: EN PC Compatible

COPERATIOS SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURSENT APPLICATION DATA:

APPLICATION NUMBER: 09-JUN-1997

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: 08/353,476

FILING DATE: 09-DEC-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Saliwanchik, David R.

REFERENCE/DOCKET NUMBER: 35,746

REFERENCE/DOCKET NUMBER: 35,746

REFERENCE/DOCKET NUMBER: GP-100C1

TELEFONDE: (352) 375-8100

TELEFONDE: (352) 375-8100
                                                                                                                                                                                1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38
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US-10-407-543-29
; Sequence 29, Application US/10407543
; Publication No. US20030175789A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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US-08-860-844-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
US-10-831-778-148
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TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A SPECIFIC SEQUENCE COMPOSITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 28, Application US/08860844
; Publication No. US20030104361A1
; GENERAL INFORMATION:
APPLICANT: Weininger, Susan
; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
; TITLE OF INVENTION: SEQUENCES: 118
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Best Local Similarity 94.1%; Pred. No. 0.019;
Matches 32; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                          ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GGGGACTITCCGCTGGGGACTITCCAGGGGGACT 34
                                                 NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEB: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 418t St., Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/407,543
FILING DATE: 03-Apr-2003
CLASSIFICATION NUMBER: US/08/860,844
FILING DATE: 09-DN-1997
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 35,746
REGISTRATION NUMBER: 35,746
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 43 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (352) 372-5
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                         STATE: Florida
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ADDRESSEE: Saliwanch
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SEQUENCE DESCRIPTION: SEQ ID NO: 28
                             TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHRACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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              TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLAKE, MARY E. GUTTERMAN, JORDAN U. HOFFMANN, JOSEPH J. BAILEY, DAVID T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 78.4%;
Best Local Similarity 93.9%;
Matches 31; Conservative
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                                                                                                                                                                                                                                            HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                    US-10-407-543-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
US-09-992-837-9
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Publication No. US20030175789A1
GENERAL INFORMATION:
APPLICANT: Weininger, Susan
Heininger, Arthur Meininger, Arthur Arthur
Heininger, Arthur SPECTION OF NUCLEIC ACIDS WITH
SPECIFIC SEQUENCE COMPOSITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 79.5%; Score 30.2; DB 2; Length 46; Best Local Similarity 91.4%; Pred. No. 0.032; Matches 32; Conservative 0; Mismatches 3; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/10/407,543
FILING DATE: 03-Apr-2003
CLASSIFICATION: 435
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION ADATA:
APPLICATION NUMBER: 08/353,476
FILING DATE: 09-DEC-1994
FILING DATE: 09-DEC-1994
FLING DATE: 09-DEC-1994
FLING DATE: 03-DEC-1994
FLING DATE: 03-DEC-1994
FLEASIFICATION NUMBER: 08/353,476
REFERENCE/POCKET NUMBER: GP-100C1
TELEPHONE: 37-8100
TELEPHONE: 37-37-8100
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st St., Suite A-1 CITY: Gainesville STATE: Florida COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-UN-1997
APPLICATION NUMBER: 08/353,476
FILING DATE: 09-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISCTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: both
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGICAL TYPE: CD
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US-10-407-543-28
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Sequence 9, Application US/09992837

Publication No. US20030039705A1

GENERAL INFORMATION:

APPLICANT: ARNTZEN, CHARLES J.

APPLICANT: BLAKE, MARY E.

APPLICANT: BLAKE, MARY E.

APPLICANT: BAILEY, DAVID T.

APPLICANT: APPLICANT: ATTERPENE COMPOSITIONS AND METHODS FOR USE THEREOF TILLE REFERENCE: CLFR:006

CURRENT APPLICATION NUMBER: US/09/992,837

FILE REFERENCE: CLFR:006

CURRENT FILING DATE: 2001-11-16

PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-19

PRIOR PLING DATE: EARLIER FILING DATE: 1998-05-19

NUMBER OF SEQ ID NOS: 9

SEQ ID NO 9

LENGTH: 44
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Pred. No. 0.046;
0; Mismatches 2; Indels
Length 46;
                                            Indels
79.5%; Score 30.2; DB 6; 91.4%; Pred. No. 0.032;
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                                              0; Mismatches
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APPLICANT: ANYLEAN.
APPLICANT: BLAKE, MARY E.
APPLICANT: BLAKE, MARY E.
APPLICANT: HOFFWANN, JOSEPH J.
APPLICANT: HOFFWANN, JOSEPH J.
APPLICANT: BAILEY, DAVID T.
APPLICANT: BAILEY, DAVID T.
APPLICANT: BAILEY, DAVID T.
APPLICANT: JAYATILAKE, GAMINI S.
TITLE OF INVENTION: TRITERPENE COMPOSITIONS AND METHODS FOR USE THEREOF FILER REFERENCE: CLFR: 1006
CURRENT APPLICATION NUMBER: US/10/000,720
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-05-19
PRIOR PLING DATE: EARLIER FILING DATE: 1999-05-19
PRIOR PILING DATE: EARLIER FILING DATE: 1998-05-03
PRIOR PLING DATE: EARLIER FILING DATE: 1998-05-03
PRIOR PLING DATE: PARLIER PILING DATE: 1998-05-19
SOFTHARE: PALENTIN VOY: 2.0
SEQ ID NO 9
APPLICANT: JAYATILAKE, GAMINI S.
TILES OF INVENTION: TRITERPENE COMPOSITIONS AND METHODS FOR USE THEREOF FILE REFERENCE: CLFR:006
CURRENT APPLICATION NUMBER: US/09/999,495
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 09/314,691
PRIOR APPLICATION NUMBER: 60/099,066
PRIOR PILING DATE: 1998-09-03
PRIOR PILING DATE: 1998-09-03
PRIOR PLING DATE: 1998-05-19
PRIOR APPLICATION NUMBER: 60/085,997
PRIOR PILING DATE: 1998-05-19
SOFTWARE: PATENTIN VOIC: 2.0
SEQ ID NOS: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.4%;
                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 44
TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Seguence
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Best Local Similarity 93.9
Matches 31; Conservative
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Best Local Similarity
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US-10-000-720-9
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RESULT 15

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Sequence 9, Application US/10238647

Publication No. US20030203049A1

GENERAL INFORMATION:

APPLICANT: ARNYZEN, CHARLES J.

APPLICANT: GITTERMAN, JORDAN U.

APPLICANT: GITTERMAN, JOSDEH J.

APPLICANT: GITTERMAN, JOSDEH J.

APPLICANT: TRITEREEN COMPOSITIONS AND METHODS FOR USE THEREOF

TILLE OF INVANTION: TRITEREEN COMPOSITIONS AND METHODS FOR USE THEREOF

FILE REFERENCE: CLFR:006

CURRENT APPLICATION NUMBER: US/10/238,647

CURRENT PILING DATE: 1999-05-19

PRIOR FILING DATE: 1999-05-19

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PATENTIN VEY: 2.0

SEQ ID NO 9

LENGTH: 44
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Publication No. US20030104361A1

GENERAL INFORMATION:

APPLICANT: Weininger, Susan

APPLICANT: Weininger, Arthur M

TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A

TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION

NUMBER OF SEQUENCES: 118

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st St., Suite A-1

CITTLE OF INVENTION: SPECIFIC SEQUENCE COUNTRY: USA
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COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-DVN-1997
CLASSIFICATION NUMBER: 08/353,476
FILING DATE: 09-DEC-1994
CLASSIFICATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: 35,746
REFERENCE/DOCKET NUMBER: 36-100C1
TELECOMMUNICATION NUMBER: 35,746
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Matches 31; Conservative
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US-08-860-844-19
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7 GGGACTTTCCGCTGGGGACTTTCCAGGGAGGCGT 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23, Application US/08860844
Publication No. US20030104361A1
GENERAL INFORMATION:
APPLICANT: Weininger, Susan
APPLICANT: Weininger, Arthur Maininger, Arthur Maininger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                              Length 45;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPRATING SYSTEM:
PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,844
PLING DATE: 09-UN-1997
CLASSIFICATION 1435
PRIOR APPLICATION 1435
PRIOR APPLICATION DATE: 09-UN-1997
CLASSIFICATION NUMBER: 08-DEC-1994
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Saliwanchik, David R.
REFERENCE/DOCKET NUMBER: 35-746
REGISTRATION NUMBER: 35-746
REFERENCE/DOCKET NUMBER: 37-86
TELEPHONE: 35-23 375-8800
INFORMATION FOR SEQ ID NO: 23:
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Pred. No. 0.08;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 GGGACTTTCCGCTGGGGACTTTCCAGGGAGGCGT 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSEE: Saliwanchik & Saliwanchik
F: 2421 N.W. 41st St., Suite A-1
Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                      76.8%;
91.2%;
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Best Local Similarity 91.2%;
Matches 31; Conservative
                                                 LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
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LENGTH: 45 base pairs
   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31; Conservative
                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                      MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                     US-08-860-844-19
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US-08-860-844-23
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2 GGGACTTTCCGCTGGGGACTTTCCAGGGGGACTT 35

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Weininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
SPECIFIC SEQUENCE COMPOSITION
                                                                                                                    Weininger, Arthur M
IIILE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
SPECIFIC SEQUENCE COMPOSITION
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                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
CORPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/407,543
FILING DATE: 03-Apr-2003
CILASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-DEC-1994
FILING DATE: 09-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 45;
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Pred. No. 0.08;
0; Mismatches 3;
                                                                                                                                                                                        NUMBER OF SEQUENCES: 118
CORRESSPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st St., Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
US-10-407-543-19; Sequence 19, Application US/10407543; Publication No. US20030175789A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23, Application US/10407543 Publication No. US20030175789A1 GENERAL INFORMATION:
                                                                                           APPLICANT: Weininger, Susan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 45 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 76.8%;
Best Local Similarity 91.2%;
Matches 31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                ZIP: 32606
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: cDNA
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Gaps
                        Gaps
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Publication No. US20050080023A1;
GENERAL INFORMATION:
APPLICANT: Aggarwal, Bharat B.
TITLE OF INVENTION:
CURRENT AFPLICATION UNBER: US/10/925,608;
CURRENT FILING DATE: 2004-08-25;
PRIOR APPLICATION NUMBER: US 60/497,841
PRIOR FILING DATE: 2003-08-26;
NUMBER OF SEQ ID NOS: 1
SEQ ID NO 1:
LENGTH: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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NAME/KEY: protein bind
OTHER INFORMATION: oligonucleotide from the human immunodeficiency
OTHER INFORMATION: virus long terminal repeat containing
OTHER INFORMATION: NF-kB binding site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Aggarwal, Bharat B.
APPLICANT: Aggarwal, Bharat B.
APPLICANT: Singh, Sujay
TITLE OF INVENTION: Selective Inhibitors of Nuclear
TITLE OF INVENTION: Factor-?B Activation And Uses Thereof
FILE REFERENCE: D6526
CURRENT APPLICATION NUMBER: US/10/981,082
CURRENT FILING DATE: 2004-11-04
PRIOR FILING DATE: 2003-11-06
NUMBER OF SEQ ID NOS: 13
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 76.8%; Score 29.2; DB 9; Best Local Similarity 91.2%; Pred. No. 0.08; Matches 31; Conservative 0; Mismatches 3;
                                                                                                   10 GGGACTTTCCGCTGGGGACTTTCCAGGGAGCCT 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAGGGGGACTT 35
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91.2%; Pred. No. 0.08;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: NF-kappB oligonucleotide US-10-925-608-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/10981082 Publication No. US20050201976A1 GENERAL INFORMATION:
  Best Local Similarity 91.2
Matches 31; Conservative
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                                                                                                                                                                                      RESULT 21
US-10-925-608-1
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US-10-981-082-1
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OTHER INFORMATION: NF- B oligonucleotide from human immunodeficiency
OTHER INFORMATION: virus-1 long terminal repeat
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Publication No. US20040058021A1
GENERAL INFORMATION:
APPLICANT: Aggarwal; Bharat
TITLE OF INVENTION: Treatment of Human Multiple Myeloma by Curcumin FILE REFERENCE: D6467
CURRENT APPLICATION NUMBER: US/10/602,303
CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: US 60/390,926
PRIOR APPLICATION NUMBER: US 60/390,926
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 4
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Pred. No. 0.08;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
                 ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st St., Suite A-1 CITY: Gainesville STATE: Florida COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAGGGGGACTT 35
                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/407,543

FILING DATE: 03-Apr-2003

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/860,844

FILING DATE: 09-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: Saliwanchik, David R.

REGISTRATION NUMBER: 35,746

REFERENCE/DOCKET NUMBER: 35,746
                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ANTI-SENSE: NO SEQUENCE DESCRIPTION: SEQ ID NO: 23: US-10-407-543-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Human immunodeficiency virus-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INPORMATION:
TELEPHONE: (352) 375-8100
ENERGAM: (352) 372-5800
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 45 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 91.2%;
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: both
    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-602-303-4
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Sequence 22, Application US/08860844

| Sequence 22, Application US/08860844
| Publication No. US20030104361A1
| GENERAL INFORMATION:
| APPLICANT: Weininger, Susan
| APPLICANT: Weininger, Atthur M
| TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
| TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
| NUMBER OF SEQUENCES: 18
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Saliwanchik & Saliwanchik | STREET: 2421 N.W. 41st St., Suite A-1 | CITY: Gainesville | STREET: Proxida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 76.3%; Score 29; DB 2; Length 46; Best Local Similarity 100.0%; Pred. No. 0.096; Matches 29; Conservative 0; Mismatches 0; Indels
                                 COMPUTER: PLOPPY disk
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PLOPPY disk
COMPUTER: PLEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-JUN-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/353,476
FILING DATE: 09-DEC-1994
CLASSIFICATION NUMBER: 08-1353,476
FILING DATE: 09-DEC-1994
CLASSIFICATION NUMBER: 08-1353,466
FILING DATE: 03-135-146
REFERENCE/DOCKET NUMBER: 35,746
REFERENCE/DOCKET NUMBER: 35,746
REFERENCE/DOCKET NUMBER: 35-160
TELEROMMUNICATION INFORMATION:
TELEROMMUNICATION INFORMATION:
TELEROMMUNICATION INFORMATION:
TELEROMMUNICATION FOR SEQ ID NO: 21:
SEQUIENCE CHARACTERISTICS:
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COUNTRY: USA

ZIP: 32606

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/060,844

FILING DATE: 09-UW1-1997

CLASSIFICATION 1435

PRIOR APPLICATION 1435

PRIOR APPLICATION NUMBER: 08/353,476

FILING DATE: 09-DEC-1994

CLASSIFICATION: 435

CLASSIFICATION: ASTONER: 08-DEC-1994

CLASSIFICATION: ASTONER: 08-DEC-1994

ATTORNEY/AGENT INPORMATION:
NAME: Saliwanchik, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GGGACTTTCCGCTGGGGACTTTCCAGGGG 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ANTI-SENSE:
US-08-860-844-21
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US-08-860-844-22
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RESULT 23
US-08-860-844-20
is Sequence 20, Application US/08860844
j Publication No. US20030104361A1
j GENERAL INFORMATION:
APPLICANT: Weininger, Susan
j APPLICANT: Weininger, ALTILE OF INVENTION:
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSE: Saliwanchik & Saliwanchik
LINEAR OF SALIWANCHIK & Saliwanchik
SURESSED: AA11 N.W. 41st St., Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Sublication No. US20030104361A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Weininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
NUMBER OF SEQUENCES:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st St., Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

CONFUREN: APPLICATION DATA:

APPLICATION NUMBER: US/08/860,844

FILING DATE: 09-UN-1997

CLASSIFICATION DATA:

APPLICATION NUMBER: 08/353,476

FILING DATE: 09-DEC-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INPORMATION:

REGISTRATION NUMBER: 35,746

REFERENCE/DOCKET NUMBER: GP-100C1

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION INFORMATION INFORMATION INFORMATI
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STRANDEDNESS: both
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGI.
MOLECULE TYPE: CD
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f: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-860-844-20
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US-08-860-844-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
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Gaps

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Length 46;

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76.3%; Score 29; DB 2; 100.0%; Pred. No. 0.096;
                         ilarity 100.0%; Pred. No. 0.0
Conservative 0; Mismatches
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                                                                                            2 GGGACTITCCGCTGGGGACTITCCAGGGG
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Best Local Similarity 100.0
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL: NO ANTI-SENSE: NO
  Query Match
Best Local Similarity
Matches 29; Conserv
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                                                                                                                                                                                                      RESULT 27
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US-08-860-844-27
; Sequence 27, Application US/08860844 ...
; Sequence 27, Application US/08860844 ...
; Publication No. US20030104361A1
; GENERAL INFORMATION:
    APPLICANT: Weininger, Susan
; APPLICANT: Weininger, Arthur M
    TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS: 1
ADDRESSE: Saliwanchik & Saliwanchik STREF: SA21 N W 418t St., Suite A-1
; CITY: Gainesville
; COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/353,476
FILING DATE: 09-DEC-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GGGACTTTCCGCTGGGGACTTTCCAGGGG 30
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REGISTRATION NUMBER: 35,746
REPERENCE/OCKET NUMBER: GP-100C1
TELEPHONE: (352) 375-8100
FELEPHONE: (352) 375-8100
FELEPHONE CAPACTERISTICS: SEQUENCE CHARACTERISTICS: LENGTH: 46 base pairs
FERMINEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SAliwanchik, David R.
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 372-8800
TELEPAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                     Query Match 76.3
Best Local Similarity 100.
Matches 29; Conservative
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STRANDEDNESS: both
                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                         ; ANTI-SENSE: NO US-08-860-844-22
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US-08-860-844-27
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Weininger, Arthur Merthur Menininger, Arthur Merthor OF DETECTION OF NUCLEIC ACIDS WITH A
TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
SPECIFIC SEQUENCE COMPOSITION
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                                                                                                                                                                                                                                                                                                                                                             ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/10/407,543

FILING DATE: 03-Apr-2003

CLASSIFICATION: 435
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                                                                                                                                                                                        NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSES: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st St., Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-UN-1997
APPLICATION NUMBER: 08/353,476
FILING DATE: 09-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 35,746
REGISTRATION NUMBER: 35,746
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
INFORMATION FOR SEQ IN NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.3%; Score 29; DB 100.0%; Pred. No. 0.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
US-10-407-543-20
; Sequence 20, Application US/10407543
; Publication No. US20030175789A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21, Application US/10407543; Publication No. US20030175789A1 GENERAL INFORMATION:
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STATE: Florida
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COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Gainesville
STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
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                                             OF DETECTION OF NUCLEIC ACIDS WITH A
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MEDIUM TYPES FORDY

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

CORPATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

PRIDA APPLICATION NUMBER: US/10/407,543

FILING DATE: 03-Apr-2003

CLASSIFICATION NUMBER: US/08/860,844

FILING DATE: 09-JUN-1997

APPLICATION NUMBER: 08/353,476

FILING DATE: 09-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: SALIWANCHOWER: 35,746

REFERENCE/DOCKET NUMBER: 35,746

TELEPHONE: (352) 375-8100

INFORMATION FOR SEQ ID NO: 21:
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n. 0.096;
0; Indels
                                                                 SPECIFIC SEQUENCE COMPOSITION
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N W. 41st St., Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st St., Suite A-1 CITY: Gainesville STATE: Florida COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.3%; Score 29; DB 100.0%; Pred. No. 0.(cive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
APPLICANT: Weininger, Susan
Weininger, Arthur M
TITLE OF INVENTION: METHOD OF D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22, Application US/10407543; Publication No. US20030175789A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucletc acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                        NUMBER OF SEQUENCES: 118
                                                                                                                                                                                                                                        ZIP: 32606
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 29; Conservative
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US-10-407-543-22
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Gaps
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TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
SPECIFIC SEQUENCE COMPOSITION
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APPLICATION NUMBER: US/10/407,543 FILING DATE: 03-Apr-2003
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/407,543
FILING DATE: 03-Apr-2003
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6;
0.096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st St., Suite A-1
                                                                                                                                        PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-UN-1997
APPLICATION NUMBER: 08/353,476
FILING DATE: 09-DEC-1994
ATTORNEY/AGENT THORNAMION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100C1
TELEFONNICATION INFORMATION:
TELEFONNICATION INFORMATION:
TELEFONNICATION (352) 372-5800
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 76.3%; Score 29; DB Best Local Similarity 100.0%; Pred. No. 0.C Matches 29; Conservative 0; Mismatches
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APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-UN-1997
APPLICATION NUMBER: 08/353,476
FILING DATE: 09-DEC-1994
ATTONREY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GGGACTITCCGCTGGGGACTITCCAGGGG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 GGGACTTTCCGCTGGGGACTTTCCAGGGG 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 27, Application US/10407543 Publication No. US20030175789A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Gaps

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Score 28.4; DB 2; Length 37;
Pred. No. 0.17;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                   RESULT 32
US-10-407-543-38
US-10-407-543-38
Sequence 38, Application US/10407543
Publication No. US20030175789A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 37 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GGGACTTTCCGCTGGGGACTT
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SEQUENCE CHARACTERISTICS:
                                  Query Match
Best Local Similarity 96.7%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 96.7%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 32606
COMPUTER READABLE FORM:
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STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Florida
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE:
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Publication No. US20030104361A1

GENERAL INFORMATION:

APPLICANT: Weininger, Susan

APPLICANT: Weininger, Arthur M

TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION

NUMBER OF SEQUENCES: 1.18

CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 76.3%; Score 29; DB 6; Length 46; Best Local Similarity 100.0%; Pred. No. 0.096; Matches 29; Conservative 0; Mismatches 0; Indels
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ZIP: 32606

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/353,476
FILING DATE: 09-DEC-1994
CLASSIFICATION: 435
ATYONEY/AGENT INFORMATION:
NAME: SAILwanchik, David R.
REGISTRATION NUMBER: 35,746
REGISTRATION PORKET DID NO: 38:
SEQUENCE CHARACTERISTICS:
LEMETHER STATES SEQUENCE: LEMETHER STATES SEQUENCE
LEMETHER STATES SEQUENCE
LEMETHER 
REGISTRATION NUMBER: 35,746
REBERENCH JOCKER TUMBER: GP-100C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFRAT. (352) 372-5800
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GGGACTITCCGCTGGGGACTTTCCAGGGG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
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STREET: 2421 N.W. 41st St., Suite A-1
                                                                                                                                                                                                                              LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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US-08-860-844-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL:
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US-08-860-844-38
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STATE:
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                                                                                                                                                                                                                                                    APPLICANT: Weininger, Susan
Weininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
SPECIFIC SEQUENCE COMPOSITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
CERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSER: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st St., Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/407,543
FILING DATE: 03-Apr-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-UN-1997
APPLICATION NUMBER: 08/353,476
FILING DATE: 09-DEC-1994
31
                                                7 GGGACTTTCCGCTGGGGACTTTCCAGGGAG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCAGGGG 31
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US-10-407-543-38
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72.6%;
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Query Match
Best Local Similarity 88.2°
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 72.6
Best Local Similarity 88.2
Matches 30; Conservative
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US-10-235-682-9/c
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                                    APPLICANT: David Baltimore et al.
TITLE OF INVENTION: NUCLEAR FACTORS ASSOCIATED WITH TRANSCRIPTIONAL REGULATION
TITLE OF INVENTION: NUCLEAR FACTORS ASSOCIATED WITH TRANSCRIPTIONAL REGULATION
CURRENT APPLICATION NUMBER: US/10/037,341
CURRENT FILING DATE: 2002-01-04
PRIOR PAPLICATION NUMBER: 08/464364
PRIOR FILING DATE: 1995-06-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.1
SEQ ID NO 53
LENGTH: 34
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Publication No. US20030104361A1

GENERAL INFORMATION:

APPLICANT: Weininger, Sugan

TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A

TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION

NUMBER OF SEQUENCES: 118

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik & Saliwanchik
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MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/353,476
FILING DATE: 09-DEC-1994
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: SALWAMOTHIK, DATIGR:
REGISTRATION NUMBER: 35,746
REFRENCE/DOCKET NUMBER: 37,746
REGISTRATION NUMBER: 35,746
REFRENCE/DOCKET NUMBER: 35,746
REGISTRATION NUMBER: 35,746
REGISTRATION NUMBER: 35,746
REFRENCE/DOCKET NUMBER: 37,746
REGISTRATION FOR SEQ ID NO: 26: SEQUENCE CHARATION FOR SEQ ID NO: 26: SEQUENCE FOR SEQ ID 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GGGACTITCCGCTGGGGACTITCCAGGG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eeeacrircecreeeacrirceaee 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28; Conservative
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TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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Best Local Similarity
Matches 28; Conserv
                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ANTI-SENSE: NO
US-08-860-844-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
CRGANISM: HIV
US-10-037-341-53
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US-08-860-844-26
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                                                    Gaps
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Weininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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CORRESPONDENCE ADDRESSE

ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st St., Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
CIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Elopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/407,543
FILING DATE: 03-Apr-2003
CLASSIFCATION ATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-UNU-1997
APPLICATION NUMBER: 08/353,476
FILING DATE: 09-UNU-1997
APPLICATION NUMBER: 08/353,476
FILING DATE: 09-DLN-1997
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                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIFIC SEQUENCE COMPOSITION
Score 27.6; DB 2;
Pred. No. 0.34;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GGGACTTTCCGCTGGGGACTTTCCAGGGGGACTT 35
                                                                                                                                                    7 eggactriccecreegactriccagagagecer 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.6%; Score 27.6; DB
88.2%; Pred. No. 0.34;
tive 0; Mismatches
                                                                                                   2 GGGACTTTCCGCTGGGGACTTTCCAGGGGGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 35,746
REBERENCE/DOCKET NUMBER: GP-100C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 26:
                                                                                                                                                                                                                                                                            Sequence 26, Application US/10407543 Publication No. US20030175789A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 9, Application US/10235682; Publication No. US20030108523A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-407-543-24;
; Sequence 24, Application US/10407543;
; Publication No. US20030175789A1;
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 25, Application US/08860844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GGGACTITCCGCTGGGGACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS:
                                                              72.1%;
83.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                 Query Match
Best Local Similarity 83.5-
-hes 31; Conservative
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MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 39
US-08-860-844-25
US-08-860-844-24
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Publication No. US20030104361A1

GENERAL INFORMATION:

APPLICANT: Weininger, Susan

APPLICANT: Weininger, Arthur M

TITLE OF INVENTION: RETHOD OF DETECTION OF NUCLEIC ACIDS WITH A

TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION

NUMBER OF SEQUENCES: 118

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: NF-kappa B DNA binding site, negative strand
US-10-235-682-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 35;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-UN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/353,476
FILING DATE: 09-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION: 435
CLASSIFICATION: 435
CLASSIFICATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 27.4; DB 5;
Pred. No. 0.41;
0; Mismatches 1;
                         APPLICANT: Catania, Anna P.
TITLE OF INVENTION: A CANCER TREATMENT SYSTEM
FILE REFERENCE: 8022.US01
CURRENT APPLICATION NUMBER: US/10/235,682
CURRENT FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/317,514
PRIOR PILING DATE: 2002-09-05
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Version 3.1
SEQ ID NO 9
LENGTH: 35
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2421 N.W. 41st St., Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEPHOR: (352) 372-5800
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 72.1%;
Best Local Similarity 96.6%;
Matches 28; Conservative
APPLICANT: Lipton, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gainesville
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 37
US-08-860-844-24
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                                                   Gaps
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                                                                                                                                                                                                                                                                                                                              Ablinevariants. Susan
APPLICANT: Weininger, Arthur M
Weininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
SPECIFIC SEQUENCE COMPOSITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
0
Score 27.4; DB 2; Length 44; Pred. No. 0.41; 0; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
CERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                             7 dedactrirccecrededactrirccededadceredec 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rccaggggactrtcc 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 418t St., Suite A-1 CITY: Gainesville STATE: Florida COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA.

APPLICATION NUMBER: US/10/407,543
FILING DATE: 03-Apr-2003
CLASSIFICATION NUMBER: US/08/60,844
FILING DATE: 09-UN-1997
APPLICATION NUMBER: US/08/60,844
FILING DATE: 09-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REFERENCE/DOCKET NUMBER: 35,746
REFERENCE/DOCKET NUMBER: 35,746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-407-543-24
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FEATURE: OTHER INFORMATION: NF-kappa B DNA binding site, positive strand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                          OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/407,543
FILING DATE: 03-Apr-2003
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'n
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Sequence 8, Application US/10235682
Fublication No. US20030108523A1
GENERAL INFORMATION:
APPLICANT: Lipton, James
TITLE OF INVENTION: A CANCER TREATMENT SYSTEM
FILE REFERENCE: 8022.US01
CURRENT APPLICATION NUMBER: US/10/235,682
CURRENT FILING DATE: 2002-09-05
FRIOR APPLICATION NUMBER: US 60/317,514
PRIOR FILING DATE: 2002-09-05
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Version 3.1
SEQ ID NO 8
LENGTH: 35
                                                                                                                                                                                                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/660,844
FILING DATE: 09-UN-1997
APPLICATION NUMBER: 08/353,476
FILING DATE: 09-DEC-1994
ATORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEPHONE: (352) 375-8100
TELEPHONE: (352) 375-8100
TELEPHONE: GPARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 69.5%; Score 26.4; DB Best Local Similarity 96.4%; Pred. No. 1; Matches 27; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 27.2; DB Pred. No. 0.49; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GGGACTTTCCGCTGGGGACTTTCCAGGGGGAC 33
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                COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 44 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 90.6%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-407-543-25
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US-10-235-682-8
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Sequence 25, Application US/10407543
Sequence 25, Application US/10407543
Fublication No. US2003017578941
GENERAL INFORMATION:
APPLICANT: Weininger, Susan
Weininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
SPECIFIC SEQUENCE COMPOSITION
Publication No. US20030104361A1
GENERAL INFORMATION:
APPLICANT: Weininger, Susan
APPLICANT: Weininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
NUMBER OF SEQUENCES:
ADDRESSEE: Saliwanchik & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-JUN-1997
CLASSIFICATION NUMBER: 08/353,476
FILING DATE: 09-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SAILwanchik, David R.
REGISTRATION NUMBER: 35,746
REGISTRATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3,
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Pred. No. 0.49;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st St., Suite A-1 CITY: Gainesville STATE: Florida COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GGGACTITCCGCTGGGGACTTTCCAGGGGGAC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: Saliwanchik & Saliwanchik
2421 N.W. 41st St., Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 71.6%;
Best Local Similarity 90.6%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                        STREET: 2421 N.W. CITY: Gainesville STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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US-10-407-543-25
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                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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Gaps

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Gaps

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Sequence 12, Application US/10659053

Sequence 12, Application US/10659053

Publication No. US20050037032A1

GENERAL INFORMATION:

APPLICANT: ZENGEN, INC.

APPLICANT: Lipton, James M.

APPLICANT: Lipton, James M.

APPLICANT: Lipton, James M.

APPLICANT: Lipton, James M.

TITLE OF INVENTION: A COMPOSITION AND METHOD OF TREATMENT FOR UROGENITAL CONDITIONS

FILE REFERENCE: 54275.8005.US03

CURRENT APPLICATION NUMBER: US/10/659,053

CURRENT APPLICATION NUMBER: US 60/126,233

FRIOR FILING DATE: 2000-03-24

FRIOR FILING DATE: 1999-03-24

FRIOR PELLING DATE: 2003-05-21

FRIOR APPLICATION NUMBER: US 60/126,233

FRIOR APPLICATION NUMBER: US 60/382,887

FRIOR APPLICATION NUMBER: US 60/382,887

FRIOR PILING DATE: 2002-05-21

FRIOR FILING DATE: 2002-05-21

SEQ ID NO 12

LENGTH: 35

FROM FILING DATE: 2002-05-21

SEQ ID NO 12

LENGTH: 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9; Length 32;
1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                    TITLE OF INVENTION: Methods For Diagnosing Autoimmune
TITLE OF INVENTION: Disease
FILE REFERENCE: 00786/457003
CURRENT APPLICATION NUMBER: US/10/775,487A
CURRENT FILING DATE: 2004-02-10
FRIOR APPLICATION NUMBER: 09/258,682
FRIOR PILING DATE: 1999-02-26
FRIOR APPLICATION NUMBER: 09/031,629
FRIOR FILING DATE: 1999-02-27
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Oligonucleotide probes for NF-kB. US-10-659-053-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 67.9%; Score 25.8; DB Best Local Similarity 93.1%; Pred. No. 1.8; Matches 27; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

68.4%; Score 26; DB

Best Local Similarity 100.0%; Pred. No. 1.5

Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCAGGG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 GGGGAGTTTCCGCTGGGGACTTTCCATGG 4
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                              APPLICANT: Faustman, Denise L.
APPLICANT: Havashi, Takuma
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ), OTHER INFORMATION: Synthetic US-10-775-487A-1
                                                      Hayashi,
  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-860-844-30
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                                                                                               APPLICANT: ZENGEN, INC.
APPLICANT: Catania, Anna P.
APPLICANT: Catania, Anna P.
APPLICANT: Catania, Anna P.
APPLICANT: Catania, Anna P.
APPLICANT: Lipton, James M.
TITLE OF INVENTION: A COMPOSITION AND METHOD OF TREATMENT FOR URGENITAL CONDITIONS
FILE REFERENCE: 54275.8005.US03
CURRENT APPLICATION NUMBER: US/10/659,053
CURRENT FILING DATE: 2003-09-08
PRIOR FILING DATE: 2003-09-08
PRIOR PILING DATE: 1999-03-24
PRIOR FILING DATE: 1999-03-24
PRIOR FILING DATE: 1999-03-24
PRIOR FILING DATE: 2003-05-21
PRIOR FILING DATE: 2003-05-21
PRIOR SPLICATION NUMBER: US 60/382,887
PRIOR FILING DATE: 2003-05-21
PRIOR SPLING DATE: 2003-05-21
PRIOR SPLING DATE: 2003-05-21
PRIOR SPLING DATE: 2003-05-21
PRIOR SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
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Patent No. US20020106689A1
GENERAL INFORMATION:
APPLICANT: Faustman
APPLICANT: Hayashi
TITLE OF INVENTION: Methods for Treating and Diagnosing Autoimmune Disease
File Reference: MGH/Faustman 17633/1030
CURRENT APPLICATION NUMBER: US/09/031,629A
CURRENT FILING DATE: 1998-02-21
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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Pred. No. 1;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Oligonucleotide probes for NF-kB. US-10-659-053-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L Similarity 100.0%; Pred. No. 1.5
26; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGGACTTTCCGCTGGGGACTTTCCATG 35
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                   ; Sequence 11, Application US/10659053; Publication No. US20050037032A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 1, Application US/10775487A; Publication No. US20050158302A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 96.4
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
US-10-659-053-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 43
US-09-031-629A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-031-629A-5
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US-10-775-487A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 11
LENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 5
LENGTH: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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Gaps

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Indels

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 CTTTCCGCTGGGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-860-844-7
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Weininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
                           GENERAL INFORMATION:
APPLICANT: Weininger, Susan
APPLICANT: Weininger, Athur M
APPLICANT: Weininger, Athur M
TILE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st St., Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: FLOTIGA

COUNTEX: USA

ZIP: 32606

COMPUTER READABLE FORM:
MEDTION TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-BOS/MS-DOS
SOFTWARE: PATENTIN RC-BOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-UN-1997
CLASSIFICATION NUMBER: 08/353,476
FILING DATE: 09-DEC-1994
CLASSIFICATION: 435
PRICE APPLICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REFERENCE/DOCKET NUMBER: 35,746
REFERENCE/DOCKET NUMBER: 37,746
REFERENCE/DOCKET NUMBER: 37,746
REFERENCE/DOCKET NUMBER: 37,746
REFERENCE/DOCKET NUMBER: 37,746
REPRENCE/DOCKET NUMBER:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st St., Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 CTTTCCGCTGGGGACTTTCCAGGGGGACTT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 crrrcccrrcccarcarrccaccacccr 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 30, Application US/10407543 Publication No. US20030175789A1 GENERAL INFORMATION:
; Publication No. US20030104361A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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MOLECULE TYPE:
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US-10-407-543-30
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Gaps
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APPLICANT: Weininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
0
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/407,543
FILING DATE: 03-Apr-2003
CLASSIFICATION NUMBER: US/08/860,844
FILING DATE: 09-JUN-1997
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-JUN-1997
APPLICATION NUMBER: 08/353,476
FILING DATE: 09-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: 35,746
TELECOMMUNICATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100C1
TELEPHONE: (352) 375-8800
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 6; Length 48;
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-UMN-1997
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/353,476
FILING DATE: 09-DEC-1994
CLASSIFICATION: 435
ATTONEY/AGENT INFORMATION:
NAME: 831/wanchik, David R.
REGISTRATION NUMBER: 35,746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 66.3%; Score 25.2; I Best Local Similarity 90.0%; Pred. No. 3; Matches 27; Conservative 0; Mismatches
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CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
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US-10-407-543-30
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Search completed: February 16, 2006, 02:34:12
Job time : 555.471 secs
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| Sequence 7, Application No. US20030175789A1
| Publication No. US20030175789A1
| GENERAL INFORMATION:
| APPLICANT: Weininger, Susan
| Weininger, Arthur M
| TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
| SPECIFIC SEQUENCE COMPOSITION
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MEDIUM TYPE: RIOPPY disk

COMPUTER: IN PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Ralease #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/407,543

FILING DATE: 03-Apr-2003

CLASSIFCATION ATA:

APPLICATION NUMBER: US/08/860,844

FILING DATE: 09-JUN-1997

APPLICATION NUMBER: 08/353,476

FILING DATE: 09-JUN-1997
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STREET: 2421 N.W. 41st St., Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INPORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-8800
INFORMATION FOR SEQ 1D NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                               65.8%; Score 25; DB illarity 100.0%; Pred. No. 3.7 Conservative 0; Mismatches
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGACTTTCCGCTGGGGACTTTCCA 27
                                                                                                                                                                                                                                                                                                                                                                                                 GGGACTITCCGCTGGGGACTITCCA 26
REFERENCE/DOCKET NUMBER: GP-100C1
TELECOMONICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 7:
SEGUIENCE CHARACTERISTICS:
LENGTH: 27 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Florida
                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                    ANTI-SENSE: NO
                                                                                                                                                                                                           MOLECULE TYPE:
HYPOTHETICAL:
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APPLICANT: Bublins, Paul D.
APPLICANT: Lu, Lina
APPLICANT: Lu, Lina
APPLICANT: Giannoukakis, Nick
TITLE OF INVENTION: FOR ENHANCING TOLEROGENICITY IN A HOST AND METHODS FOR
TITLE OF INVENTION: MAKING THE SAME
FILE REPERENCE: AP32737 / 072396.0225
CURRENT APPLICATION NUMBER: 2001-04-27
FRICK APPLICATION NUMBER: 60/200,479
PRIOR APPLICATION NUMBER: 60/200,479
PRIOR PILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 1
SEQ ID NO 1
LENGTH: 25
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                                                  Gaps
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DB 6; Length 27; 3.7;
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                                                0; Indels
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; OTHER INFORMATION: Synthesized nucleotide sequence
US-09-844-915-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3;
9.1;
Query Match 65.8%; Score 25; DB Best Local Similarity 100.0%; Pred. No. 3.7 Matches 25; Conservative 0; Mismatches
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                                                                                                     56
                                                                                                                                        3 GGGACTTTCCGCTGGGGACTTTCCA 27
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                                                                                                                                                                                                                                                         US-09-844-915-1; Sequence 1, Application US/09844915; Sequence 1, Application US/09844915; Patent No. US20020048564A1; GENERAL INFORMATION:
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Run

Sequence:

Searched:

Database

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Sequence 31496, A
Sequence 310956,
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1 US-11-136-527-139991

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US-10-310-914A-767705

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US-11-36-527-318422

US-11-36-527-318428

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21940, A
103498,
260545,
507340,
528104,
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                                                                              February 16, 2006, 02:03:53; Search time 354.248 Seconds (without alignments) 98.157 Million cell updates/sec
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/ cgn2_6/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
             GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-175-859-100529
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US-11-175-859-66382
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US-11-121-849-3316
US-11-121-849-43102
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US-11-131-849-55779
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US-11-175-859-21940
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Maximum Match 100%
Listing first 300 summaries
                                                          - nucleic search, using sw model
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Match
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Sequence 34784, A Sequence 47813, A Sequence 98013, A

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Result No.

15.6

Sequence 139984, Sequence 148772, Sequence 213033, Sequence 213054, Sequence 255943, Sequence 264919,

Sequence 318422 Sequence 323032,

Sequence 295909

Sequence 1042809, Sequence 860573,

Sequence 337618

Sequence 369219, Sequence 411393, Sequence 577777, Sequence 34784, A

Sequence 115454, Sequence 515523, Sequence 603980, Sequence 625609, Sequence 664250, Sequence 664250,	Sequence equence equence equence	Sequence 1216378, Sequence 1216555, Sequence 487014,	edneuce	equence equence equence	equence 1334567 Sequence 2166, sequence 56581	Sequence 36301, A Sequence 63156, A Sequence 76904, A	87010, 150850	Sequence 210823, Sequence 232914,	Sequence 234662, Sequence 236300,	Sequence 277374, Sequence 509586, Sequence 585616.	Sequence 585617, Sequence 139988,	Sequence 139994, Sequence 200554, Sequence 216717,	Sequence 218537, Sequence 222021,	Sequence 243777, Sequence 264917,	Sequence 344781, Sequence 344817,	5466/0 58648, 5	Sequence 4612, Ap	23877,	30372,	34982,	63177,	88574,	Sequence 92135, Sequence 105891	equence	ednence	ednence	Sequence 67829, A Sequence 277280,	equence	ednence
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11 US-11-175-859-16894 Sequence 16894, A II US-11-175-859-29564 Sequence 29564, A II US-11-175-859-78404 Sequence 78404, A II US-11-175-859-78404 Sequence 108242, II US-11-175-859-11846 Sequence 111846, T US-10-310-914A-481857 Sequence 63781, Sequence 63781,	7 US-10-310-914A-940417 Sequence 940417, 9 US-11-101-244-1342196 Sequence 1342196, 10 US-11-083-784-1342196 Sequence 1342196, 7 US-10-310-914A-400362 Sequence 400362, 7 US-10-310-914A-400362 Sequence 400362,	7 US-10-310-914A-983911 Sequence 983911, 7 US-10-770-726-1531 Sequence 1531, Ap 7 US-10-310-914A-470528 Sequence 470528,	7 US-10-314A-1229615 Sequence 1229615, c 11 US-11-001-347-2195 Sequence 2195, Ap c 7 US-10-310-914A-1229664 Sequence 1229664, c	7 US-10-310-914A-515600 Sequence 515600, c 7 US-10-310-914A-220517 Sequence 920517, c 7 US-10-310-914A-1227854 Sequence 1227854, c	11 US-11-121-849-92973 Sequence 92973, A C 11 US-11-121-849-123890 Sequence 123890, C C	11 US-11-121-849-245310 Sequence 245310,	11 US-11-121-849-394406 Sequence 494405, 11 US-11-121-849-480753 Sequence 490753, 11 TS-11-121-849-514563 Sequence 514563.	11 US-11-121-849-574900 Sequence 574900,	11 US-11-121-849-574901 Sequence 574901, 11 US-11-136-527-52210 Sequence 52210, A	11 US-11-136-527-52215 Sequence 52215, A C 11 US-11-136-52220 Sequence 52220, A C 2 US-11 US-11-136-527-5220 Sequence 52220, A C C C C C C C C C C C C C C C C C C	11 US-11-175-859-241 Sequence 241, App c 11 US-11-175-859-241 Sequence 240, App c 11 US-11-175-859-24603 Sequence 24603, A	11 US-11-175-859-62229 Sequence 62229, II US-11-175-859-73037 Sequence 73037, II US-11-175-859-7307	11 US-11-175-859-114859 Sequence 114859, 7 US-10-310-914A-458309 Sequence 458309,	7 US-10-310-914A-643683 Sequence 643683, 7 US-10-310-914A-1017158 Sequence 1017158,	7 US-10-310-914A-1020590 Sequence 7 US-10-310-914A-24012 Sequence	7 US-10-310-914A-1090819 Sequence 7 US-10-310-914A-1242049 Sequence	7 US-10-310-914A-1298143 Sequence 1289143,	7 US-10-310-914A-166305 Sequence 8519, Ap	11 US-11-121-849-29916 Sequence 29916, A 11 US-11-121-849-50786 Sequence 50786, A	11 US-11-121-849-60898 Sequence 60898, A 11 US-11-121-849-61350 Sequence 61350, A	11 US-11-121-849-363099 Sequence 11 US-11-121-849-374844 Sequence	11 US-11-121-849-399270 Sequence 399270, 11 US-11-121-849-423422 Sequence 423422,	11 US-11-136-527-148785 Sequence 148785, C	11 US-11-136-527-273444 Sequence 273444,	11 US-11-136-52/-323329 Sequence 323329, 7 US-10-310-914A-637718 Sequence 637718,	<pre>11 US-11-175-859-19585 Sequence 19585, A 11 US-11-175-859-27865 Sequence 27865, A</pre>	11 US-11-175-859-34114 Sequence 34114, A 11 US-11-175-859-44652 Sequence 44652, A	11 US-11-175-859-63852 Sequence 63852, A	11 US-11-17-859-70800 Sequence 00000, A 11 US-11-175-859-73803 Sequence 73803, A 11 US-11-175-859-86934 Sequence 86934, A
US-11-175-859-16694 Sequence 16894, A US-11-175-859-29564 Sequence 29564, A US-11-175-859-7844 Sequence 78404, A US-11-175-859-108242 Sequence 108242, US-11-175-859-111846 Sequence 111846, US-10-310-9144-481857 Sequence 63781, US-10-310-9144-65781	37.4 19 7 US-10-310-914A-940417 Sequence 940417, 37.4 19 9 US-11-101-244-1342196 Sequence 1342196, 37.4 19 10 US-11-083-784-1342196 Sequence 1342196, 37.4 20 7 US-10-914A-400362 Sequence 400362, 37.4 20 7 US-10-914A-400362 Sequence 800362,	37.4 20 7 US-10-914A-880143 Sequence 880143, 37.4 21 7 US-10-914A-983911 Sequence 1531, Ap 37.4 21 7 US-10-770-726-1531 Sequence 1531, Ap 37.4 21 7 US-10-914A-470528 Sequence 470528,	37.4 21 7 US-10-914A-1229615 Sequence 1229615, c 37.4 21 11 US-11-001-347-2195 Sequence 2195, Ap c 37.4 22 7 US-10-914A-1229664 Sequence 1229664, c	37.4 23 7 US-10-310-914A-515600 Sequence 515600, c 37.4 23 7 US-10-310-914A-220517 Sequence 920517, c 37.4 23 7 US-10-914A-1227854 Sequence 1227854, c	37.4 25 11 US-11-121-849-92973 Sequence 92973, A 2 25 11 US-11-121-849-123890 Sequence 123890, C	37.4 25 11 US-11-121-849-245310 Sequence 2545310,	37.4 25 11 US-11-121-849-324406 Sequence 324406, 37.4 25 11 US-11-121-849-480753 Sequence 480753, 37.4 25 11 US-11-121-849-514563 Sequence 514563.	37.4 25 11 US-11-121-849-514504 Sequence 514564, 37.4 25 11 US-11-121-849-574900 Sequence 574900,	37.4 25 11 US-11-121-849-574901 Sequence 574901, 37.4 25 11 US-11-136-527-52210 Sequence 52210, A	37.4 25 11 US-11-136-527-52215 Sequence 52215, A C 37.4 25 11 US-11-136-52220 Sequence 52220, A C 37.4 25 11 US-11-136-527-5220	37.4 25 11 US-11-135-24-244 Sequence 241, App c 37.4 50 11 US-11-175-859-241 Sequence 241, App c 37.4 50 11 US-11-175-859-24603 Sequence 24603, A	2 37.4 50 11 US-11-175-859-62229 Sequence 62229, 2 37.4 50 11 US-11-175-859-73037 Sequence 73037, 2 37.4 50 11 US-11-175-859-73037 Sequence 73037, 2 37.4 50 11 US-11-175-859-73037	2 37.4 50 11 US-11-175-889-114859 Sequence 158309, 4 36.8 22 7 US-10-310-914A-458309 Sequence 458309,	4 36.8 23 7 US-10-310-914A-643683 Sequence 643683, 4 36.8 23 7 US-10-310-914A-1017158 Sequence 1017158,	4 36.8 23 7 US-10-310-914A-1020590 Sequence 4 36.8 24 7 US-10-310-914A-24012 Sequence	4 36.8 24 7 US-10-310-914A-1090819 Sequence	4 36.8 24 / US-10-312-9144-1290143 Sequence 8219, Ap	4 36.8 25 / US-10-750-623-8519 Sequence 8519, Ap. 4 36.8 25 7 US-10-310-914A-166305 Sequence 166305,	4 36.8 25 11 US-11-121-849-29916 Sequence 29916, A 4 36.8 25 11 US-11-121-849-50786 Sequence 50786, A	4 36.8 25 11 US-11-121-849-60898 Sequence 60898, A 4 36.8 25 11 US-11-121-849-61350 Sequence 61350, A	4 36.8 25 11 US-11-121-849-363099 Sequence 4 36.8 25 11 US-11-121-849-374844 Sequence	4 36.8 25 11 US-11-121-849-399270 Sequence 399270, 4 36.8 25 11 US-11-121-849-423422 Sequence 423422,	c 36.8 25 11 US-11-136-527-148785 Sequence 148785, c 25 11 US-11-136-527-255946 Sequence 255946, c	4 36.8 25 11 US-11-136-527-273444 Sequence 273444,	4 36.8 25 II US-II-146-52/-342329 Sequence 323323, 4 36.8 28 7 US-10-310-914A-637718 Sequence 637718,	4 36.8 50 11 US-11-175-859-19585 Sequence 19585, A 4 36.8 50 11 US-11-175-859-27865 Sequence 27865, A	4 36.8 50 11 US-11-175-859-3414 Sequence 3414, A 4 36.8 50 11 US-11-175-859-44652 Sequence 44652, A	4 36.8 50 11 US-11-775-889-63852 Sequence 63852, A	36.8 50 11 US-11-175-859-73803 Sequence 73803, A 36.8 50 11 US-11-175-859-73803 Sequence 73803, A 36.8 50 11 US-11-175-859-86934 Sequence 86934, A

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Publication No. US20060019907A1
GENERAL INFORMATION:
APPLICANT: AGGARMAL, BHARAT
APPLICANT: SHISHODIA, SHISHIR
TITTLE OF INVENTION: I B KINASE
TITLE OF INVENTION: I B KINASE
TITLE OF INVENTION: ACTIVATION AND USES THEREOF
FILE REFERENCE: CLFR:255US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: AGGARNAL, BHARAT
APPLICANT: SHIGHODIA, SHIGHIR
TITLE OF INVENTION: GUGGULSTERONE: AN INHIBITOR OF NUCLEAR FACTOR- B AN
TITLE OF INVENTION: B KINASE
TITLE OF INVENTION: ACTIVATION AND USES THEREOF
FILE REFERENCE: CLFR: 2551S
CURRENT FILING DATE: 2005-07-12
PRIOR PLICATION NUMBER: 60/587,187
PRIOR PLICATION NUMBER: 60/587,187
NUMBER OF SEQ ID NOS: 6
SCOTWARE PATENTING DATE: 2004-07-12
NUMBER OF SEQ ID NOS: 6
SCOTWARE PATENTING DATE: 2014-07-12
NUMBER OF SEQ ID NOS: 6
SCOTWARE PATENTING DATE: 2014-07-12
NUMBER OF SEQ ID NOS: 6
SCOTWARE PATENTING DATE: 211
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100.0%; Score 38; DB 11;
Best Local Similarity 100.0%; Pred. No. 6.9e-06;
Matches 38; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Synthetic oligonucleotide US-11-127-654-141
                TILLE OF INVENTION: INVENTANTALION: DISEASES CURRENT APPLICATION NUMBER: US/11/127,654 CURRENT FILLING DATE: 2005-005-12 PRIOR APPLICATION NUMBER: US 10/112,653 PRIOR PILING DATE: 2002-03-29 PRIOR FILING DATE: 2001-03-29 NUMBER OF SEQ ID NOS: 1040 SOFTWARE: Patentin version 3.2 LENGTH: 38
      TITLE OF INVENTION: INFLAMMATORY DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/11179321; Publication No. US20060019907A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial sequence
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US-11-179-321-5
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US-11-179-321-1
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; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1096857,
Sequence 1225293,
Sequence 1111949,
Sequence 1111949,
Sequence 118497,
Sequence 128559,
Sequence 128959,
Sequence 273870,
Sequence 287193,
Sequence 287193,
Sequence 287193,
Sequence 374271,
Sequence 374271,
Sequence 374271,
Sequence 426843,
Sequence 426843,
Sequence 426843,
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Sequence 189633,
Sequence 362316,
Sequence 313593,
Sequence 5115, App
Sequence 5115, App
Sequence 5615, App
Sequence 22627, A
Sequence 1106, A
Sequence 31060, A
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Sequence 1178527,
Sequence 942238,
Sequence 942238,
Sequence 1129011,
Sequence 656686,
Sequence 87624,
Sequence 914648,
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Sequence 1245002,
Sequence 1364403,
Sequence 231296,
Sequence 391707,
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Sequence 823213,
Sequence 1096071,
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Sequence 1337223
      Sequence 504569
                                                  Sequence 6
Sequence 1
US-10-310-914A-504569
US-10-310-914A-627070
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US-10-310-914A-126502
US-10-310-914A-1364403
US-10-310-914A-31296
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US-10-310-914A-823213
US-10-310-914A-1096071
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US-10-310-914A-1355293
US-10-310-914A-1355369
US-10-310-914A-1355369
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US-11-121-849-64678

US-11-121-849-218959

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US-11-121-849-2189334

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US-11-121-849-576158

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US-11-136-527-356316

US-11-175-859-5615

US-11-175-859-5618

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US-10-310-914A-1178527
US-11-101-244-942238
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US-10-310-914A-1129011
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US-10-310-914A-1337223
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US-11-127-654-141
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Gaps

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60.5%; Score 23; DB 8; Length 23; 100.0%; Pred. No. 3.7;

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Best Local Similarity 100.0%; Pred. No. 3.7
Matches 23; Conservative 0; Mismatches
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 US-11-175-815-3
                                         Query Match
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US-11-175-815-3
US-11-175-815-3
Sequence 3, Application US/11175815
Sequence 3, Application US/2006002932A1
Sequence 3, Application No. US2006002932A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: 2048/50875-DAA/JPW/AJD
CURRENT PELING DATE: 2005-07-05
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 3
LENGTH: 23
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                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                           ) OTHER INFORMATION: Description of Artificial Sequence:
) OTHER INFORMATION: Primer
US-11-179-321-5
                                                                                                                                                                                                                                                                                                                          3;
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Pred. No. 0.017;
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US-11-116-746-12

Sequence 12, Application US/11116746

Publication No. US20060020114A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: Baker, Kevin

APPLICANT: Gurney, Austin

APPLICANT: Gurney, Austin

APPLICANT: Gurney, Austin

FILE REFERENCE: P1110

CURRENT FILING DATE: 2005-04-28

PRIOR APPLICATION NUMBER: US/11/116,746

CURRENT FILING DATE: 2005-04-28

PRIOR FILING DATE: 1997-06-18

SEQ ID NO 12

LENGTH: 29

LENGTH: 29
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CURRENT APPLICATION NUMBER: US/11/179,321
CURRENT FILING DATE: 2005-07-12
PRIOR APPLICATION NUMBER: 60/587,187
PRIOR FILING DATE: 2004-07-12
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 5
LENGTH: 45
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                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 91.2%;
Matches 31; Conservative
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US-11-116-746-12
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Best Local Similarity
Matches 24; Conserva'
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THOUSE OF UNIVERSITY SHISHIR
TITLE OF INVENTION:
TITLE OF SPECIAL STREAM
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TITLE OF SPECIAL SONS-07-12
THOMBER OF SEQ ID NOS:
SONS-07-12
NUMBER OF SEQ ID NOS:
SOFTWARE: PARCHIN VOR: 2.1
TITLE OF SPECIAL STREAM
THORETING DATE: 2004-07-12
THOMBER OF SEQ ID NOS:
SOFTWARE: PARCHIN VOR: 2.1
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Sequence 6, Application US/11179321

Sequence 6, Application US/11179321

Sequence 6, Application Wo. US2060019907A1

SERNERAL INFORMATION:

APPLICANT: AGGARWAL

TITLE OF INVENTION: GUGGULGTERONE:

TITLE OF INVENTION: GUGGULGTERONE:

TITLE OF INVENTION: ACTIVATION AND USES THEREOF

TITLE OF INVENTION: ACTIVATION AND USES THEREOF

TITLE OF INVENTION: ACTIVATION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/11/179,321

CURRENT FILING DATE: 2005-07-12

PRIOR PILING DATE: 2005-07-12

PRIOR PILING DATE: 2004-07-12
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Pred. No. 17;
0; Mismatches 6;
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1 GGGACTTTCCGCTGGGGACTTTC 23
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Best Local Similarity 80.6%;
Matches 25; Conservative
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 45
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Publication No. US20060024715A1
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US-11-121-849-3916/c
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TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR PILING DATE: 2005-05-05
NUMBER OF SEQ ID NOS: 362830
SSCTWABER PATENTIN Version 3.2
LENGTH: 25
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APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
FILE REFERENCE: 36601.
CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT APPLICATION NUMBER: US 60/585,352
PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR FILING DATE: 2004-07-02
PRIOR FILING DATE: 2004-07-02
SRIOR PRIOR FILING DATE: 2004-07-02
SRIOR PRIOR PRIOR DATE: 2004-07-02
SRIOR PRIOR DATE: 2004-07-02
SOFTWARE: Patentin version 3.2
SEQ ID NO 100529
LENGTH: 50
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47.4%; Score 18; DB 11; Length 50;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 24; Conservative 1; Mismatches 11; Indels
                       6; Indels
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                                                                   5 ACTITICGCTGGGGACTITICCAGGGGGACTT 35
                                                                                             13 ACTITCGGCTGCTCACTITCCAGGGAGGCGT 43
  Pred. No. 17;
0; Mismatches
                                                                                                                                                                                                                          ; Sequence 100529, Application US/11175859; Publication No. US20060024715A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 200528, Application US/11136527 Publication No. US20050287570A1 GENERAL INFORMATION:
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Best Local Similarity 80.6%;
Matches 25; Conservative
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Matches 19; Conservative
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US-11-175-859-100529
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ORGANISM: Artificial
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US-11-175-859-32817/c
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US-11-175-859-100529
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US-11-136-527-200528
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Sequence 3916, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded String Reference: 3.684.1
; TILLE OF INVENTION: Microarrays
; TILLE OF INVENTION: Microarrays
; TILLE OF INVENTION: Microarrays
; FILE REFRENCE: 3.684.1
; CURRENT PILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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GENERAL INFORMATION:

APPLICANT: Affymetrix, Inc.

APPLICANT: Liu, Guoying et al.

TITLE OF INVENTION: Method of Analysis of Human Polymorphism
FILE REFERENCE: 36601.

CURRENT PILING DATE: 2005-07-05

PRIOR PILING DATE: 2006-07-02

PRIOR FILING DATE: 2004-07-02

NUMBER OF SEQ ID NOS: 116251

SOFTWARE: Patentin version 3.2

LENGTH: 50
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; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.11/175,859
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR PILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SEQ ID NO 65382
; LENGTH: 50
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43.2%; Score 16.4; DB 11;
Best Local Similarity 71.4%; Pred. No. 1.4e+03;
Matches 20; Conservative 1; Mismatches 7;
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Pred. No. 7e+02;
1; Mismatches 9;
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Best Local Similarity 68.8<sup>†</sup>
Matches 22; Conservative
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COGANISM: homo sapien
US-11-175-859-32817
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CORGANISM: homo sapien
US-11-175-859-66382
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US-11-136-527-273210/C
US-11-136-527-273210/C
US-11-136-527-273210/Application US/11136527

| Sequence 273210, Application US/11136527
| Publication No. US20050287570A1
| GENREAL INFORMATION:
| APPLICANT: Wyeth
| APPLICANT: Wyeth
| TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
| TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
| TITLE OF INVENTION: DAIDS: 2005-05-25
| FILE REFERENCE: 2005-05-25
| FRIOR APPLICATION NUMBER: US 60/574,294
| PRIOR FILING DATE: 2005-05-26
| NUMBER OF SEQ ID NOS: 362830
| SOFTWARE: Patentin version 3.2
| SEQ ID NO 273210
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Publication No. US20050287570A1
Publication No. US20050287570A1
Publication No. US20050287570A1
APPLICANT: Wyeth
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
TITLE OF INVERTION Probe Arrays For Expression Profiling of Rat Genes FILE REPERBURE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
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41.1%; Score 15.6; DB 11; Length 25;
Best Local Similarity 81.8%; Pred. No. 2.6e+03;
Matches 18; Conservative 0; Mismatches 4; Indels
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Publication No. US20060024715A1
GENERAL INFORMATION:
APPLICANT: Affymetrix, Inc.
APPLICANT: Liu, Guoying et al.
ITILE OF INVENTION: Method of Analysis of Human Polymorphism
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Pred. No. 2.6e+03;
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SOFTWARE: Patentin version 3.2
SEQ ID NO 273212
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 81.8%;
Matches 18; Conservative
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ORGANISM: Artificial
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US-11-175-859-21940/c
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US-11-121-849-43102
US-11-121-849-43102
Sequence 43102, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: 'Obn Palma
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
FILE REPERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO. 62
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US-11-121-849-565799/c

US-11-121-849-565799, Application US/11121849

Publication No. US2000272080A1

Publication No. US2000272080A1

GENERAL INFORMATION:

APPLICANT: John Palma

TITLE OF INVENTION: Microarrays

TITLE OF INVENTION: Microarrays

TITLE OF INVENTION: Microarrays

TITLE OF INVENTION WUMBER: US/11/121,849

CURRENT APPLICATION NUMBER: 60/567,949

PRIOR FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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                                                                                                                    Score 16; DB 11; Length 25; Pred. No. 1.9e+03; 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16; DB 11; Length 25; Pred. No. 1.9e+03; O; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                        10 CCGCTGGGGACTTTCCAGGGGGAC 33
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                                                                                                                      42.1%;
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Best Local Similarity 79.2%;
Matches 19; Conservative (
                                                                                                                                                                       19; Conservative
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US-11-121-849-43102
                                              ; ORGANISM: Homo sapien
US-11-121-849-3916
                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapien
US-11-121-849-565799
LENGTH: 25
                            TYPE: DNA
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US-11-121-849-507340
US-11-121-849-507340
US-11-121-849-507340
Sequence 507340, Application US/11121849
Sequence 507340, Application No. US20050272080A1
SEQUENCE 10 THORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded String TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarray
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2004-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
SUFFWARE Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 507340
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 528104, Application US/11121849
; Sequence 528104, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
    APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S:
    TITLE OF INVENTION: Microarrays
; TITLE OF INVENTION: Microarrays
; FILE REPERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673804
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 528104
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  Length 25;
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Pred. No. 3.2e+03;
0; Mismatches 6;
Query Match 40.5%; Score 15.4; DB 11; Best Local Similarity 76.0%; Pred. No. 3.2e+03; Matches 19; Conservative 0; Mismatches 6;
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76.0%; Pred. No. 3.2e+03;
:ive 0; Mismatches 6;
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; Publication No. US20050287570A1
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                                                                                                        11 CGCTGGGGACTTTCCAGGGGGACTT 35
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Best Local Similarity 76.0%;
Matches 19; Conservative (
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Best Local Similarity 76.09
Matches 19; Conservative
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CORGANISM: Homo sapien
US-11-121-849-507340
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CORGANISM: Homo sapien
US-11-121-849-528104
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US-11-121-849-528104/c
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US-11-121-849-103498/c
; Sequence 103498, Application US/11121849
; Publication No. US2000272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION WUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 103498
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US-11-121-849-260545/C
US-11-121-849-260545/C
Sequence 260545, Application US/11121849
Sequence 260545, Application US/11121849
Sequence 260545, Application No. US20050272080A1
GENERAL INFORMATION:
APPLICANT John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded STITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTHARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 260545
LENGTH: 25
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Best Local Similarity 76.0%; Pred. No. 3.2e+03;
Matches 19; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
     FILE REFERENCE: 3690.1
CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR FILING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 116251
SOFTWARE: PATENTIN VEXBION 3.2
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                                                                                                                                                                                                                                                                                                                                     41.1%;
75.0%;
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CORGANISM: homo sapien
US-11-175-859-21940
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US-11-121-849-103498
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CORGANISM: Homo sapien
US-11-121-849-260545
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Matches 18; Conserv
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LENGTH: 50
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Sequence 2, Application US/11032236
Publication No. US20050273867A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BRULET, PHILIPPE
APPLICANT: PICAD:, SANDRINE
APPLICANT: PICAD:, SANDRINE
TITLE OF INVENTION: OF LOCAL CA2+ DYNAMICS IN LIVING ORGANISMS
                                                                                                                                                                                                               Gaps
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| Publication No. US20060024715A1
| GENERAL INFORMATION:
| APPLICANT: Affymetrix, Inc.
| APPLICANT: Affymetrix, Inc.
| APPLICANT: Liu, Guoying et al.,
| TILE OF INVENTION: Method of Analysis of Human Polymorphism
| FILE REFERENCE: 3690.1
| CURRENT FILING DATE: 2005-07-05
| PRIOR FILING DATE: 2006-07-02
| NUMBER OF SEQ ID NOS: 116251
| SOFTWARE: PatentIn version 3.2
| SEQ ID NO 66869
| TYPE: DNA
| TYPE: DNA
| TYPE: DNA
| TYPE: DNA
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                                                                                                                                                            Score 15.4; DB 7; Length 26; Pred. No. 3.2e+03; 0; Mismatches 6; Indels
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40.5%; Score 15.4; DB 11;
Best Local Similarity 66.7%; Pred. No. 3.4e+03;
Matches 22; Conservative 0; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 03495.0328
CURRENT APPLICATION NUMBER: US/11/032,236
CURRENT FILING DATE: 2005-01-11
FRIOR APPLICATION NUMBER: 60/543,659
FRIOR FILING DATE: 2004-02-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 3.3
LENGTH: 41
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 767705
LENGTH: 26
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                                                                                                                                                                 Query Match
Best Local Similarity 76.0%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                6 CTTTCCGCTGGGGACT1
                                                                                            ; ORGANISM: Human
US-10-310-914A-767705
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                                                                           TYPE: RNA
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Sequence 767705, Application US/10310914A

Sequence 767705, Application US/10310914A

Sequence 767705, Application US/10310914A

Sequence 767705, Application US/1031041

Sequence 767705, Application US-1031041

GENERAL INFORMATION: USB as accompanies of novel regulatory genes and TITLE OF INVENTION: USB thereof

FILE REFERENCE: 06087.0200.CPUS01

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION UNDER: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402
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                                       APPLICANT: Mounts, William M
TILE REPERENCE: 031896-04100 (AMI01086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US/11/136,527
PRIOR APPLICATION NUMBER: US/11/136,527
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR PILING DATE: 2005-05-05
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR PAPLICATION NUMBER: US/11/136,294
PRIOR FILING DATE: 2006-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
LENGTH: 25
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Pred. No. 3.2e+03;
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3.2e+03;
6;
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Pred. No. 3.2e+03;
0; Mismatches 6;
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Best Local Similarity 76.0%;
Matches 19; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 76.0%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Probe US-11-136-527-139991
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                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial
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US-11-136-527-213042/c
    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                               TYPE: DNA
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APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
CURRENT REPERSENCE: 06087.0200.CEVESO1
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 663779
LENGTH: 23
TYPE: RNA
OPCANT.
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TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded St
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded St
FITLE OF INVENTION: Microarrays
FITLE OF INVENTION: Microarrays
FILLE REPRENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR PILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 454114
LENGTH: 25
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1 Similarity 85.0%; Pred. No. 3.8e+03;
17; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 15.2; DB 7;
Pred. No. 3.7e+03;
6; Mismatches 3;
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; Sequence 454114/ Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
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Best Local Similarity 55.0%;
Matches 11; Conservative
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ORGANISM: Homo sapien
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Best Local Similarity
Matches 17; Conserva
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ORGANISM: Human
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Publication No. US20660003322A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TAPPLICANT: Bentancing and Applicant Shiler, Kvuzat
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06097.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
LENGTH: 23
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APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
FILE REFERENCE: 3669.1
CURRENT PILIOS DATE: 2005-07-05
CURRENT PILIOS DATE: 2005-07-05
PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR APPLICATION NUMBER: US 60/585,352
NUMBER OF SEQ ID NOS: 116251
SOFTWARE PatentIn version 3.2
SOFTWARE PatentIn version 3.2
LENGTH: 50
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40.0%; Score 15.2; DB 7; Length 23;
Best Local Similarity 70.0%; Pred. No. 3.7e+03;
Matches 14; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                               Best Local Similarity 70.4%; Pred. No. 3.4e+03;
Matches 19; Conservative 1; Mismatches 7; Indels
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US-10-310-914A-663779
; Sequence 663779, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
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Matches 19; Conservative
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US-11-175-859-103464
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US-10-310-914A-298241
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US-10-310-914A-298241
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US-11-175-859-103464
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Sequence 196232, Application US/11121849

Fagurence 196232, Application US/11121849

Fublication No. US20050272080A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded Statistic OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
CURRENT FILING DATE: 2005-05-03

FRIOR FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SEQ ID NO 196232

LENGTH: 25
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Sequence 815249, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Benivach, Isaac
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 815249
LENGTH: 24
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     APPLICANT: Affymetrix, Inc.
APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
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39.5%; Score 15; DB 7; I
Best Local Similarity 65.2%; Pred. No. 4.5e+03;
Matches 15; Conservative 3; Mismatches 5;
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                                                                          FILE REFERENCE: 3690.1

CURRENT APPLICATION NUMBER: US/11/175,859

CURRENT FILING DATE: 2005-07-05

PRIOR APPLICATION NUMBER: US 60/585,352

PRIOR FILING DATE: 2004-07-02

NUMBER OF SEQ ID NOS: 116251

SOFTWARE: PatentIn version 3.2

LENGTH: 50
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US-11-175-859-66764
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US-11-121-849-196232/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-815249
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                                                                                                                                                                                                                                                                                                                TYPE: DNA
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TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION WUMBER: US/10/310,914A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1393495
LENGTH: 27
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; Publication No. US20060024715A1
; GABERAL INFORMATION:
    APPLICANT: Affmetrix, Inc.
    APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; PILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT APPLICATION NUMBER: US 60/585,352
; PRIOR APPLICATION NUMBER: US 60/585,352
; ROTHWARE OF SEQ ID NOS: 116251
; SEQ ID NO 44456
; LENGTH: 50
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Score 15.2; DB 7; Length 26;
Pred. No. 3.8e+03;
4; Mismatches 3; Indels
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Pred. No. 4.1e+03;
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                                                                                                                                                                                                                                 RESULT 32
US-10-310-914A-1383495
US-10-310-914A-1383495, Application US/10310914A; Sequence 1383495, Application US/10310914A; Publication No. US20060003322A1; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
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; Publication No. US20060024715A1
; GENERAL INFORMATION:
                                                                                                         1 GGGGACTITCCGCTGGGGAC 20
                                                                                                                                         7 GAGGACUUUGCCCUGGGGAC 26
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Best Local Similarity 65.0%;
Matches 13; Conservative
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1 Similarity 66.7%;
20; Conservative
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Best Local Similarity
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US-11-175-859-43456/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-11-175-859-43456
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; Sequence 280766, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
    APPLICANT: Wyeth
    APPLICANT: Wyeth
    APPLICANT: Wheth
    APPLICANT: Wheth
    APPLICANT: Woults, William M
    TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
    FILE REFERENCE: 031896-041000 (AM101086)
    CURRENT FILING DATE: 2005-05-25
    PRIOR APPLICATION NUMBER: US 60/574,294
    PRIOR PLING DATE: 2005-05-26
    NUMBER OF SEQ ID NOS: 362830
    SOFTWARE: PatentIn version 3.2
    SEG ID NO 280766

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| Sequence 314081, Application US/11136527
| Publication No. US20050287570A1
| Publication No. US20050287570A1
| GENERAL INFORMATION:
| APPLICANT: Wyeth
| APPLICANT: Wyeth
| TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
| FILE REFERENCE: 031896-041000 (AM101086)
| CURRENT FILING DATE: 2005-05-25
| PRIOR APPLICATION NUMBER: US/11/136,527
| PRIOR PILING DATE: 2005-05-26
| NUMBER OF SEQ ID NOS: 362830
| SOFTWARE: Patentin version 3.2
| SEQ ID NO 314081
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APPLICANT: Wyeth
APPLICANT: Wounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION UMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 25;
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Best Local Similarity 78.3%; Pred. No. 4.5e+03;
Matches 18; Conservative 0; Mismatches 5;
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; Publication No. US20050287570A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 CGCTGGGGACTTTCCAGGGGGAC 33
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                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-11-136-527-318283
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Publication No. US20050272080A1

GENERAL INPORMATION:
APPLICANTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded & TITLE OF INVENTION: Microarrays

TITLE OF INVENTION: Microarrays

TITLE OF INVENTION: Microarrays

TITLE APPLICATION NUMBER: US/11/121,849

CURRENT APPLICATION NUMBER: 00/567,949

PRIOR APPLICATION NUMBER: 00/567,949

PRIOR FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
                                                                                                                                                                                                                                                                                                               J. Sequence 378884, Application US/11121849
Sequence 378884, Application US/11121849
Publication No. US200502720801
GENERAL INFORMATION:
APPLICAMT: John Palma
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
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                                                                 Length 25;
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SOFTHARBE Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 378884
LENGTH: 25
                                                                                                               0: Indels
                                                               39.5%; Score 15; DB 11; I 100.0%; Pred. No. 4.5e+03; tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 GGGGACTTTCCAGGGGGACTTTC 37
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                                                                                                                                                           5 ACTITCCGCTGGGGA 19
                                                                                                                                                                                                       22 ACTITCCGCTGGGGA 8
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Best Local Similarity 78.3.
                                              Query Match
Best Local Similarity 100.
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, ORGANISM: Homo sapien
US-11-121-849-510666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapien
US-11-121-849-378884
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US-11-136-527-280766/c
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US-11-121-849-510666
                     US-11-121-849-196232
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APPLICANT: Worth
APPLICANT: Wounts, William M
FILE REPERENCE: 031896-041000 (AMI01086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SEQ ID NO 358480
LENGTH: 25
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; Sequence 11173, Application US/11175859
; Publication No. US2066024715A1
; GENERAL INFORMATION:
APPLICANT: Affymetrix, Inc.;
TILLE OF INVENTION: Method of Analysis of Human Polymorphism
FILE REFERENCE: 3690.1
; CURRENT APPLICATION UNDRER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR APPLICATION NUMBER: US 60/585,352
; RIUNG DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SEQ ID NO 11773
: LENGTH: 50
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PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                   3 GGACTITCCGCTGGGGACTITCC 25
                                                                                                                                                                                                                                                                                                                                                                                                         2 GGACTAGCAGCTGGGGTCTTTAC 24
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                                                                                                                                                                                                     ) OTHER INFORMATION: Probe US-11-136-527-318283
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US-11-175-859-11173
                                                                                                                                      TYPE: DNA ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial
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Best Local Similarity
Matches 18; Conserv
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US-11-136-527-358480
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US-11-175-859-11173
                                                                                          SEQ ID NO 318283
LENGTH: 25
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                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                    Sequence 74560, Application US/11175859
; Sequence 74560, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTYON: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT APPLICATION NUMBER: US 60/585,352
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR APPLICATION NUMBER: US 60/585,352
; RIUNDER OF FLING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SEQ ID NO 74560
; LENGTH: 50
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Publication No. US20060024715A1
GENERAL INFORMATION:
APPLICANT: Affymerix, Inc.
APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
FILE REPERSINGE: 3690.1
CURRENT FILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR FILING DATE: 2004-07-02
    39.5%; Score 15; DB 11; Length 50; 78.3%; Pred. No. 4.9e+03;
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39.5%; Score 15; DB 11; Length 50
Best Local Similarity 78.3%; Pred. No. 4.9e+03;
Matches 18; Conservative 0; Mismatches 5; Indels
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Pred. No. 4.9e+03;
0; Mismatches 10
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                                                   0, Mismatches
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US-10-310-914A-252171/c
; Sequence 252171, Application US/10310914A
                                                                                               2 GGGACTTTCCGCTGGGGACTTTC 24
                                                                                                                                 2 GGGTATTTCTGCTGGTGATTTTC 24
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SOFWRARE: Patentin version 3.2
SEQ ID NO 104360
LENGTH: SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 39.5%;
Best Local Similarity 67.7%;
Matches 21; Conservative
Query Match
Best Local Similarity 78.33
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CORGANISM: homo sapien
US-11-175-859-74560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: homo sapien
US-11-175-859-104360
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US-11-175-859-104360
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US-11-175-859-74560
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Sequence 571272, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
TITLE REPERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
PRIOR PELICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
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                                                                                        Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
FILE REFERENCE: 3690.1
CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR FILING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 116251
SOFTWARE: Patentin version 3.2
LENGTH: 50
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                                                                                   Score 14.8; DB 11;
Pred. No. 5.4e+03;
0; Mismatches 2;
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Pred. No. 5.9e+03;
1; Mismatches 13;
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; Publication No. US20060024715A1
; GENERAL INFORMATION:
APPLICANT: Affymetrix, Inc.
                                                                                                                                                                                 14 TGGGGACTTTCCAGGGGG 31
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                                                                                      Query Match 38.9%;
Best Local Similarity 88.9%;
Matches 16; Conservative
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Best Local Similarity 61.1%;
Matches 22; Conservative
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Matches 16; Conservative
                     ; ORGANISM: Homo sapien
US-11-121-849-569838
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US-11-121-849-571272
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US-11-175-859-1145
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US-11-175-859-1145/c
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, TYPE: DNA
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                                        APPLICANT: Benewich, Isaac
APPLICANT: Banier, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: USES thereof
FILE REFERENCE: 06087.0200. CPUSO1
CURRENT PILINGATICATION WINBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 252171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 508653, Application US/11121849
Publication No. US200502720803.
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
FILE REPERENCE: 3684.1
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR PILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 508663
LENGTH: 25
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Sequence 569838, Application US/11121849
Publication No. US2050272080A1
SEQUENCE 569838, Application US/11121849
Publication No. US2050272080A1
SERNEAL INFORMATION:
APPLICANT:
JOHN PALMA
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarray
TITLE OF INVENTION: Microarray
STORTENT FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 569838
LENGTH: 25
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Pred. No. 5.4e+03;
0; Mismatches 2; Indels
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88.9%;
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Best Local Similarity 88.9%;
Matches 16; Conservative (
  Publication No. US20060003322A1
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Best Local Similarity
                          GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                               US-10-310-914A-252171
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US-11-121-849-569838
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US-11-121-849-508663
                                                                                                                                                                                                                                                                                                      TYPE: RNA
ORGANISM: Human
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Search completed: February 16, 2006, 02:53:06 Job time : 357.248 secs

us-09-669-187a-148.szlm50.rnpbn

A28677 Oligonucleo A28678 Oligonucleo A28674 dsRNA with A28685 Oligonucleo	CQ003486 Sequence CQ003487 Sequence	CQ006799 Sequence CQ006770 Sequence BD202727 Method an AR110134 Sequence	141099 Sequence 2 A23688 L. monocyto	A23689 b. monocyto AX058552 Sequence	AX519178 Sequence	BD078171 Modulator BD078223 Modulator	AR121366 Sequence AR213275 Semience	AR202976 Sequence	AX158895 Sequence	AR630012 Sequence	AR137709 Sequence	CQ892090 Sequence CS130448 Sequence	CS130449 Sequence	AR182883 Sequence	AR607446 Sequence AX045778 Sequence	AX045788 Sequence	AX10405 Sequence	AXI04338 Sequence AXI04339 Sequence	AX104619 Sequence	AXIO5235 Sequence	AX355141 Sequence	AX355401 Sequence AX355402 Sequence	AX477342 Sequence AX547118 Sequence	AX547391 Sequence	AXS47672 Sequence	AX54/848 Sequence AX664309 Sequence	AX664310 Sequence	A28676 deRNA with	ARO/4234 Sequence ARO84522 Sequence	AR084523 Sequence	I21020 Sequence 3	AX023407 Sequence	AX032596 Sequence	A40420 Sequence	AR010036 Sequence	AR034//I Sequence AR152031 Sequence	BD138633 Soluble M	103043 Sequence 8 124744 Sequence 7	AX104236 Sequence AX104771 Sequence
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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocc	- nucleic search, using sw model	February 15, 2006, 17:51:58 ; Search (without a 2369.293 M	US-09-669-187A-906	••	e: IDENTITY NUC	Gapext 1.0	5883141 seqs, 28421725653 residues	of hits satisfying chosen parameters:	seq length: 0	20	Maximum	Listing first 300 summaries	GenEmbl:*	2: gb_in:*	3: gb_env:* 4: gb_om:*	5: gb_ov:*	7: gb ph:	8: gb_pr:* 9: gb_ro:*	10: gb_sts:*	12: gb_un:*	14: gb_htg:*		No. is the number of results predicted by chance greater than or equal to the score of the result	derived by analysis of the total	SUMMARIES	Query	core Match Length DB ID	100.0 20 6	100.0 20 6	20 100.0 50 6	.4 87.0 27 6	.4 87.0 27 6	4 87.0 27 6	4 87.0 30 6	4 87.0 39 6	4 87.0 39 6	4 82.0 50 6	16 80.0 17 6 .8 79.0 20 6	.8 79.0 26 6 BD078154 .8 79.0 42 6 AR362756
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AR080892 Sequence AR173722 Sequence AX033315 Sequence AX520121 Sequence AX513947 Sequence AX513947 Sequence AX5139851 Sequence	თ თ თ თ თ o	AR531433 Sequence AR582752 Sequence AX158894 Sequence X84968 H.sapiens t AR006855 Sequence AR080893 Sequence AR173723 Sequence	AX033314 Sequence AX094559 Sequence BD138044 Expressio BD237692 Therapeut AR473408 Sequence AX278210 Sequence AX278210 Sequence BD078200 Modulator AR018187 Sequence	AR430823 Sequence 101689 Sequence 1135088 Mus musculu AX157237 Sequence AR284627 Sequence AR080903 Sequence AR080903 Sequence AR13733 Sequence CQ005982 Sequence AX190214 Sequence AX190214 Sequence AX190214 Sequence	AR594206 Sequence AX513870 Sequence AX513870 Sequence AX515849 Sequence AX519146 Sequence AX220098 Sequence AX220098 Sequence AX220098 Sequence AX620119 Sequence AX600119 Sequence AX600119 Sequence AX600119 Sequence AX600119 Sequence AX600119 Sequence	0 0 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	AX3974b sequence AR30315 Sequence AX104367 Sequence AX547420 Sequence
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Thu Feb 16 12:20:53 2006

VERSION KEYMORDS SOURCE SOURCE ORGANISM Synthetic construct ORGANISM ORDER synthetic construct ORGANISM ORDER squences; artificial sequences.  REFERENCE AUTHORS TITLE TITLE JOURNAL PATENTS PATENTS TOTE OF TOWA RESEARCH FOUNDATION (US); Coley Pharmaceutical MNIVERSITY OF TOWA RESEARCH FOUNDATION (US); Coley Pharmaceutical MNIVERSITY OF TOWA RESEARCH FOUNDATION (US); Coley Pharmaceutical Cource Account of the foundation of t	>- C	AX547767  AX547767  LOCUS  LOCUS  LOCUS  AX547767  AX547767  AX547767  VERSION  VERSION  AX547767  VERSION  AX547767  VERSION  AX547767  VERSION  AX547767  VERSION  AX547767  AX547767  VERSION  AX547767  Glession  AX547767  AX5477  AX547767  AX5477  AX5477  AX5477  AX5477  AX5477  AX5477  AX5477  AX5477  AX547  AX5477  AX5477  AX5477  AX5477  AX5477  AX5477  AX5477  AX747  AX5477  AX547  AX547  AX547  AX547  AX547  AX547  AX547  AX7	Ouery Match Query Match Query Match Best Local Similarity 100.0%; Score 20; DB 6; Length 20; Best Local Similarity 100.0%; Pred. No. 9.7e+02; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Qy	RESULT 3 AX05849 LOCUS LOCUS DEFINITION Sequence 1 from Patent WO0077250. ACCESSION AX058549 VERSION AX058549 VERSION AX058549.1 GI:12310891 KEYWORS SOURCE SYNCHETIC CONSTRUCT ORGANISM SYNCHETIC CONSTRUCT OF THE SEQUENCES ARTIFICIAL SEQUENCES.
AX557192 Sequence AR006856 Sequence AR006858 Sequence AR080894 Sequence AR080895 Sequence AR080896 Sequence AR173724 Sequence AR173725 Sequence AR173726 Sequence AR173726 Sequence AR173726 Sequence AR145961 Sequence BD245235 Method of BD245235 Method of BD337693 Therapeut CS088786 Sequence	AR364012 Sequence AR473409 Sequence AX278211 Sequence BD078173 Modulator I39398 Sequence 48 I87969 Sequence 48 AR681017 Sequence AR168792 Sequence AR168792 Sequence AR206251 Sequence	AKA2293 Sequence AX318196 Sequence AX318205 Sequence AX318213 Sequence AX318213 Sequence AX45605 Sequence AX45605 Sequence AX56363 Sequence XX60426 G.lamblia t A4044 Sequence X60426 G.lamblia t A40444 Sequence X118D087471 De novo o BD087471 De novo o BD087477 De novo o BD087477 De novo o BD087475 De novo o AX182066 Sequence AX182066 Sequence AX182066 Sequence AX18206 Sequence AX184070 Sequence AX261487 Sequence	AR261492 Sequence AR261494 Sequence BD087461 De novo o BD087461 De novo o BD087463 De novo o BD087463 De novo o BD087464 De novo o BD087464 De novo o BD087465 De novo o	BD087467 De novo o BD087468 De novo o BD087469 De novo o BD087472 De novo o BD087479 De novo o
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Escude, C., Garestier, T., Helene, C. and Roulon, T. Method for circularizing oligonucleotides around a double stranded nucleic acid, resulting structures and uses thereof

REFERENCE AUTHORS TITLE

PAT 30-APR-2001

linear

DNA

AX104714 20 bp I Seguence 906 from Patent WO0122972. AX104714

RESULT 1
AX104714
LOCUS
DEFINITION
ACCESSION

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1 (bases 1 to 27)
Woo,S.L.C., Smith,L.C., Cristiano,R.J., Gottchalk,S. and Sparrow,J.
Nucleic acid transporter system and methods of use
Patent: US 5994109-A 15 30-NOV-1999;
Location/Qualifiers
                                                                                                                                                                             PAT 07-SEP-2000
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llarity 94.7%; Pred. No. 8.8e+03;
Conservative 0; Mismatches 1;
            Score 17.4; DB 6;
Pred. No. 8.8e+03;
0; Mismatches 1;
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Pred. No. 8.8e+03;
0; Mismatches 1;
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1 (bases 1 to 27)

Woo,S.L.C., Smith,L.C., Cristiano,R.J.,

Nucleic acid transporter systems

Patent: US 6177554-A 14 23-JAN-2001;

Location/Qualifiers
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/mol_type="unassigned DNA"
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Sequence 15 from patent US 6177554.
AR125630
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Sequence 15 from patent US 5994109.
AR091425.1 GI:10018180
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/organism="unknown"
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Wolbases 1 to 27)
Woo, S.L.C., Smith, L.C., Cristiano, R.J., Gottchalk, S. and Sparrow, J.
Wooleic acid transporter system and methods of use
Patent: US 5994109-A 14 30-NOV-1999;
Location/Qualifiers
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Method for circularizing oligonucleotides around a double stranded
nucleic acid, resulting structures and uses thereof
bether, WO 0077250-A 2 1-DEC-2000.
INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM)
(PR) ; CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
Location/Qualifiers
Patent: WO 0077250-A 1 21-DEC-2000;
INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM)
(FR) ; CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
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100.0%; Pred. No. 8.5e+02;
cive 0; Mismatches 0;
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100.0%; Pred. No. 8.5e+02;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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/organism="synthetic construct"
//mol_type="unassigned DNA"
/db_xref="teaxon:28630"
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/mol_type="unassigned DNA"
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                                                                                                                     /note="Oligonucleotide"
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PAT 07-SEP-2000

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Uniquesized (1 to 39)

Woo,S.L.C., Smith,L.C., Cristiano,R.J., Gottchalk,S. and Sparrow,J.

Wucleic acid transporter system and methods of use
Patent: US 5994109-A 13 30-NOV-1999;

Location/Qualifiers
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Woo,S.L.C., Smith,L.C., Cristiano,R.J., Gottchalk,S. and Sparrow,J.

Nucleic acid transporter systems
Patent: US 6177554-A 13 23-JAN-2001;

Location/Qualifiers
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llarity 94.7%; Pred. No. 8.7e+03;
Conservative 0; MiSmatches 1;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/noTe="Primer ON-TATADE1"
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Sequence 13 from patent US 6177554.
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Sequence 13 from patent US 5994109.
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/mol_type="unassigned DNA"
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/wol_type="unassigned DNA"
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Woo'S.LC., Smith, L.C., Cristiano, R.J., Gottchalk, S. and Sparrow, J.
Woo, S.LC., Smith, L.C., Systems
Nucleic acid transporter systems
Patent: US 6177554-A 15 23-JAN-2001;
Location/Qualifiers
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Thf-inducible promoters and methods for using
Patent: WO 0246433-A 43 13-JUN-2002;
Saus, Juan (ES)
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Pred. No. 8.7e+03;
0; Mismatches 1;
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/noCe="primer ON-TATADE1"
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Patent: WO 0246378-A 43 13-JUN-2002;
Saus, Juan (ES)
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/mol_type="unassigned DNA"
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Sequence 43 from Patent WO0246433.
AX477591
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Sequence 43 from Patent W00246378.
AX505011 GI:23386333
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1 Similarity 94.7%;
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oc A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
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27-MAR-1998 US 60/079678
PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
JAMES A MCSWIGGEN
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 17)
Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J.A. Method and reagent for treating diseases or conditions concerning molecule participating in vacculogenic response
Patent: JP 2002509721-A 5754 02-APR-2002;
RIBOZYME PHARMACEUTICALS, INC
                                                                                                                                                                                                                                                                                                                                                                                                              C12N15/09, A61K31/7088, A61K31/7125, A61K48/00, A61P3/10, A61P17/06,
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1 (bases 1 to 20)
1 (bases 2
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80.0%; Score 16; DB 6; Le
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 16; Conservative 0; Mismatches 0;
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    /organism="synthetic construct"
/mol_type="genomic DNA"

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/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"
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JP 2002509721-A/5754
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Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response.

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JP 2002509721-A/5754.
Homo sapiens (human)
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1 (bases 1 to 50)
Kunsch,C.A., Choi,G.A., Barash,S.C., Dillon,P.J., Fannon,M.R. and
                                                                                                                                                                                                                                                                          1 (bases 1 to 50)
Kunsch, C.A., Choi, G.H., Barash, S., Dillon, P.J., Fannon, M.R. and
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89.5%; Pred. No. 1.9e+04;
tive 0; Mismatches 2; Indels
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89.5%; Pred. No. 1.9e+04;
ive 0; Mismatches 2; Indels
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Patent: US 6737248 A. 2153 18-MAY-2004;
Human Genome Sciences, Inc.; Rockville, MD
Location/Qualifiers
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                                                                   Sequence 2153 from patent US 6593114.
AR356035.1 GI:33762119
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/organism="unknown"
/mol_type="genomic DNA"
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SHORT THERAPEUTIC GARNA OF DEFINED Patent: WO 9014090-A 5 29-NOV-1990; Location/Qualifiers
                                                     /organism="unknown"
/mol_type="genomic DNA"
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Biogen, Inc.; Cambridge, MA; EPX;
                            Location/Qualifiers
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Best Local Similarity 89.5%;
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Matches 17; Conservative
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Modulator of DNA cytosine-5 methyltransferase and method of
using the same
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Unclassified.
1 (bases 1 to 42)
11let,B. and Kawashima,E.H.
Expression systems for overproduction of desired proteins Patent: US 5182196-A 21 26-JAN-1993;
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                                       Score 15.8; DB 6; Length 20;
Pred. No. 3.7e+04;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                    PAGENT: JP 2001514862-A 38 18-SEP-2001;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
OS Unidentified
PN JP 2001514862-A/38
PD 18-SEP-2001
PF 12-JUN-1998 JP 2000508978
PR 29-AUG-1997 US 60/057411
PI NORBERT O REICH, JAMES FLYNN
PC C12N9/10,C12Q1/48//C12N15/00
CC Strandedness: Double;
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/organism='Unidentified'
Location/Qualifiers
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Sequence 21 from patent US 5182196.
AR362756
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
    /db xref="taxon:32630"
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JP 2001514862-A/38.
unidentified
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Reich, N.O. and Flynn, J.
                                         Query Match
Best Local Similarity 89.5%;
Matches 17; Conservative
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AR362756
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                                  2; Indels
   Length
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Pred. No. 3.3e+04;
0; Mismatches 2;
Score 15.8; DB 6;
Pred. No. 3.3e+04;
0; Mismatches 2;

    .43
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|mol type="unassigned DNA"
|db_xref="taxon:32630"

    .43
    forganism="synthetic construct"
|mol type="unassigned DNA"
|db_xref="taxon:32630"

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1 (bases 1 to 43)
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1 (bases 1 to 43)
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Gaps

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2; Indels

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and

PAT 16-JAN-2004

linear

DNA

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
Patent: WO 04944-A 2127 05-JUL-2001;
Curagen Corporation (US)
Location/Qualifiers
                                                                      Shimkets, R.A. and Leach, M.

Nucleic acids containing single nucleotide polymorphisms methods of use thereof

Patent: WO 0147944-A 2126 05-JUL-2001;

Curagen Corporation (US)

Location/Qualifiers
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/note="Nucleotide deleted between bases 25 and :
Accession number cg44131752"
                                                                                                                                                                         /organism="Homo sapiens"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
25. .26
/note="Nucleotide deleted between bases 25
Accession number cg441131752"
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/organism="Homo sapiens"
/mol type="unassigned DNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                 1. .44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
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synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 44)
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synthetic construct
other sequences, artificial sequences.
1 (bases 1 to 47)
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Homo sapiens
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Oligonucleotide 9.
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PAT 16-JAN-2004

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85.0%;
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JP 2002509721-A/5753.
Homo sapiens (human)
Homo sapiens
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                Chordata; Craniata; Vertebrata; Euteleostomi;
Euarchontoglires; Primates; Catarrhini;
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
Patent: WO 0147944-A 5340 05-JUL-2001;
Curagen Corporation (US)
                                                                    Shimkets, R.A. and Leach, M.
Nucleic acids containing single nucleotide polymorphisms and methods of use thereof f
Patent: WO 0147944-A 5339 05-JUL-2001;
Curagen Corporation (US)
                                                                                                                                                                                                                   25.7.26
/note="Nucleotide deleted between bases 25 and 26
Accession number cg43267341"
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/note="Nucleotide deleted between bases 25 and decession number cg43267341"
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89.5%; Pred. No. 3.2e+04;
ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                         Length 50;
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                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                          79.0%; Score 15.8; DB 6;
89.5%; Pred. No. 3.2e+04;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
25...26
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/db_xref="taxon:9606"
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/organism="Homo sapiens"
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 Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                        Local Similarity 89.5
ses 17; Conservative
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Matches 17; Conservative
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                                             Hominidae; Homo
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CQ006700
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Matches
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                                                       REFERENCE
AUTHORS
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VERSION
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Homo sapiens (human)
JP 2002509721-A/5753
02-APR-2002
24-MAR-1999 JP 2000541291
27-MAR-1999 JS 60/079678
PAMELA A PACCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT, JAMES A MCSWIGGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (Bases 1 too 17)
Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J.A. Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response Participating in vasculogenic response RIBOZYME PHARMACEUTICALS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                 OS Homo sapiens (human)

PN 2002509721-A/5753

PD 20-APR-2005

PF 24-MAR-1999 JP 2000541291

PR 27-MAR-1999 US 60/079678

PR 27-MAR-
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C A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00,
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Patent: US 6114154-A 2 05-SEP-2000;
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Pred. No. 5.6e+04;
0; Mismatches 3; Indels
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participating in vasculogenic response
Kev
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77.0%; Score 15.4; DB 6;
Best Local Similarity 94.1%; Pred. No. 5.3e+04;
Matches 16; Conservative 0; Mismatches 1;
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 2 from patent US 6114154.
AR110134.1 GI:12826410
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/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"
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Gaps

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METHODS OF DETECTING OR QUANTITATING NUCLEIC ACIDS AND OF PRODUCING LABELLED INVARDELIZED DUCLEIC ACIDS
Patent: WO 9304199-A 5 G4-MAR-1993;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escude,C., Garestier,T., Helene,C. and Roulon,T.
Method for circularizing oligonucleotides around a double stranded
nucleic acid, resulting structures and uses thereof
Patent: WO 0077250-A 4 21-DEC-2000;
INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM)
(FR); CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
Location/Qualifiers
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Detection of genetic polymorphisms
Patent: WO 02052044-A 1181 04-JUL-2002;
Riken (JP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 75.0%; Score 15; DB 6; Le Best Local Similarity 100.0%; Pred. No. 7.6e+04; Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                          76.0%; Score 15.2; DB 6;
85.0%; Pred. No. 5.5e+04;
tive 0; Mismatches 3;
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                                                                                                                          1. .41
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/mol type="unassigned DNA"
/db_xref="taxon:32630"
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other sequences; artificial sequences.
1 (bases 1 to 41)
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Sequence 4 from Patent WO0077250.
AX058552
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synthetic construct
                                                                                                                                                                                                                              Query Match
Best Local Similarity 85.0
Matches 17; Conservative
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ACCESSION
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KEYWORDS
SOURCE
ORGANISM
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ORGANISM
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AUTHORS
TITLE
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                         RESULT 32
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PATENT: WO 93104199-A 4 04-MAR-1993;
Location/Qualifiers
                                                                        PAT 13-MAY-1997
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Noonberg, S. B. and Hunt, C. Anthony.
In vivo oligonucleotide generator, and methods of testing the binding affinity of triplex forming oligonucleotides derived therefrom Patent: US 5624803-A 2 29-APR-1997;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                          linear

    .41
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|mol type="unassigned DNA"
|db_xref="taxon:32630"

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L. monocytogenes HlyA gene probe-primer.
A23689
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L. monocytogenes HlyA gene probe-primer.
A23688
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synthetic construct
other sequences, artificial sequences.
1 (bases 1 to 41)

    .38
    /organism="unknown"
    /mol_type="unassigned DNA"

                                                                   38 bp
Sequence 2 from patent US 5624803.
141099
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BD078223 26 bp DNA linear PAT 27-AUG-2002 Modulator of DNA cytosine-5 methyltransferase and method of using
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Reich, N.O. and Flynn, J.
Modulator of DNA cytosine-5 methyltransferase and method of using the same
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29-AUG-1997 US 60/057411
NORBERT O REICH, JAMES FLYNN
C12N9/10, C12Q1/48/C12N15/09, C12N15/00
Strandedness: Double;
Topology: Linear;
Modulator of DNA cytosine-5 methyltransferase and method of using the same
Strandedness: Double;
Topology: Linear;
Modulator of DNA cytosine-5 methyltransferase and method of
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THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
OS Unidentified
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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18-SEP-2001
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JP 2001514862-A/107.
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Reich,N.O. and Flynn,J.
Modulator of DNA cytosine-5 methyltransferase and method of using
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Modulator of DNA cytosine-5 methyltransferase and method of using
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Patent: WO 02052044-A 5376 04-JUL-2002;
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THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
OS Unidentified
PN JP 2001514862-A/55
PD 18-SEP-2001
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29-AUG-1997 US 60/057411
NORBERT O REICH, JAMES FLYNN
C12N9/10, C12Q1/48//C12N15/09,C12N15/00
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Seguence 5376 from Patent WO02052044.
AX519178

    .41
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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PAT 20-APR-2005

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Unknown.
Unclassified.
Unclassified.

(I (bases I to 31)

Hayashizaki,Y. and Watahiki,M.

RNA polymerase

Patent: US 6867027-A 17 15-MAR-2005;

Patent: US 6867027-A 17 15-MAR-2005;

Lich Institute of Physical and Chemical Research, Nippon Gene Co., 1td., and Nippon Genetech Co., 1td.; Wako;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shimkets, R.A. and Leach, M. Nucleic acids containing single nuclectide polymorphisms and methods of use thereof Patent: WO 0140521-A 2220 07-JUN-2001; Curagen Corporation (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="unassigned DNA"
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25.—26.
/note="Nucleotide deleted between bases 25 and 26
                                                                                                            Query Match 74.0%; Score 14.8; DB 6; Length 31; Best Local Similarity 88.9%; Pred. No. 8.2e+04; Matches 16; Conservative 0; Mismatches 2; Indels
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ilarity 88.9%; Pred. No. 8.2e+04;
Conservative 0; Mismatches 2;
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Seguence 2220 from Patent WO0140521.
AXIS8892
 Patent: US 6365350-A 31 02-APR-2002;
                                                                                                                                                                                                                                                                                                          Sequence 17 from patent US 6867027. AR643452 AR643452.1 GI:62781753
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AR643452
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1 (Dases I to 30)
Murachima.K., Moriya.T., Hamaya,T., Koga,J., Sumida,N., Aoyagi,K.,
Murakami,T. and Kono,T.
Enzyme endoglucanase and cellulase preparations containing the same
Patent: US 6159720-A 18 12-DEC-2000;
Location/Qualifiers
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larity 88.9%; Pred. No. 8.2e+04;
Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                74.0%; Score 14.8; DB 6; Length 30; llarity 88.9%; Pred. No. 8.2e+04; Conservative 0; Mismatches 2; Indels
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Sequence 25 from patent US 6403362.
AR213275
AR213275.1 GI:23310445
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Sequence 31 from patent US 6365350.
AR202976
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/organism="unknown"
/wol_type="unassigned DNA"
Sequence 18 from patent US 6159720.
AR121366
AR121366.1 GI:14104942
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/organism="unknown"
/mol_type="genomic DNA"
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Hayashizaki, Y.
Method of DNA sequencing
                                                                                                                                                                                                                                                                                                                                                                 1 AGGGGAGGGGAGG 18
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Best Local Similarity
Matches 16; Conserv
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AR213275/c
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AR202976
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PAT 22-JUN-2001

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PAT 06-FEB-2002
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                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 20)
Lin,S.-L., Chuong,C.-M. and Ying,S.-Y.
Method for generating full-length cDNA library from single cells
Patent: US 6197554-A 2 06-WAR-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                 Kim, J.P., Starr, D.B., Tam, A.W., Laurance, M.E., Michelotti, E.F., Velligan, M.D., Latour, D.R., Thomas, R.L., Kongpachith, A., Sheppard, L.T., Lim, M.Y. and Bruice, T.W.
Promoters for regulated gene expression
Patent: WO 0194600-A 66 13-DEC-2001;
GENELABS TECHNOLOGIES, INC. (US)
Location/Qualifiers
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larity 93.8%; Pred. No. 1.2e+05;
Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 bp DNA Sequence 133 from Patent WO2004087203. CQ892090.1 GI:55164648
                                                                         DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA
                                                                                                                                                                                                                                                                                                                                                                 1. .25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="unassigned DNA"
                                                                        25 bp
Sequence 66 from Patent WO0194600.
AX351114
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Sequence 2 from patent US 6197554.
AR137709
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/organism="unknown"
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                                                                                                                                                     Homo sapiens (human)
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Matches 15; Conserv
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Matches 16;
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Unclassified.
1 (bases 1 to 25)
1 (kases 1 to 25)
2 (kin, J. E., Start, D. B., Tam, A. W., Laurance, M. E., Michelotti, B. F., Velligan, M. D., Latour, D. R., Thomas, R. L., Kongpachith, A., Sheppard, L. T., Kim, M. Y. and Bruice, T. W.
Sheppard, L. T., Kim, M. Y. and Bruice, T. W.
Sheppard, E. T., Kim, M. Y. and Bruice, T. W.
Sheppard, L. G. Sandard gene expression
Patent: US 6838556-A 66 04-JAN-2005,
Genelabs Technologies, Inc.; Redwood City, CA
Location/Qualifiers
                                         /note="2 of 2 allelic variants (2219 is other entry)"
                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                       Unknown.
Unknown.
Unclassified.
1 (bases 1 to 20)
Pescovitz,0.H.
Use of GHRH-RP to stimulate stem cell factor production
Patent: US 6159934-A 16 12-DEC-2000;
Patent: US cls9934-A 16 12-DEC-2000;
Patent: US cls9934-A 16 12-DEC-2000;
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                                                                                       74.0%; Score 14.8; DB 6; Length 88.9%; Pred. No. 7.6e+04; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                     DNA
Accession number cg39331132"
26
                                                                                                                                                                                                                                                                   20 bp Sequence 16 from patent US 6159934.
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Seguence 66 from patent US 6838556.
AR630012
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                                                                                                                                                                         39 GGGAAGGAAGGGGAGGGG 22
                                                                                                                                                     3 GGGAGGGAGGGAGGGG 20
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                                                                                       Query Match
Best Local Similarity 88.9
Matches 16; Conservative
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Matches 15; Conservative
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Best Local Similarity 93.8
Matches 15; Conservative
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AR121583/c
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AR630012
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Length 20;

PAT 27-APR-1998

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I (bases 1 to 20)
Misuguchi,M., Kurosaki,N., Makino,K., Koyanagi,Y. and Yamamoto,N.
Misuguchi,M., Rurosaki,N., Makino,K., Koyanagi,Y. and Yamamoto,N.
Misuguchi,M., 1 ANTI-SENSE OLIGONUCLEOTIDE
Parent: JP 1997052898-4 9 25-FEB-1997;
SOYAKU GIJUTSU KENKYUSHO:KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-1995 JP 1995224606
MIZUGUCHI MASATSUGU, KUROSAKI NAOKO, MAKINO KEISUKE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism='Artificial sequences'.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.0%; Score 14.2; DB 6; Length 20; larity 84.2%; Pred. No. 1.5e+05; Conservative 0; Mismatches 3; Indels
                                                                   /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="texton:3562"
/noTe="phosphorothioate or phosphodiester"
                                                                                                                                                                    Query Match 71.0%; Score 14.2; DB 6; Best Local Similarity 84.2%; Pred. No. 1.5e+05; Matches 16; Conservative 0; Mismatches 3;
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Patent: WO 2005063300-A 4 14-JUL-2005;
Phenion GmbH & Co KG (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                               20 bp DNA
Anti-HTLV-1 antisense oligonucleotide.
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Sequence 55 from patent US 6339068.
AR182883.1 GI:20226090
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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CO7H21/04//A61K31/70;
strandedness: Single;
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JP 1997052898-A/9
25-FEB-1997
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hypothetical: No;
anti-sense: Yes;
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JP 1997052898-A/9.
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PF 09-AUG-1995
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KOYANAGI YOSHIO,
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Cosmetic or pharmaceutical preparations containing nucleic acid sequences forming a superstructure sequences forming a superstructure Patent: WO 2005063300-A 3 14-JUL-2005; Phenion GmbH & Co KG (DE)
Location/Qualifiers
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                                                                   Davis, H.L. and Mccluskie, M.J.
Immunostimulatory nucleic acid oil-in-water formulations and related methods of use
Patent: WO 2004087203-A
Coley Pharmaceutical Group, Ltd. (CA)
Location/Qualifiers
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/organism="synthetic construct"
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PAT 20-APR-2002

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REFERENCE I to 20)
AUTHORS Krieg, A.M., Davis, H.L., Wu, T. and Schorr, J.
AUTHORS Krieg, A.M., Davis, H.L., Wu, T. and Schorr, J.
AUTHORS Location/Qualifiers
JOURNAL Patent: US 6339668-A 55 15-JAN-2002;
FEATURES
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1. 20
AUTHORS
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Adf82761 Antiviral
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Ad808441 Poly-C pr
Adv99321 PCR prime
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Ad194441 Human ATP
Ad194436 Human Det
Ad194426 Human Det
Ad19623 MCRR1 loc
Ad176662 MCRR1 loc
Ad176662 MCRR1 loc

ALIGNMENTS

AAF99701 standard; DNA; 20 BP

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                                                                   Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic; immunostimulatory; tumour; viral infection; bacterial infection; fungal infection; parasitic infection; cancer; asthma: infections allergy; immune deficiency; phosphorothioate; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.
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27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
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Aag6972 Herpes si Aax64234 HSV-1 b'g Aax76438 Sequencin Aax17522 Test sequ Aaa38175 Primer us Aah44830 Probe use Abx683013 DNA bindi Abz02124 Human leu Abz02124 Human leu

Micro gol Human DNA Duplex ol Chimeric

Adc56859 1 Adg33323 1 Ade80552

Adc56858 Micro gol

Human ACh Human Vbe

Adi83485 HCV DNAzy

Abz04828 Human leu Abz04829 Human leu

4

Synthetic

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The invention describes a method of treating non-allergic inflammatory disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases, such as psoriasis, eczema, allergic context dermatitis, latex dermatitis or inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease. This sequence represents an immunostimulatory nucleic acid
                                                                                                                                                                                                                                        Treating non-allergic inflammatory diseases, such as psoriasis, eczallergic contact dermatitis, latex dermatitis or inflammatory bowel disease by administering an immunostimulatory nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ds; allergy; asthma; poly-G nucleic acid; aerosol formulation; hypo-responsive subject; immunostimulatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 20; DB 9; Length 20;
Pred. No. 6e+02;
; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 4 A; 0 C; 16 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunostimulatory nucleic acid #817.
                                                                                                                                                                                                                                                                                                                              Disclosure; Page 32; 229pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AGGGGAGGGGAGGGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AGGGAGGGAGGGGGG 20
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  29-MAR-2002; 2002US-00112653
                                           29-MAR-2001; 2001US-0279642P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADB37203 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bratzler RL, Petersen DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20; Conservative
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                                                                                                                                                                                                 WPI; 2003-521815/49.
                                                                                                                                                      Krieg AM, Berg DJ;
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(PETE/) PETERSEN D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                    (KRIE/) KRIEG A M. (BERG/) BERG D J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PETE/) PETERSEN
(FOUR/) FOURON Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2003087848-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to inhibiting angiogenesis in a subject, comprising administering at least one antiangiogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lesfon, rheumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, observable syndrome, mocatagial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, intestinal adhesions, atheroscierosis, scleroderma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.
rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
plaque neovascularisation; telangiectasia; haemophiliac joint;
angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
scleroderma; hypertrophic scar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypertrophic scars. The present sequence is an antiangiogenic nucleic acid of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunostimulatory; antiinflammatory; dermatological; antipsoriatic; antiulcer; gene therapy; vaccine; non-allergic inflammatory disease; psoriasis; eczema; allergic contact dermatitis; latex dermatitis; lafidamatory bowel disease; ulcerative colitis; crohn's disease; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 20; DB 6; Length 20; 100.0%; Pred. No. 6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 35; 276pp; English
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                                                                                                                                                                                                                                        14-DEC-2001; 2001WO-US048458.
                                                                                                                                                                                                                                                                                                                              (COLE-) COLEY PHARM GROUP INC
                                                                                                                                                                                                                                                                                     14-DEC-2000; 2000US-0255534P.
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                                                                                                                                                      WO200253141-A2
                                                                                                                                                                                                                                                                                                                                                                            Bratzler RL;
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                                                                                                                                                                                                 11-JUL-2002
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Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.

Disclosure; Page 17; 221pp; English

US2003050268-A1

Synthetic.

ACH03240;

RESULT

Query Match Matches

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Gaps

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The invention relates to a method of suppressing a symptom of an allergic response in a subject by administering a first and second dose of an immunostimulatory nucleic acid that comprises a nucleotide sequence comprising 5'-cg-3', and where the second dose is administered from 1 day to 8 weeks after the first dose. The methods and compositions of the present invention are useful for the treatment or prevention of asthma and allergy, including rhinitis, urticaria and atopic dermatitis, using an immunostimulatory nucleic acid alone or in combination with other medicaments. They can also be used in preventing bacterial and viral infections. This sequence represents an oligonucleotide used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Suppressing allergies, including asthma, rhinitis, urticaria and atopic dermatitis, in a subject, comprises administering a first and second dose of an immunostimulatory nucleic acid.
The invention relates to a method of treating or preventing allergy or asthma which comprises administering to a subject a poly-G nucleic acid in an aerosol formulation. The methods and compositions of the present invention are useful for diagnosing and/or treating asthma and allergy especially in a hypo-responsive subject. The present sequence represents an immunostimulatory nucleic acid of the invention.
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ss; antiasthmatic; antiallergic; dermatological; antiinflammatory; antibacterial; virucide; immunoglobulin E antagoniet; allergy; immunostimulator; asthma; rhinitis; urticaria; dermatitis; bacterial infection; viral infection.
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                                                                                                                                                              Score 20; DB 9; Length 20;
Pred. No. 6e+02;
                                                                                                                                                                                                 0; Indels
                                                                                                                            Sequence 20 BP; 4 A; 0 C; 16 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Allergic response suppressor oligonucleotide #906.
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100.0%; Pred. No. co.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fouron Y;
                                                                                                                                                                                                                                                          1 AGGGAGGGAAGGGAAGGG 20
                                                                                                                                                                                                                                     1 AGGGAGGGAGGGGG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bratzler RL, Petersen DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BRAT/) BRATZLER R L. (PETE/) PETERSEN D M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-833006/82.
                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2004235774-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         10-FEB-2005
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Circularizing oligonucleotide around double-stranded nucleic acid, useful e.g. for detecting mutations, using target-binding oligonucleotide with complementary end sequences.
                                                                                                                                                                                                                                                                                              Nucleic acid detection; nucleic acid labelling; gene therapy;
nucleic acid purification; androgen receptor promoter; triple helix; ss.
                            Gaps
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                                                                                                                                                                                                                                                                     Sequence of a fragment of the murine androgen receptor promoter
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                            Indels
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 Pred. No. 6e+02;
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(CNRS ) CNRS CENT NAT RECH SCI.
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100.08; FL.
                                                                                 1 AGGGGAGGGGAGGGG 20
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                                                           1 AGGGGAGGGGAGGGG
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                                                                                                                                                                       ABL56735 standard; DNA; 50
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                            20; Conservative
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           Best Local Similarity
Matches 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                 Synthetic.
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ABL56735
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RESULT 7 ABL56736/c

DB 13; Length 20;

100.0%; Score 20;

Query Match

93US-00167641.

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14-DEC-1993;
                                    US6033884-A
                                                           07-MAR-2000
            Synthetic
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                                                                                                                                                                                                                                                                                                                                       ....uarizing oligonucleotide around double-stranded nucleic acid, useful
e.g. for detecting mutations, using target-binding oligonucleotide with
complementary end sequences.
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                                                                                          Nucleic acid detection, nucleic acid labelling, gene therapy, nucleic acid purification; androgen receptor promoter, triple helix; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transporter system; nucleic acid delivery; gene therapy; cancer; carcinogenesis; cardiovascular disease; infection; ss.
                                                                        Sequence of a fragment of the murine androgen receptor promoter.
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Pred. No. 5.5e+02;
                                                                                                                                                                                                                                                                 & RECH MEDICALE
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                                                                                                                                                                                                                                                                                                       Helene C,
                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 20; 91pp; French
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ABL56736 standard; DNA; 50 BP
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                                                                                                                                                                                                                  14-JUN-2000; 2000WO-FR001655.
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                                                                                                                                                                                                                                                                                                      Garestier T,
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wes 20; Conserv
                                                                                                                                                                     WO200077250-A2
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                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                       Escude C,
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                      ABL56736
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The present invention relates to a transporter system for delivering nucleic acid to a cell. The system comprises a nucleic acid binding complex, complex, consisting of a binding molecule bonded non-covalently to the nucleic acid, and covalently to a surface ligand, and a lytic agent. The binding molecule is spermine or a spermidine derivative. Nucleotide sequences AAA36632 and peptide sequences AAA3663-A36652 and peptide sequences AAA36650 are used in the construction of the transporter system of the invention. The transporter system is used in gene therapy, particularly to deliver transporter system is used in gene therapy, particularly to deliver nucleic acids to hepatocytes, muscle cells or bone forming cells, e.g for treating cardiovascular disease, cancer, and infection. The transporter systems are also used to create transgenic animals (as models for human carcinogenesis or disease or for drug testing). Other uses include transforming cells to produce proteins, or transfecting cells in vitro to study the function of the nucleic acid. The use of a surface ligand allows specific targeting of selected cells and tissues. The lytic agent provides for release of the nucleic acid into the cellular interior, from
                                                                                                                                                                                                                                                                            System for transporting nucleic acid into cells, useful e.g. in gene therapy and for generating transgenic animals, comprises binding agent linked to nucleic acid, surface ligand and lytic agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        endosomes, without requiring endosomal or lysosomal degradation
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                                                                                                                                                        Smith LC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.0%; Score 17.4; DB 3; Length 27; 94.7%; Pred. No. 4.2e+03; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 27 BP; 13 A; 0 C; 14 G; 0 T; 0 U; 0 Other;
                                                                                                                                                        Sottchalk S, Sparrow J, Cristiano RJ, Woo SLC,
                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 15a; 108pp; English
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                                                                                         COLLEGE MEDICINE
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                          93WO-US002725.
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92US-00855389
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nes 18; Conserv
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19-MAR-1993;
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14-DEC-1993;
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                                                         WOO SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
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                                                                                                                                                                                    The present invention relates to a transporter system for delivering nucleic acid to a cell. The system comprises a nucleic acid binding complex, consisting of a binding molecule bonded non-covalently to the nucleic acid, and covalently to a surface ligand, and a lytic agent. The binding molecule is spermine or a spermidine derivative. Nucleotide sequences AAA36633-A36652 and peptide sequences AAY98456-Y98500 are used in the construction of the transporter system of the invention. The transporter system is used in gene therapy, particularly to deliver nucleic acids to hepatocytes, muscle cells or bone forming cells, e.g for treating cardiovascular disease, cancer, and infection. The transporter systems are also used to create transport sesting). Other uses include carcinogenesis or disease or for drug testing). Other uses include transforming cells to produce proteins, or transfecting cells in vitro carcinogenesis on of the nucleic acid. The use of a surface ligand allows specific targeting of selected cells and tissues. The lytic agent provides for release of the nucleic acid into the cellular interior, from endosomes, without requiring endosomal or lysosomal degradation
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                                                                                                                   System for transporting nucleic acid into cells, useful e.g. in gene therapy and for generating transgenic animals, comprises binding agent linked to nucleic acid, surface ligand and lytic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                    Smith LC;
                                                                                                                                                                                                                                                                                                                                                                                                                                 87.0%; Score 17.4; DB 3; Length 27;
llarity 94.7%; Pred. No. 4.2e+03;
Conservative 0; Mismatches 1; Indels
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/*tag= a
/note= "all C's are methylcytosines"
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 27 BP; 0 A; 14 C; 0 G; 13 T; 0 U; 0 Other;
                                                                      WOO SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Template pyrimidine series sequence in a ligand.
                                                                      Cristiano RJ,
                                                                                                                                                                  Disclosure; Fig 15a; 108pp; English.
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                                             (BAYU ) BAYLOR COLLEGE MEDICINE
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            92US-00855389.
93WO-US002725.
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                                                                      Gottchalk S, Sparrow J,
                                                                                             WPI; 2000-281993/24
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hes 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified base
            20-MAR-1992;
19-MAR-1993;
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AAZ39496/c
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The invention relates to a nucleic acid transport system (NTS) for delivering nucleic acid into a cell. The NTS contains but is not limited to 5 components: (a) the nucleic acid or a macromolecule to be delivered; (b) a moiety that recognizes and binds to a cell surface receptor or antigen or is capable of entering a cell through cytosis; (c) a nucleic acid or macromolecular molecule binding moiety; (d) a moiety that is capable of moving or initiating movement through a nuclear membrane; and/or (e) a lysis moiety that enables the transport of the entire complex from the cell surface directly into the cytoplasm of the cell. The NTS cellivers nucleic acid into the cellular interior as well as the nucleus of specific cells. The NTS can be used to treat disorders by targeting specific nucleic acid accordingly. The NTS can also be used to create transgenic animals for assessing human disease, such as cancer, in an animal model. The NTS can be used in vitro with tissue culture cells. The NTS can be used in vitro with tissue culture cells. The yes agent within the NTS avoids the problem of endosomal/lysosomal
                                                                                                                                                                                                                                                                                                          Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model.
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                                                                                                                                                                           Smith LC;
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                                                                                                                                                                           Sparrow J,
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                                                                                                    (BAYU ) BAYLOR COLLEGE MEDICINE.
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93WO-US002725.
93US-00167641.
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                                                                                                                                                                           Cristiano RJ,
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Matches 18; Conserv
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                                                                                                            The invention relates to a nucleic acid transport system (NTS) for delivering nucleic acid into a cell. The NTS contains but is not limited to 5 components: (a) the nucleic acid or a macromolecule to be delivered; (b) a moiety that recognizes and binds to a cell surface receptor or artigen or is capable of entering a cell through cytosis; (c) a nucleic acid or macromolecular molecule binding moiety; (d) a moiety that is capable of moving or initiating movement through a nuclear membrane; and or (e) a lysis moiety that enables the transport of the entire complex from the cell surface directly into the cytolasm of the cell. The NTS delivers nucleic acid into the cellular interior as well as the nucleus of specific cells. The NTS can be used to treat disorders by targeting transgenic animals for assessing human disease, such as cancer, in an animal model. The NTS can be used in vitro with tissue culture cells animal model. The NTS can be used in vitro with tissue culture cells which allows the role of various nucleic acids to be studied by targeting specific expression into specifically targeted tissue culture cells. The last agent within the NTS avoids the problem of endosomal/lysosomal
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                                           Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model.
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Pred. No. 4.2e+03;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 27 BP; 13 A; 0 C; 14 G; 0 T; 0 U; 0 Other;
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                                                                                      Disclosure; Fig 15A; 107pp; English.
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93US-00167641.
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Best Local Similarity 94.7%
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             WPI; 2000-038262/03
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                                                                                                                                                                                                                                                                                                                                                                          degradation
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Nucleic acid transporter system for delivering nucleic acid into a cell, useful for delivering proteins and polypeptides to cells, including

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This invention describes a novel system (1) for delivering a nucleic acid to a cell, comprising a binding complex comprising a ligand binding molecule noncovalently bound to a nucleic acid and covalently linked to a curface ligand, and a second binding complex comprising a second binding complex comprising a second binding molecule noncovalently bound to a nucleic acid and covalently linked to a nuclear ligand. The complexes are simultaneously bound to the nucleic acid transporter system can also be used in a method for the in vivo targeting of the insertion of DNA into a cell. It can also be used in processes for producing transformed cell lines. The system can be used to deliver a variety or proteins and polypeptides, such as hormones, growth factors, enzymes, clotting factors, apolipoproteins, receptors, drugs, oncogenes, tumor antigens, tumor appropriate system uses lysis agents to overcome the problems of endosomal/lysosomal degradation seen with prior art systems
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 87.0%; Score 17.4; DB 4; Length 27; Best Local Similarity 94.7%; Pred. No. 4.2e+03; Matches 18; Conservative 0; Mismatches 1; Indels
growth factors, enzymes, hormones, and tumor suppressors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid transporter system primer SEQ ID NO 14.
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27 BP; 13 A; 0 C; 14 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note = "5-methylcytosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "5-methylcytosine"
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/note= "5-methylcytosine"
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/mod_base= Other
/note= "5-methylcytosine"
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                                         Disclosure; Col 97-98; 105pp; English
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/mod_base= Other
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/mod_base= Other
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AGGGGAGGGGAGGG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC82866 standard; DNA; 27 BP
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Gaps

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Length 27; Indels

87.0%; Score 17.4; DB 4; 94.7%; Pred. No. 4.2e+03; ive 0; Mismatches 1;

1 AGGGGAGGGGAGGG 19

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Conservative

Local Similarity nes 18; Conserv

Query Match Best Loc Matches 24 AAGGGAGGGAGGGAGGG 6

AAS08476/c ID AAS08476 standard; DNA; 27

RESULT 14

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Nucleic acid transporter system for delivering nucleic acid into a cell, useful for delivering proteins and polypeptides to cells, including growth factors, enzymes, hormones, and tumor suppressors.
                                                                                                                                                                                                                                                                                                                                                            WOO SLC;
                                                                                                                                                                                                                                                                                                                                                            Smith LC,
                                     *tag= h
mod_base= Other
note= "5-methylcytosine"
                                                                                                                                                                                                                                       /mod_base= Other
/note= "5-methylcytosine"
                      note = "5-methylcytosine"
                                                                                     note= "5-methylcytosine"
                                                                                                                    note = "5-methylcytosine"
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note= "5-methylcytosine"
                                                                                                                                                                                                                                                                                                                                                           Sparrow J, Cristiano RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Col 97-98; 105pp; English.
                                                                    *tag= i
mod_base= Other
                                                                                                    *tag= j
mod base= Other
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mod_base= Other
       *tag= g
mod_base= Other
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                                                                                                                                                                                                                                                                                                           92US-00855389.
93WO-US002725.
93US-00167641.
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modified base
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                                                                                                                                                                                                                                                                                                                                                            Gottchalk S,
                                                                                                                                                                                                                                                                                             05-JUN-1995;
                                                                                                                                                                                                                                                                                                              20-MAR-1992;
                                                                                                                                                                                                                                                                                                                    19-MAR-1993;
14-DEC-1993;
                                                                                                                                                                                                                                                               US6150168-A.
                                                                                                                                                                                                                                                                              21-NOV-2000.
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This invention describes a novel system (I) for delivering a nucleic acid to a cell, comprising a binding complex comprising a ligand binding molecule noncovalently bound to a nucleic acid and covalently linked to a nucleic acid and covalently linked to a nucleic acid and covalently linked to a nuclear ligand. The complexes are simultaneously bound to the nucleic acid and covalently linked to nuclear ligand. The complexes are simultaneously bound to the nucleic acid. The nucleic acid transporter system can also be used in a method for the in vivo targeting of the insertion of DNA into a cell. It can also be used in processes for producing transformed cell lines. The system can be used to deliver a variety or proteins and polypeptides, such as hormones, growth factors, enzymes, clotting factors, apolipoproteins, receptors, drugs, oncogenes, tumor antigens, tumor cauptoproteins, receptors, drugs, oncogenes, tumor antigens, tumor the transporter system uses lysts agents to overcome the problems of endosomal/lysosomal degradation seen with prior art systems

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Sequence 27 BP; 0 A; 14 C; 0 G; 13 T; 0 U; 0 Other;
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The sequence represents the pyrimidine-rich oligonucleotide #5 used in a nucleic acid transporter system. The nucleic acid transporter system uses mucleic acid binding complexes containing surface ligands which are capable of binding to a cell surface receptor and entering the cell through cytosis. The compounds of the invention are either ligands,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model.
                                                         Pyrimidine-rich oligonucleotide #5 used in nucleic acid transport system.
                                                                              Nucleic acid transport, cytosis; ligand; lysis agent; spacer molecule; gene therapy; hepatocyte; muscle; bone forming cell; oligonucleotide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sparrow J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith LC, Cristiano RJ, Gottchalk S,
                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 15; 111pp; English.
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/mod_base= m5c
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/mod_base= m5c
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'mod_base= m5c
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93WO-US002725.
93US-00167641.
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19-MAR-1993;
14-DEC-1993;
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                                      23-OCT-2001
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                                                                                                                 Synthetic.
                  AAS08476;
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AAD41066 standard; DNA; 30

RESULT 16

AAD41066

AAD41066;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model.
binding molecules (surface ligands), lysis agents, spacer molecules or their intermediates. The ligands, binding molecules, lysis agents and spacer molecules are used in nucleic acid transporter lystems to deliver nucleic acid into specific cells e.g. in gene therapy to deliver acid into hepatocytes, muscle cells or bone forming cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid transport; cytosis; ligand; lysis agent; spacer molecule; gene therapy; hepatocyte; muscle; bone forming cell; oligonucleotide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Purine-rich oligonucleotide #5 used in nucleic acid transporter system.
                                                                                                                                                                                       Gaps
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                                                                                                                                             Query Match 87.0%; Score 17.4; DB 4; Length 27; Best Local Similarity 94.7%; Pred. No. 4.2e+03; Matches 18; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 17.4; DB 4; Length 27;
Pred. No. 4.2e+03;
0; Mismatches 1; Indels
                                                                                                          Sequence 27 BP; 0 A; 14 C; 0 G; 13 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gottchalk S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 15; 111pp; English
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94.7%; Pred
0; 1
                                                                                                                                                                                                                       1 AGGGGAGGGGAGGG 19
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                                                                                                                                                                                                                                              24 AAGGGAGGGAGGGAGGG 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92US-00855389.
93WO-US002725.
93US-00167641.
                                                                                                                                                                                                                                                                                                                                                   AAS08477 standard; DNA; 27 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-365933/38
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19-MAR-1993;
14-DEC-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                        AAS08477;
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                                                                                                                                                                                                                                                                                                                   RESULT 15
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The invention relates to a tumour necrosis-factor TNP inducible promoters.

The invention is useful for identifying candidate TNP inducible promoters by aligning a test sequence consisting of a nucleic acid sequence with a comparison sequence selected from the invention, using a gap opening penalty of 50 and a gap extension penalty of 3 to define a test alignment, shuffling the nucleic sequence of the test sequence at least one hundred times, while maintaining its length and composition, to produce a series of randomised sequences, aligning the randomised and appearance of 3, to produce a series of randomised calignments, where the average alignment quality of the randomised alignments represent an alignment quality of the randomised alignments represent an alignment expected by chance, comparing the test alignment with the average alignment quality of the randomised and identifying a test alignment with a probability value of less than to 0.05 that the alignment is obtained by chance as a candidate TNF inducible promoter. The invention is useful for identifying candidate compounds for treating or preventing autoimmune disorders or cancer. The present sequence is a primer used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel tumor necrosis-factor inducible promoter useful for identifying candidate compounds for treating/preventing autoimmune disorders/cancer, or for identifying promoters that are regulated by tumor necrosis factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                               Tumour necrosis-factor; TNF; promoter; autoimmune disorder; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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Pred. No. 4.2e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 30 BP; 6 A; 4 C; 17 G; 3 T; 0 U; 0 Other;
                                                                                          Primer ON-TATADel used for DNA sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example; Page 17; 95pp; English.
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ilarity 94.7%;
Conservative C
                                                                                                                                                                                                                                                                                                  07-DEC-2001; 2001WO-EP014412.
                                                                                                                                                                                                                                                                                                                                    08-DEC-2000; 2000US-0254649P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AGGGGAGGGAGGGTGGG
                                                      30-OCT-2002 (first entry)
                                                                                                                                                  therapy; primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-519670/55
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                                                                                                                                                                                                                          WO200246433-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Simil
Matches 18; C
                                                                                                                                                                                                                                                                                                                                                                       (SAUS/) SAUS
                                                                                                                                                                                     Unidentified
                                                                                                                                                                                                                                                               13-JUN-2002
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Local Similarity es 18; Conserv

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New isolated DNA polymerase, pol kappa 76, useful in identifying autoimmune disorders and in treating cancer and autoimmune disorders by
                                                                                                                                                    Example; Page 6; 54pp; English.
         08-DEC-2000; 2000US-0254649P.
                                                                                                                             modifying its expression.
                                                                               WPI; 2003-479531/45.
                                 (SAUS/) SAUS
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                                                                                                                                                                                                                                                                                                                                                                 The present invention provides the protein and coding sequences of human DNA polymerase pol kappa 76. The gene is found on human chromosome 5q12-13, in a head-to-head arrangement with the Goodpasture antigen binding protein (GPBP). The detection of the coding sequence can be used for diagnosing an autoimmune condition and identifying cells undergoing applytosis, and the sequences can be used in the treatment of autoimmune diseases and cancer. The present sequence is a sequencing primer
                                                                                                                                                                                                                                                                                                 Novel isolated pol kappa76 polypeptide, a 76 kDa alternatively spliced variant of DNA polymerase kappa, useful as target for treating a patient with autoimmune disorder or cancer.
                                                      Human; pol kappa 76; Goodpasture antigen binding protein; GPBP;
chromosome 5q12-13; apoptosis; autoimmune disorder; cancer; cytostatic;
immunosuppressive; PCR; primer; sequencing; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; ss; Goodpasture antigen binding protein; GPBP; COL4A3BP; collagen 4 alpha 3 binding protein; DNA polymerase kappa; Pol kappa; Goodpasture disease; cutaneous lupus; polK76; bi-directional promoter; autoimmune disease; cancer; antisense therapy; PCR; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human bi-directional promoter PCR/sequencing primer ON-TATADel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 17.4; DB 6; Length 30;
Pred. No. 4.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                  Human pol kappa 76 DNA polymerase sequencing primer #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 30 BP; 6 A; 4 C; 17 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                 Example, Page 15, 90pp, English
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                                                                                                                                                                                                     08-DEC-2000; 2000US-0254649P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 87.0%;
1 Similarity 94.7%;
18; Conservative (
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            (first entry)
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Best Local Similarity
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                                                                                                                              WO200246378-A2
                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                            (SAUS/) SAUS
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            18-SEP-2002
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                                                                                                                                                       13-JUN-2002
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                                                                                                                                                                                                                                                   Saus J;
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The invention relates to an isolated pol kappa (k) 76 polypeptide (an alternatively spliced form of DNA polymerase kappa), appearing as ADD13492). The gene for AB007327 (encoded by the CDNA appearing as ADD13492). The gene for POLkappa is located on chromosome 5q12-13 in a head-head arrangement with the gene encoding Goodpasture antigen binding protein (GDBP or collagen 4 alpha 3 binding protein (CDL4A3bp), associated with autoimmune diseases cuch as Goodpasture's disease and cutaneous lupus) i.e. has a bi-comprising the polK76 cDNA, a host cell transfected with the vector, detecting (M1) polK76 (comprising providing a protein sample to be corrected, contacting the protein sample to be screened, complexes, where the presence of the antibody-polypeptide complexes in a sample (comprising contacting the sample with one or more polK76 pcrimer, carrying out PCR to generate PCR products, and identifying the comprising providing a tissue of body fluid sample from the patient, comprising providing a tissue or body fluid sample in which no autoimmune condition is present, and detecting an increase in pol K76 RNA expression in the tissue of body fluid sample compared to the control sample, where the increase indicates the presence of an autoimmune condition) and the tissue of body fluid sample compared to the control sample, where the increase indicates the presence of an autoimmune disorder or cancer by modifying the expression or activity of polK76 or polK76 increasing their expression or activity of polK76 increasing produce is a PCR and/or sequencing primer used in the analysis of bi-directional promoters of encer in the present sequence is a PCR and/or sequencing cancer. The present sequence is a PCR and/or sequencing in the present sequence is a PCR and/or sequencing in the present sequence is a PCR and/or sequence is a PCR and/or seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human tumour necrosis factor (TNF) inducible promoter PCR primer #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             compared to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    whose structure and sequence were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.2e+03;
ches 1;
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); Mismatches
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Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polkappa/GPBP)
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ADA97805
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The present invention relates to a transporter system for delivering nucleic acid to a cell. The system comprises a nucleic acid binding complex, consisting of a binding molecule bonded non-covalently to the nucleic acid, and covalently to a surface ligand, and a lytic agent. The binding molecule is spermine or a spermidine derivative. Nuclectide sequences AAP36633-A3662 and peptide sequences AAP36456-Y98500 are used in the construction of the transporter system of the invention. The transporter system is used in gene therapy, particularly to deliver transporter systems are also used to create transporter and infection. The transporter systems are also used to create transport and infection. The transporter systems are also used to create transport and infection. The transporter cransforming cells to produce proteins, or transfecting cells in vitro transforming cells to produce proteins, or transfecting cells in vitro to study the function of the nucleic acid. The use of a surface ligand allows specific targeting of selected cells and tissues. The lytic agent provides for release of the nucleic acid into the cellular interior, from condosomes, without requiring endosomal or lysosomal degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model.
System for transporting nucleic acid into cells, useful e.g. in gene therapy and for generating transgenic animals, comprises binding agent linked to nucleic acid, surface ligand and lytic agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid transport system; NTS; cell surface receptor; cytosis nuclear membrane; lysis moiety; transgenic animal; human disease; nucleic acid delivery; cancer; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.0%; Score 17.4; DB 3; Length 39; 94.7%; Pred. No. 4.1e+03; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 39 BP; 13 A; 6 C; 14 G; 6 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Target sequence in a double stranded vector.
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                                                                                 Disclosure; Fig 15a; 108pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 15A; 107pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AGGGGAGGGAGGG 19
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93US-00167641.
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14-DEC-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  promoter. Also disclosed are an expression vector comprising one or more trumour necrosis factor inducible promoters and a recombinant host cell transfected with one or more expression vectors. The TNF inducible promoters, expression vectors and host cells are useful for identifying promoters that are regulated by tumour necrosis factor or for identifying promoters that compounds for treating or preventing autoimmune disorders or candidate compounds for treating or preventing autoimmune disorders or necrosis factor inducible promoter of the invention.
                                                                                                                                                                                                                                                                                             New tumor necrosis factor inducible promoters, useful for identifying promoters that are regulated by tumor necrosis factor, or for identifying candidate compounds for treating or preventing autoimmune disorders or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a tumour necrosis factor (TNF) inducible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transporter system; nucleic acid delivery; gene therapy; cancer; carcinogenesis; cardiovascular disease; infection; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 30 BP; 6 A; 4 C; 17 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                             Example, Page 7; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA36645 standard; cDNA; 39 BP
                                                                                                                                          08-DEC-2000; 2000US-0254649P.
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                                                                                                   07-DEC-2001; 2001US-00008721
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                      US2003082745-A1
                                                                                                                                                                               (SAUS/) SAUS
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                                                                                                                                                                                                                      Saus J;
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delivering nucleic acid into a cell. The NTS contains but is not limited to 5 components: (a) the nucleic acid or a macromolecule to be delivered; (b) a moiety that recognizes and binds to a cell surface receptor or acting or is capable of entering a cell through cytosis; (c) a nucleic acid or macromolecular molecule binding moiety; (d) a moiety that is capable of moving or initiating movement through a nuclear membrane; and/or (e) a lysis moiety that enables the transport of the entire complex from the cell surface directly into the cytoplasm of the cell. The NTS delivers nucleic acid into the cellular interior as well as the nucleus of specific cells. The NTS can be used to treat disorders by targeting specific nucleic acid acordingly. The NTS can also be used to create transgenic animals for assessing human disease, such as cancer, in an animal model. The NTS can be used in vitro with tissue culture cells. Which allows the role of various nucleic acids to be studied by targeting specific expression into specifically targeted tissue culture cells. The last agent within the NTS avoids the problem of endosomal/lysosomal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel system (1) for delivering a nucleic acid to a cell, comprising a binding complex comprising a ligand binding molecule noncovalently bound to a nucleic acid and covalently linked to a surface ligand, and a second binding complex comprising a second binding molecule noncovalently bound to a nucleic acid and covalently linked to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid delivery; nucleic acid transporter system; hormone; enzyme; growth factor; clotting factor; apolipoprotein; receptor; drug; oncogene; tumor antigen; tumor suppressor; viral antigen; parasitic antigen; bacterial antigen; primer; ses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               into a cell,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                             87.0%; Score 17.4; DB 3; Length 39; 94.7%; Pred. No. 4.1e+03; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOO
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                                                                                                                                                                                                                                                                                                                                                             Sequence 39 BP; 13 A; 6 C; 14 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith LC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AGGGGAGGGAGGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC82865 standard; DNA; 39 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93US-00167641.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sparrow J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-049093/06.
                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gottchalk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence represents the double-stranded vector target sequence #5 used in a nucleic acid transporter system. The nucleic acid transporter system uses nucleic acid binding complexes containing surface ligands which are capable of binding to a cell surface receptor and entering the cell through cytosis. The compounds of the invention are either ligands, binding molecules (surface ligands), lysis agents, spacer molecules or their intermediates. The ligands, binding molecules, lysis agents and spacer molecules are used in nucleic acid transporter systems to deliver nucleic acid into hepatocytes, muscle cells e.g. in gene therapy to deliver nucleic acid into hepatocytes, muscle cells or bone forming cells
nuclear ligand. The complexes are simultaneously bound to the nucleic acid. The nucleic acid transporter system can also be used in a method for the in vivo targeting of the insertion of DNA into a cell. It can also be used in processes for producing transformed cell lines. The system can be used to deliver a variety or proteins and polypeptides, such as hormones, growth factors, enzymes, clotting factors, apolipoproteins, receptors, drugs, oncogenes, tumor antigens, tumor suppressors, viral antigens, parasitic antigens, and bacterial antigens. The transporter system uses lysis agents to overcome the problems of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid transport, cytosis; ligand; lysis agent; spacer molecule; gene therapy; hepatocyte; muscle; bone forming cell; ds.
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vector target sequence #5 used in nucleic acid transporter system.
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                                                                                                                                                                                                                                                 Match
Local Similarity 94.7%; Pred. No. 4.1e+03;
es 18; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                endosomal/lysosomal degradation seen with prior art systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 17.4; DB 4; Length 39;
Pred. No. 4.1e+03;
                                                                                                                                                                                                                       Sequence 39 BP; 13 A; 6 C; 14 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 39 BP; 13 A; 6 C; 14 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith LC, Cristiano RJ, Gottchalk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Fig 15; 111pp; English.
                                                                                                                                                                                                                                                                                                                                      1 AGGGGAGGGGAGGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                           10 AAGGGAGGGAGGGAGGG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
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93WO-US002725.
93US-00167641.
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94.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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Best Local Similarity
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19-MAR-1993;
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Matches
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artiple-helix computation triangle helical nucleic acid computation triangle and second substantially complementary strands, and an oligonuclectide bound to a purine-rich target sequence within the double helical nucleic acid, where the oligonuclectide binds in a parallel and antiparallel orientation, respectively, to target sequences on alternate strands of the double helical nucleic acid. The method has therapeutic applications, where gene expression is controlled by selective triple-helix formation within expression regulatory sequences of a target gene. The oligonuclectides can be used to form triple-helices, and are useful to cletcet the presence or absence of specific sequences within genomic DNA for diagnostic and therapeutic purposes. The oligonuclectides can be selected to specifically bind to pathogenic double-stranded DNA including selected to specifically bind to pathogenic bacteria or viruses for replication or virulence, reducing their pathogenicity. Alternatively, the oligonuclectides can be chosen to target a unique sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention relates to methods and oligonucleotides for forming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   parnogen which is not found in the genome of pathogen's host. The suppression of specific oncogenes including those of endogenous or viral origin. Such therapeutic oligonucleotides are capable of forming triple-helices with such sequences in cancer tries of endogenous or viral origin. Such therapeutic oligonucleotides are capable of forming triple-helices with such sequences in cancernal origin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   helices with such sequences in cancerous cells containing the activated oncogene, so preferentially killing or repressing the cancer causing cell. The present sequence represents a DNA sequence used in the methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A triple-helix comprising a double helical nucleic acid (DHNA) and an oligonuclectide which binds in parallel and antiparallel orientation, respectively, for targetting sequences on alternate strands of DHNA to control gene expression.
                                                                                                                                                                                                                                                                                                                                                                        Triple-helix formation; purine-rich target sequence; double-helix DNA; gene expression; regulatory sequence; pathogenic double-stranded DNA; pathogenic bacteria; virus; replication; virulence; cancer; cancer oncogene suppression; cancervus cell; cytostatic; antimicrobial; ss.
Gaps
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  Indels
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  1;
                                                                                                                                                                                                                                                                                                                                 Triple helix forming associated DNA sequence #19.
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CALY ) CALIFORNIA INST OF TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; Fig 8B; 108pp; English.
                                           1 AGGGGAGGGGAGGG 19
                                                                                    10 AAGGGAGGGAGGGAGGG 28
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                                                                                                                                                                                                  ABK98155 standard; DNA; 39 BP
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                                                                                                                                                                                                                                                                                      (first entry)
  18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-536030/57.
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                                                                                                                                                                                                                                                                                      07-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-JUN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                           ABK98155;
  Matches
                                                                                                                                                      RESULT 24
                                                                                                                                                                             ABK98155
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Score 17.4; DB 6; Length 39;

87.0%;

Query Match

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The present invention relates to methods and oligonucleotides for forming a triple-helix comprising a double helical nucleic acid comprising first and second substantially complementary strands, and an oligonucleotide bound to a purine-rich target sequence within the double helical nucleic acid, where the oligonucleotide binds in a parallel and antiparallel acid, where the oligonucleotide binds in a parallel and antiparallel configuration, respectively, to target sequences on alternate strands of the double helical nucleic acid. The method has therapeutic applications, where gene expression is controlled by selective triple-helix formation within expression regulatory sequences of a target gene. The oligonucleotides can be used to form triple-helices, and are useful to detect the presence or absence of specific sequences within genomic DNA for diagnostic and therapeutic purposes. The oligonucleotides can be selected to specific sequences required by pathogenic bacteria or viruses for replication or virulence, reducing their pathogenicity. Alternatively,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the oligonucleotide are chosen to target a unique sequence of the pathogen which is not found in the genome of pathogen's host. The oligonucleotides can be used in cancer treatment by way of triple-helix suppression of specific oncogenes including those of endogenous or viral origin. Such therapeutic oligonucleotides are capable of forming triple-helices with such sequences in cancerous cells containing the activated oncogene, so preferentially killing or repressing the cancer causing cell. The present sequence represents a DNA sequence used in the methods of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A triple-helix comprising a double helical nucleic acid (DHNA) and an oligonucleotide which binds in parallel and antiparallel orientation, respectively, for targetting sequences on alternate strands of DHNA to control gene expression.
                                                                                                                                                                                                                                                                                                                                                                        Triple-helix formation; purine-rich target sequence; double-helix DNA; gene expression; regulatory sequence; pathogenic double-stranded DNA; pathogenic bacteria; virus; replication; virulence; cancer; oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
                       Gaps
                     ;
0
                     Indels
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Pred. No. 4.1e+03;
                                                                                                                                                                                                                                                                                                                                    Triple helix forming associated DNA sequence #18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CALY ) CALIFORNIA INST OF TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; Fig 8B; 108pp; English.
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                                                            19
                                                                                                  28
                                                              1 AGGGGAGGGAGGGG
                                                                                                    10 AAGGGAGGGAGGGGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93US-00168920.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92US-00946976.
94.78;
                                                                                                                                                                                                            ABK98154 standard; DNA; 39
                                                                                                                                                                                                                                                                                           (first entry)
                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beal PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-536030/57.
  Best Local Similarity
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                                                                                                                                                                                                                                                                                         07-OCT-2002
                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                    ABK98154;
                       Matches
                                                                                                                                                                     RESULT 25
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A triple-helix comprising a double helical nucleic acid (DHNA) and an oligonuclectide which binds in parallel and antiparallel orientation, respectively, for targetting sequences on alternate strands of DHNA to
                                                                                                                                                                                                Triple-helix formation; purine-rich target sequence; double-helix DNA gene expression; regulatory sequence; pathogenic double-stranded DNA; pathogenic bacteria; virus; replication; virulence; cancer; oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
                            Gaps
                           ;
0
       Score 17.4; DB 6; Length 39;
Pred. No. 4.1e+03;
0; Mismatches 1; Indels
                                                                                                                                                                              Triple helix forming associated oligonucleotide #3.
                                                                                                                                                                                                                                                                                                                                                     (CALY ) CALIFORNIA INST OF TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Col 29; 108pp; English.
87.0%; Scc...
94.7%; Pred
0;
                                               1 AGGGGAGGGGAGGG 19
                                                                  30 AAGGGAGGGAGGGGAGGG 12
                                                                                                                    BP
                                                                                                                                                                                                                                                                                                                                   92US-00946976.
                                                                                                                   ABK98106 standard; DNA; 43
                                                                                                                                                           (first entry)
                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     respectively, for target
control gene expression
                                                                                                                                                                                                                                                                                                                                                                         Dervan PB, Beal PA;
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-536030/57.
                 Local Similarity
nes 18; Conserv
                                                                                                                                                                                                                                                                       US6403302-B1
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                                                                                                                                                           07-OCT-2002
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                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                        ABK98106;
         Query Match
                   Best Loc
Matches
                                                                                                RESULT 26
                                                                                                           ABK98106
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The present invention relates to methods and oligonucleotides for forming a triple-helix comprising a double helical nucleic acid comprising first and second substantially complementary strands and an oligonucleotide bound to a purine-rich target sequence within the double helical nucleic acid, where the oligonucleotide binds in a parallel and antiparallel crientation, respectively, to target sequences on alternate strands of the double helical nucleic acid. The method has therapeutic application, where gene expression is controlled by selective triple-helix formation oligonucleotides can be used to form triple-helics, and are useful to eligonucleotides can be used to form triple-helices, and are useful to detect the presence or absence of specific sequences within genomic DNA cor diagnostic and therapeutic purposes. The oligonucleotides can be selected to specific sequences required by pathogenic double-stranded DNA including specific sequences required by pathogenic double-stranded DNA including specific sequences required by pathogenic bacteria or viruses for replication or virulence, reducing their pathogenicity. Alternatively, the oligonucleotide can be chosen to target a unique sequence of the propertion of the oligonucleotide can be chosen to target a unique sequence of the propertion of the oligonucleotide can be chosen to target a unique sequence of the propertion of the oligonucleotide can be chosen to target a unique sequence. The oligonucleotides can be used in cancer treatment by way of triple helix suppression of specific oncogenes including those of endogenous or viral origin. Such therapeutic oligonucleotides are capable of forming triple helices with such sequences in cancerous cells containing the activated oncogene, so preferentially killing or repressing the cancer causing cell. The present sequence represents an oligonucleotide used in the the present invention methods of

Sequence 43 BP; 15 A; 6 C; 14 G; 8 T; 0 U; 0 Other;

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a triple-hellx comprising a double helical nucleic acid comprising first and second substantially complementary strands, and an oligonucleotide bound to a purine-rich target sequence within the double helical nucleic acid, where the oligonucleotide binds in a parallel and antiparallel corid, where the oligonucleotide binds in a parallel and antiparallel corid the double helical nucleic acid. The method has therapeutic applications, where gene expression is controlled by selective triple-helix formation within expression regulatory sequences of a target gene. The oligonucleotides can be used to form triple-helices, and are useful to detect the presence or absence of specific sequences within genomic DNA for diagnostic and therapeutic purposes. The oligonucleotides can be selected to specific sequences required by pathogenic bacteria or viruses for replication or virulence, reducing their pathogenicity. Alternatively, the oligonucleotides can be chosen to target a unique sequence of the pathogen which is not found in the genome of pathogen's host. The pathogen which is not found in the genome of pathogen's host. The oligonucleotides can be used in cancer treatment by way of triple-helix origin. Such therapeutic oligonucleotides are capable of forming triple-helices with such sequences in cancerous cells containing the activated concepted. The present sequence represents a DNA sequence used in the methods cell. The present sequence represents a DNA sequence used in the methods
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention relates to methods and oligonucleotides for forming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A triple-helix comprising a double helical nucleic acid (DHNA) and an oligonuclectide which binds in parallel and antiparallel orientation, respectively, for targetting sequences on alternate strands of DHNA to
                                                                                                                                                                                                                                                                                                                                                                         Triple-helix formation; purine-rich target sequence; double-helix DNA; gene expression; regulatory sequence; pathogenic double-stranded DNA; pathogenic bacteria; virus; replication; virulence; cancer; concogene suppression; cancerous cell; cytostatic; antimicrobial; 88.
                                                   Gaps
                                                   ;
                                                   Indels
             Length
4; DB 6; 4e+03;
                                                                                                                                                                                                                                                                                                                                       Triple helix forming associated DNA seguence #1.
             Score 17.4; DB
Pred. No. 4e+03
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CALY ) CALIFORNIA INST OF TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; Col 29; 108pp; English.
                                                                                      1 AGGGGAGGGAGGG 19
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0
                                                                                                                                                                                                                         ABK98104 standard; DNA; 19 BP
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               87.0%;
94.7%;
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                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         control gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beal PA;
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                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-SEP-1992;
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                                                     18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                              ABK98104;
               Query Match
Best Local 8
                                                   Matches
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                                                                                                                                                                                       RESULT 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a kit for diagnosing and treating T-cell associated diseases which comprises a panel of nucleic acid primers specifically priming and allowing amplification of each Wbeta gene, WbetaRNA or CDNA. The kit is useful for diagnosing organ transplant rejection and diagnosing and treating T-cell associated diseases including autoimmune diseases, degenerative nervous system diseases, graft versus host disease. Autoimmune diseases include Addison's diseases and neoplastic diseases. Autoimmune diseases include Addison's disease, arcphic gastritis. Degenerative nervous system diseases include multiple sclerosis and Alzheimer's disease. Hypersensitivity diseases include multiple sclerosis and Li hypersensitivities such as contact with allergens that lead to Goodpasture's syndrome and Type IV hypersensitivities such as those manifested in leprosy. Infectious diseases include viral infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kit for diagnozing and treating T-cell associated diseases e.g. autoimmune, degenerative nervous system and infectious disease, comprises nucleic acid primers specifically priming and allowing amplification of a
                                                                                                                                                                                                                                                                     human; T-cell associated disease; Vbeta; autoimmune disease; degenerative nervous system disease; graft versus host disease; hypersensitivity disease; infectious disease; neoplastic disease; Addison's disease; atrophic gastritis; degenerative nervous system disease; multiple sclerosis; Alzheimer's disease; hypersensitivity disease; type I hypersensitivity; Goodpasture's syndrome; type II hypersensitivity; Goodpasture's syndrome; type IV hypersensitivity; leptosy; infectious disease; viral infection; HIV; fungal infection, Candida; parasitic infection; schistosome; filaria; bacterial infection; Mycobacterium; neoplastic disease; lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
                                                     Gaps
                                                     ö
                        85.0%; Score 17; DB 6; Length 19; 100.0%; Pred. No. 5.9e+03;
                                                  0; Indels
Sequence 19 BP; 5 A; 0 C; 14 G; 0 T; 0 U; 0 Other;
                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 699; 164pp; English.
                                                                                                                                                                                                                                                 Human Vbeta gene repeat sequence #295.
                                                   ö
                                                                             3 GGGAGGGGAGGGG 19
                                                                                                      GGGAGGGAGGGGAGGG 18
                                                                                                                                                                      ADH70505 standard; DNA; 23 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-00309335.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-00263959
                                                                                                                                                                                                                       (first entry)
                                                   17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-059052/06
                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hood LE, Rowen L;
                                                                                                                                                                                                                                                                                                                                                                                                                        breast cancer; ds.
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Б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2002150891-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROWEN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo gapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-SEP-1994;
19-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HOOD/) HOOD
(ROWE/) ROWEN
                                                                                                                                                                                                                       25-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vbeta gene
                                                                                                                                                                                              ADH70505;
                           Query Match
                                                   Matches
                                                                                                                                            RESULT 28
ADH70505/
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caused by viruses such as HIV, fungal infections such as those caused by the yeast genus Candida, parasitic infections such as those caused by schistosomes, filaria and bacterial infections such as those caused by Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
                                                                                                                                      such as leukaemias, lymphomas and cancers such as cancer of the brain, breast. The present sequence represents a Voeta gene repeat sequence.
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Duplex, T4 polynucleotide kinase, nebularine, triple helix; triplex,
detection; diagnosis, pathogen; bacteria, virus; virulence; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Triple helix formation for diagnosis and therapy - by specific recognition by oligo:nucleotide probe of target sequence in doublestranded nucleic acid.
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                                                                                                                                                                                                                                                                                                            84.0%; Score 16.8; DB 12; Length 23; 90.0%; Pred. No. 6.7e+03; ive 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                             Sequence 23 BP; 1 A; 17 C; 1 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C or T"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AGGGGAGGGAGGGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CALY ) CALIFORNIA INST OF TECHN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGGGGGGGAGGTGAGGGG 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/note= "A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39mer duplex forming DNA.
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24-MAR-1994
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                                                                                                                                                                                                                                                                                                            Query Match
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correct PN field.)
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24-MAR-1994
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                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                          AAQ46256;
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Best Local S
                                                                              Matches
                                                                                                                                                                        RESULT 31
                                                                                                                                                                                      AAQ46256
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                                                                                                                                                                                                               The sequences given in AAQ46256-57 form a duplex which was used to evaluate the binding of trplix forming oligomers (TFO). The annealed coligomers form a purine-rich target sequence to which the TFO which contain a nebularine nucleotide binds, bind, forming a triple helix. These triplex-forming oligomers may be used to detect the presence or specific sequences within genomic DNA by the formation in situ or in vivo of triple helices for diagnostic and therapeutic purposes. TFO can be selected which specifically bind to pathogenic double-stranded DNA or in vivo of triple helices for diagnostic and therapeutic purposes. TFO can be selected which specifically bind to pathogenic double-stranded DNA including specific sequences required by pathogenic bacteria or viruses including specific sequence. Alternatively, TFO can be chosen to target a unique sequence of the pathogen which is not found in the genome of the pathogen which is not found in the genome of the pathogen witch is not found in the call containing it. Triple helix technology can also be used for cancer treatment by way of triple helix suppression of specific oncogenes including those of endogenous or viral origin. (Updated on 25-MAR-2003 to
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therapeutic agent to kill the pathogen or the cell containing it. Triple helix technology can also be used for cancer treatment by way of triple helix suppression of specific encogenes including those of endogenous or viral origin. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Triple helix formation for diagnosis and therapy - by specific recognition by oligo:nucleotide probe of target sequence in doublestranded nucleic acid.
                                                                                                                                                                                                                                                                                                                                                       T4 polynucleotide kinase; nebularine; triple helix; triplex
on; diagnosis; pathogen; bacteria; virus; virulence; cancer;
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0
                                                                                         Query Match 82.0%; Score 16.4; DB 2; Length 43; Best Local Similarity 89.5%; Pred. No. 8.6e+03; Matches 17; Conservative 0; Mismatches 2; Indels
                                                                 Sequence 43 BP; 14 A; 6 C; 14 G; 8 T; 0 U; 1 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 23; 42pp; English.
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                                                                                                                                              1 AGGGAGGGGAGGG 19
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                                                                                                                                                                                                                                        AAQ46257 standard; DNA; 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/note= "A,
                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                            (revised)
                                                                                                                                                                                                                                                                                                                                  Duplex forming DNA #2.
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                                                                                                                                                                                                                                                                                                                                                                                        oncogene; ss.
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24-MAR-1994
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                                                                                                                                                                                                                                                                                                                                                                           detection;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
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                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Duplex, T4 polynucleotide kinase; nebularine; triple helix; triplex;
detection; diagnosis; pathogen; bacteria; virus; virulence; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Triple helix formation for diagnosis and therapy - by specific recognition by oligo nucleotide probe of target sequence in doublestranded nucleic acid.
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                                                            Length 43;
                                                                                                                      Indels
Sequence 43 BP; 7 A; 15 C; 7 G; 13 T; 0 U; 1 Other;
                                                            Score 16.4; DB 2;
Pred. No. 8.6e+03;
); Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G, C or T"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER
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                                                                                                                                                                                                                                                                                                                                                                                      BP.
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                                                            82.0%;
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/note= "A,
                                                                                                                                                                                                                                                                                                                                                                                      AAQ46256 standard; DNA; 43
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/mod_base=
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                                                                                        Local Similarity 89.5
nes 17; Conservative
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modified_base
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including those of endogenous

suppression of

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The present invention relates to methods and oligonucleotides for forming a triple-helix comprising a double helical nucleic acid comprising first and second substantially complementary strands, and an oligonucleotide bound to a purine-rich target sequence within the double helical nucleic acid, where the oligonucleotide binds in a parallel and antiparallel or respectively, to target sequences on alternate strands of the double helical nucleic acid. The method has therapeutic applications, where gene expression is controlled by selective triple-helix formation within expression regulatory sequences of a target gene. The oligonucleotides can be used to form triple-helices, and are useful to detect the presence or absence of specific sequences within genomic DNA collected to specifically bind to pathogenic double-stranded DNA selection sequences required by pathogenic double-stranded DNA including specific sequences required by pathogenic double-stranded DNA the oligonucleotide can be chosen to target a unique sequence of the pathogen which is not found in the genome of pathogen; The pathogen which is not found in the genome of pathogen; The
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treatment by way of triple helix suppression of specific oncogenes including those of endogenous or viral origin. (Updated on 25-WAR-2003 correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A triple-helix comprising a double helical nucleic acid (DHNA) and an oligonuclectide which binds in parallel and antiparallel orientation, respectively, for targetting sequences on alternate strands of DHNA to
                                                                                      record issued on 21-OCT-2004 : Correction to feature table key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Triple-helix formation; purine-rich target sequence; double-helix DNA; gene expression; regulatory sequence; pathogenic double-stranded DNA; pathogenic bacteria; virus; replication; virulence; cancer; oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
                                                                                                                                                                                                           Gaps
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                                                                                                                                                                  82.0%; Score 16.4; DB 2; Length 43; 89.5%; Pred. No. 8.6e+03;
                                                                                                                                                                                                         2; Indels
                                                                                                                           Sequence 43 BP; 14 A; 6 C; 14 G; 8 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Triple helix forming associated DNA sequence #21.
                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                          14 AAGGGNGGGGAGGG 32
                                                                                                                                                                                                                                                                                                                                                                                       ABK98158 standard; DNA; 43 BP.
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                                                                                                                                                                                                         17; Conservative
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                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                            ABK98158;
                                                                                                                                                                    Query Match
                                                                                        Revised
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                                                                                                                                                                                                                                                                                                                                            RESULT 32
ABK98158/
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pathogen which is not found in the genome of pathogen's host. The oligonucleotides can be used in cancer treatment by way of triple-helix

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The present invention relates to methods and oligonucleotides for forming a triple-helix comprising a double helical nucleic acid comprising first and second substantially complementary strands, and an oligonucleotide bound to a purine-rich target sequence within the double helical nucleic acid, where the oligonucleotide binds in a parallel and antiparallel or riempartively, to target sequences on alternate strands of the double helical nucleic acid. The method has therapeutic applications, where gene expression is controlled by selective triple-helix formation within expression regulatory sequences of a target gene. The oligonucleotides can be used to form triple-helices, and are useful to detect the presence or absence of specific sequences within genomic DNA for diagnostic and therapeutic purposes. The oligonucleotides can be selected to specifically bind to pathogenic double-stranded DNA including specific sequences required by pathogenic bacteria or viruses for replication or virulence, reducing their pathogenicity. Alternatively, the oligonucleotide can be chosen to target a unique sequence of the the pathogen which is not found in the genome of pathogen's host. The
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               origin. Such therapeutic oligonucleotides are capable of forming triple-
helices with such sequences in cancerous cells containing the activated
oncogene, so preferentially killing or repressing the cancer causing
cell. The present sequence represents a DNA sequence used in the methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oligonucleotide which binds in parallel and antiparallel orientation, respectively, for targetting sequences on alternate strands of DHNA to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     triple-helix comprising a double helical nucleic acid (DHNA) and an
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                                                                                                                                                                                                                         Gaps
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0
                                                                                                                                                                                Length 43;
                                                                                                                                                                              82.0%; Score 16.4; DB 6; Length 4 Larity 89.5%; Pred. No. 8.6e+03; Conservative 0; Mismatches 2; Indels
                                                                                                                                       Sequence 43 BP; 7 A; 15 C; 7 G; 13 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Triple helix forming associated DNA sequence #3.
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                                                                                                                                                                                                                                                                  1 AGGGGAGGGAGGG 19
                                                                                                                                                                                                                                                                                                         AAGGGNGGGAGGGAGGG 16
                                                                                                                                                                                                                                                                                                                                                                                                                 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                 the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 control gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-536030/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beal PA;
                                                                                                                                                                                                    Local Similarity
nes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-DEC-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
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                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                           34
                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                      RESULT 33
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The present invention relates to methods and oligonuclectides for forming a triple-helix comprising a double helical nucleic acid comprising first and second substantially complementary strands, and an oligonuclectide bund to a purine-rich target sequence within the double helical nucleic acid, where the oligonuclectide binds in a parallel and antiparallel corientation, respectively, to target sequences on alternate strands of the double helical nucleic acid. The method has therapeutic applications, where gene expression is controlled by selective triple-helix formation within expression regulatory sequences of a target gene. The oligonuclectides can be used to form triple-helices, and are useful to detect the presence or absence of specific sequences within genomic DNA for diagnostic and therapeutic purposes. The oligonuclectides can be seed to granding their pathogenic double-stranded DNA including selected to specifically bind to pathogenic double-stranded DNA including replication or virulence, reducing their pathogenicity. Alternatively, the oligonuclectide can be chosen to target a unique sequence of the
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oligonucleotides can be used in cancer treatment by way of triple-helix suppression of specific oncogenes including those of endogenous or viral origin. Such therapeutic oligonucleotides are capable of forming triple-helices with such sequences in cancerous cells containing the activated oncogene, so preferentially killing or repressing the cancer causing cell. The present sequence represents a DNA sequence used in the methods of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A triple-helix comprising a double helical nucleic acid (DHNA) and an oligonuclectide which binds in parallel and antiparallel orientation, respectively, for targetting sequences on alternate strands of DHNA to
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                                                                                                                                                                                                                           82.0%; Score 16.4; DB 6; Length 43;
89.5%; Pred. No. 8.6e+03;
ive 0; Mismatches 2; Indels
                                                                                                                                                                                     Sequence 43 BP; 7 A; 15 C; 7 G; 13 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Triple helix forming associated DNA sequence #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CALY ) CALIFORNIA INST OF TECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                    1 AGGGGAGGGGAGGG 19
                                                                                                                                                                                                                                                                                                                                                    34 AAGGGNGGGAGGGAGG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABK98111 standard; DNA; 43 BP
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                                                                                                                                                                                                                                                    Local Similarity 89.5
les 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               control gene expression.
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                                                                                                                                                                                                                                Query Match
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a triple-helix comprising a double helical nucleic acid comprising first and second substantially complementary strands, and an oligonucleotide bound to a purine-rich target sequence within the double helical nucleic acid, where the oligonucleotide binds in a parallel and antiparallel or acid, where the oligonucleotide binds in a parallel and antiparallel or crientation, respectively, to target sequences on alternate strands of the double helical nucleic acid. The method has therapeutic applications, which expression is controlled by selective triple-helix formation within expression regulatory sequences of a target gene. The oligonucleotides can be used to form triple-helices, and are useful to detect the presence or absence of specific sequences within genomic DNA controlled by a controlled by a controlled by a controlled by a controlled by pathogenic double-stranded DNA including specific sequences required by pathogenic double-stranded DNA including specific sequences required by pathogenic bacteria or viruses for replication or virulence, reducing their pathogenicity. Alternatively,
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                                                              origin. Such therapeutic oligonucleotides are capable of forming triple-helices with such sequences in cancerous cells containing the activated oncogene, so preferentially killing or repressing the cancer causing cell. The present sequence represents a DNA sequence used in the methods
pathogen which is not found in the genome of pathogen's host. The digonucleotides can be used in cancer treatment by way of triple-helix suppression of specific oncogenes including those of endogenous or viral origin. Such therapeutic oligonucleotides are capable of forming triple-
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                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                        Score 16.4; DB 6; Length 43; Pred. No. 8.6e+03; Mismatches 2; Indels
                                                                                                                                                                                               Sequence 43 BP; 14 A; 6 C; 14 G; 8 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Triple helix forming associated oligonucleotide #4.
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                                                                                                                                                                                                                                                                                                                                  1 AGGGGAGGGAGGGAGGG 19
                                                                                                                                                                                                                                                                                                                                                                         14 AAGGGNGGGGAGGGGG 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                           82.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                    Query Match
Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                     of the present invention
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the oligonucleotide can be chosen to target a unique sequence of the pathogen which is not found in the genome of pathogen's host. The oligonucleotides can be used in cancer treatment by way of triple-helix suppression of specific oncogenes including those of endogenous or viral origin. Such therapeutic oligonucleotides are capable of forming triple-helices with such sequences in cancerous cells containing the activated oncogene, so preferentially killing or repressing the cancer causing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A triple-helix comprising a double helical nucleic acid (DHNA) and an oligonucleotide which binds in parallel and antiparallel orientation, respectively, for targetting sequences on alternate strands of DHNA to control gene expression.
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                                                                                                                                                                                                                    Gaps
                                                                                                           cell. The present sequence represents an oligonucleotide used in the methods of the present invention
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                                                                                                                                                                                 Score 16.4; DB 6; Length 43;
Pred. No. 8.6e+03;
0; Mismatches 2; Indels
                                                                                                                                                       Seguence 43 BP; 14 A; 6 C; 14 G; 8 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Triple helix forming associated DNA sequence #20.
                                                                                                                                                                          82.0%; Scor.
89.5%; Pred. No. 6...
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                                                                                                                                                                                                                                                1 AGGGGAGGGGAGGGGAGGG 19
                                                                                                                                                                                                                                                                          14 AAGGGNGGGGAGGGAGGG 32
                                                                                                                                                                                                                                                                                                                                                    ABK98157 standard; DNA; 45 BP.
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                                                                                                                                                                                                                 17; Conservative
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                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                       RESULT 36
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The present invention relates to methods and oligonucleotides for forming a triple-helix comprising a double helical mucleic acid comprising first and second substantially complementary strands, and an oligonucleotide bound to a purine-rich target sequence within the double helical nucleic acid, where the oligonucleotide binds in a parallel and antiparallel orientation, respectively, to target sequences on alternate strands of the double helical nucleic acid. The method has therapeutic applications, where gene expression is controlled by selective triple-helix formation within expression regulatory sequences of a target gene. The oligonucleotides can be used to form triple-helices, and are useful to detect the presence or absence of specific sequences within genomic DNA for diagnostic and therapeutic purposes. The oligonucleotides can be selected to specifically bind to pathogenic double-stranded DNA including specific sequences required by pathogenic bacteria or viruses for

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replication or virulence, reducing their pathogenicity. Alternatively, the oligonucleotide can be chosen to target a unique sequence of the pathogen which is not found in the genome of pathogen's host. The oligonucleotides can be used in cancer treatment by way of triple-helix suppression of specific oncogenes including those of endogenous or viral origin. Such therapeutic oligonucleotides are capable of forming triple-helices with such sequences in cancerous cells containing the activated oncogene, so preferentially killing or repressing the cancer causing cell. The present sequence represents a DNA sequence used in the methods of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  syndrome, etc. Organisms transformed with the DNA sequences can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide(s) and proteins derived from Staphylococcus aureus -
stored on computer readable medium and used in the production of anti-
                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                             Sequence 45 BP; 14 A; 7 C; 14 G; 9 T; 0 U; 1 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus contig SEQ ID #2153.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barash SC,
                                                                                                                                                                                                                                                                                                                                                                    1 AGGGGAGGGGAGGG 19
                                                                                                                                                                                                                                                                                                                                                                                                             AAGGGNGGGAGGGAGGG 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV76464 standard; DNA; 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                       Best Local Similarity 89.5
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADH70729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hood LE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ROWE/)
                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
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888888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
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                                                                                                                                                                                                                                                                                             ö
                           (and their fragments) are useful as primers or probes for isolating homologues of any of the S aureus DNA sequences contained on the computer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ribozymes for modulating the synthesis, expression and/or stability mRNA encoding an angiogenic factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention describes enzymatic nucleic acid molecules with RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic; ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; verruce automascular glaucoma; tuberous sclerosis; pot-wine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
for recombinant production of the polypeptides. The new DNA sequences
                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                  Score 16.4; DB 2; Length 50;
Pred. No. 8.5e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Integrin subunit beta 3 substrate sequence SEQ ID NO:5754.
                                                                                                                                                            Seguence 50 BP; 0 A; 46 C; 1 G; 2 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coeshott C,
                                                                                                                                                                                                                  Match 82.0%; Score 16.4; I Local Similarity 89.5%; Pred. No. 8.5e es 17; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                      2 GGGGAGGGAGGGGG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (RIBO-) RIBOZYME PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-591315/50.
                                                                                               readable medium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9950403-A2
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                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA22528;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 degenerative nervous system disease; graft versus host disease; hypersensitivity disease; infectious disease; neoplastic disease; hydrion's disease; atrophic gastritis; degenerative nervous system disease; multiple sclerosis; Alzheimer's disease; hypersensitivity disease; type I hypersensitivity; Goodpasture's syndrome; type II hypersensitivity; Goodpasture's syndrome; type II hypersensitivity; infections disease; viral infection; HIV; fungal infection; Candida; parasitic infection; schistosome; filaria; bacterial infection; Mycobacterium; neoplastic disease; lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
stability of an mRNA encoding angiogenic factor, especially ARNT, integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are especially used to treat cancer, diabetic retinopathy, age related macular degeneration (ARMD), inflammation, and arthritis, as well as neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris, angiofibroma of tuberous sclerosis, por wine stains, Sturge Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Reber-Rendu syndrome, and other syndrome and diseases related to the levels of ARNT, Tie-2,
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a kit for diagnosing and treating T-cell associated diseases which comprises a panel of nucleic acid primers specifically priming and allowing amplification of each Wheta gene, WhetaRNA or cDNA. The kit is useful for diagnosing organ transplant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human; T-cell associated disease; Vbeta; autoimmune disease;
                                                                                                                                                                                                                                                          80.0%; Score 16; DB 2; Length 17; 100.0%; Pred. No. 1.3e+04; ive 0; Mismatches 0; Indels
                                                                                                                                                                           integrin subunit alpha-6, or integrin subunit beta-3
                                                                                                                                                                                                                      Seguence 17 BP; 0 A; 13 C; 1 G; 0 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 923; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Vbeta gene repeat sequence #519.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADH70729 standard; DNA; 19 BP
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                                                                                                                                                                                                                                                                                                                                                  3 GGGAGGGGAGGGAGG
                                                                                                                                                                                                                                                                                                                                                                                             16 GGGAGGGGAGGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-2004 (first entry)
                                                                                                                                                                                                                                                                                                       16; Conservative
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                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          breast cancer; ds.
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E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2002150891-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             поор (/поор)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-SEP-1994;
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                                                    atrophic gastritis. Degenerative nervous system diseases include multiple soletosis and Alzheimer's disease. Hypersensitivity diseases include Type I hypersensitivities such as contact with allergens that lead to allergies, Type II hypersensitivities such as those present in Goodpasture's syndrome and Type IV hypersensitivities such as those manifested in leprosy. Infectious diseases include viral infections caused by the yeast genus Candda, parasitic infections such as those caused by the yeast genus Candda, parasitic infections such as those caused by Mycobacterium. Neoplastic diseases include lymphoproliferative diseases such as leukaemias, lymphomas and cancers such as cancer of the brain, breast. The present sequence represents a Vbeta gene repeat sequence.
              including autoimmune diseases, degenerative nervous system diseases, graft versus host disease, hypersensitivity diseases, infectious diseases and neoplastic diseases. Autoimmune diseases include Addison's disease,
                                                                                                                                                                                                                                                                                                               Gaps
rejection and diagnosing and treating T-cell associated diseases
                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                Score 15.8; DB 12; Length 19;
Pred. No. 1.5e+04;
); Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide purification; liquid chromatography; hydrophobic protective group; deprotection; ds.
                                                                                                                                                                                                                                                    Sequence 19 BP; 1 A; 2 C; 16 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                             2 GGGGAGGGGAGGGG 20
                                                                                                                                                                                                                                                                                                                                                                         1 GGGGCGGGAGGGGCGGGG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF99947 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic oligonucleotide #13
                                                                                                                                                                                                                                                                                79.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 89.5
Matches 17; Conservative
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soluble organic solvent at a suitable concentration gradient to elute the deprotected oligonucleotides; and (e) removal of the solvent and the salt from the eluted oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA cytosine methyltransferase modulator containing 5-C methylcytosine used to inhibit methylation of DNA, and proliferation of cancer cells.
                                                                                                                                                                                                                                                                                                                                                                                                                          DNA cytosine methyltransferase; DCMTase; binding discrimination; C-5 methylcytosine; allosteric site; synthetic inhibitor; cancer cell; proliferation; development disorder; Huntington's disease;
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                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide used for screening DCMTase binding discrimination.
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                                                                                                   Score 15.8; DB 4; Length 20;
Pred. No. 1.5e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and disorders associated with a Hox gene
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Pred. No. 1.4e+04;
0; Mismatches 2; Indels
                                                                                                                                    2; Indels
                                                                     T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 26 BP; 3 A; 1 C; 20 G; 2 T; 0 U; 0 Other;
                                                                                                                                    0; Mismatches
                                                                     Sequence 20 BP; 1 A; 1 C; 17 G; 1
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                                                                                                                                                                      2 GGGGAGGGAGGGGG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Down's syndrome; Hox gene; ss.
                                                                                                                                                                                                                                                                                           BP
                                                                                                    79.0%;
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                                                                                                                                                                                                                                                                                           AAX40753 standard; DNA; 26
                                                                                                                                                                                                                                                                                                                                                              16-JUN-1999 (first entry)
                                                                                                      Query Match
Best Local Similarity 89.5
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reich NO, Flynn J;
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es 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Down's syndrome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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Matches
                                                                                                                                                                                                                                                           RESULT 41
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The present sequence is an oligonucleotide provided in a specification relating to the simplified purification of oligonucleotides by liquid chromatography. The process comprises: (a) pouring oligonucleotides protected with a hydrophobic group and oligonucleotide with no protective group into a liquid chromatography column packed with an acid and alkali resistant packing agent, such as polystyrene resin; (b) pouring a mixed developing solvent composed of a buffer made from a volatile salt and a water soluble organic solvent at a suitable concentration gradient into the column; (c) pouring an acid, particularly 6-16 v/v* acetic acid, into the column to deprotect the oligonucleotides protected with the hydrophobic group; (d) pouring a mixed developing solvent composed of a buffer made from a volatile salt, particularly 0.05-0.5 N aqueous ammonium hydrogencarbonate solution adjusted at pH 8-10, and a water

process for purification of oligonucleotides using liquid

WPI; 2001-268251/28

Example 1; Page 4; 13pp; Japanese.

chromatography

Neuroprotective; nootropic; antidepressant; tranquilizer; anticonvulsant; cardiant; antiasthmatic; antiinflammatory; human; GABA; promoter; CNS; gamma-amino butyric acid B receptor 1; splice isoform; spinal spasticity; transcription modulator; central nervous system disorder; dementia; muscle relaxation; Alzhaimer's disease; depression; anxiety; epilepsy; cardiovascular disorder; asthma; irritable bowel syndrome; emesis; reflux disease; neurological disease; PCR primer; ss.

Human GABA(b) receptor 1 promoter P1b primer 2058 PR1b CGVI Rev.

09-APR-2001 (first entry)

AAF28801;

AAF28801 standard; DNA; 27 BP

AAF28801

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the invention relates to novel nucleic acid molecules constituting the human gamma-amino butyric acid (GABA)B receptor 1 promoters Pla and/or human gamma-amino butyric acid (GABA)B receptor 1 promoters Pla and/or corms or active fragments. PCR primers AAF28788-AAF28805 were used for corms or active fragments. PCR primers AAF28788-AAF28805 were used for CFR mutagenesis of the GABA(b) promoter sequences for mutational analysis of promoter element function. Nucleic acid molecules containing the human GABAB receptor 1 promoters pla and/or plb are useful for screening therapeutic agents that selectively regulate the expression of GABAB receptor la- and lb-type splice isoforms. These compounds, which are condulators of GABAB receptor 1 transcription, are potentially useful in the treatment of disorders that are related to neurally-controlled physiological responses regulated by GABAB receptors such as central nervous system (CNS) disorders, e.g. muscle relaxation in spinal spatinity, Alzheimer's disease and other dementias, psychiatric and neurological disorders, asthum, gut motility disorders, e.g. irritable cardiovascular disorders, asthum, gut motility disorders, e.g. irritable
                                                                                                                                                                                                                  Neuroprotective, nootropic, antidepressant, tranquilizer, anticonvulsant, cardiant, princher, promoter, CNS; gardiant, princher, continuintammatory, human, GABA, promoter, CNS; gamma-amino butyric acid B receptor 1; splice isoform, spinal spasticity, transcription modulator; central nervous system disorder; dementia, transcription, Alzaheimer's disease, depression, anxiety; epilepsy; cardiovascular disorder; asthma; irritable bowel syndrome; emesis; reflux disease; neurological disease; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid molecules constituting the human gamma amino butyric acid-B receptor 1 promoters, useful for screening modulators of the receptors transcription or therapeutic agents regulating the expression
                                                                                                                                                                           Human GABA(b) receptor 1 promoter P1b primer 2057 PR1b CGVI Fwd.
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Pred. No. 1.4e+04;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 27 BP; 3 A; 16 C; 2 G; 6 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 6; Page 21; 46pp; English
                                           AAF28800 standard; DNA; 27 BP.
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Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-MAY-2000; 2000WO-SE000878
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                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Edlund A,
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                                                                                                                                 09-APR-2001
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                                                                                       AAF28800;
RESULT 42
AAF28800/c
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New nucleic acid molecules constituting the human gamma amino butyric acid-B receptor 1 promoters, useful for screening modulators of the receptors transcription or therapeutic agents regulating the expression of its splice isoforms.

Leonardsson G;

Johansson T,

Ekstrand J, Edlund A, (ASTR ) ASTRAZENECA AB

WPI; 2001-024861/03.

04-MAY-2000; 2000WO-SE000878.

WO200068268-A1 Homo sapiens.

16-NOV-2000.

99SE-00001659

06-MAY-1999;

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The invention relates to novel nucleic acid molecules constituting the human gamma-amino butyric acid (GABA)B receptor 1 promoters Pla and/or bub (AAP28781 and AAF28782). Or their functionally equivalent modified forms or active fragments. PCR primers AAF2878865 were used for forms or active fragments. PCR primers AAF2878865 were used for CC FCR mutagenesis of the GABA(b) promoter sequences for mutational analysis of promoter element function. Nucleic acid molecules containing the human CC GABAB receptor 1 promoters pla and/or Plb are useful for screening therapeutic agents that selectively regulate the expression of GABAB receptor la- and 1b-type splice isoforms. These compounds, which are modulators of GABAB receptor 1 transcription, are potentially useful in the treatment of disorders that are related to neurally-controlled physiological responses regulated by GABAB receptors such as central nervous system (CNS) disorders, e.g. muscle relaxation in spinal nervous system (CNS) disorders, e.g. muscle relaxation in spinal courties, all disorders, e.g. depression, anxiety or epilepsy, cardiovascular disorders, asthma, gut motility disorders, e.g. irritable bowel syndrome, emesis or reflux disease
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AAL28918 standard; DNA; 50 BP RESULT 44
AAL28918/c
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RESULT 46
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                                                                                                                      Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopoietin; apoptosis related protein; catherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinase; cytokine; interferon; minterleukin; Grprotein coupled receptor; thioesterase; intlammation; multifactorial disease; autoimmune disease; infection; nervous system disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections.
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Pred. No. 1.3e+04;
0; Mismatches 2; Indels
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                                                                                   Human SNP oligonucleotide #2126.
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27-DEC-2000; 2000US-00173419.
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Best Local Similarity 89.5%;
Matches 17; Conservative
                                          (first entry)
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AAL28918
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BP

AAL32132 standard; DNA; 50

RESULT 45 AAL32132

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(first entry)

24-JAN-2002

AAL32132;

SXXXE

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The present invention relates to oligomucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, appprosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins coupled receptors and thloesterases. The present sequence is one such oligomucleotide. The oligomucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's diseases), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, concerning the protein of pathogenic concerning.
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                                                  Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopoietin; appoposis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinase; cytokine; interferon; interferum; multifactorial disease; autoimmune disease; infection; nervous system disease; so.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections.
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Human SNP oligonucleotide #5340.
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27-DEC-2000; 2000US-00173419.
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Matches 17; Conservative
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The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apptoais related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins coupled receptors and thioseterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, clastemic lupus erythromatosus and Gravé a disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic
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Immunosuppressive, immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; anglopoietin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cycochrome; kinase; cytokine; interferon; interleukin; G-protein coupled receptor; thioesterase; inflammation; multifactorial disease; autoimmune disease; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections.
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Pred. No. 1.3e+04;
0; Mismatches 2; Indel8
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89.5%; Pred
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AAL28919 standard; DNA; 50
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KW amy]
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The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apptoais related proteins, oadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins coupled receptors and thioseferases. The present sequence is one cuch oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune consistency of the may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune systemic lupus erythromatosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, concerned the contraction of pathogenic contractions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinesin; cytokine; interferon; interleakin; d-protein coupled receptor; thioesterase; inflammation; multifactorial disease; autoimmune disease; infection; nervous system disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic; ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARND; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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1.3e+04;
2;
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; Mismatches
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27-DEC-2000; 2000US-00173419.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA22527 standard; RNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUN-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-465210/50.
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nes 17; Conserv
                                                                                                                                                                  WO200147944-A2.
                                                                                                                            Homo sapiens.
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The present interaction describes enzymatic nuclear data morecules with knapper cleaving activity, which specifically cleave RNA encoded by an arth KNA decarbon nuclear transporter (ARNT) gene, an integrin alpha 6 subunit gene, an integrin subunit beta 3 cene, an integrin alpha 6 subunit gene, or a flate-2 gene. AAA1761 to AAA1762 to Peresent ribozyme sequences for ARNT, and AAA17169 to AAA17560 and AAA17623 to AAA17684 represent their corresponding target sequences; AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19087 to AAA19155 to AAA19152 represent their corresponding target sequences; and AAA19155 to AAA19150 to AAA19155 to AAA19150 to AAA1950 to AAA21960 and AAA1595 to AAA21961 and AAA21501 to AAA2159 represent ribozyme sequences for integrin alpha 6 subunit, and AAA20362 to AAA21360 and AAA21896 to AAA21896 to AAA21891 represent ribozyme sequences for integrin subunit beta 3, and AAA23342 represent ribozymes of the invention are used for modulating the synthesis, expression and/or stability of an mRNA encoding angiogenic factor, especially ARNT, integrin subunit beta-3, integrin subunit alpha 6, or Tie-2. They are specially used to treat cancer, diabetic retinopathy, age related macular degeneration (ARND), inflammation, and arthritis, as well as angiofibroma of tuberosis, pot-wine starins, surreas vulgaris, and angiofibroma of tuberosis, pot-wine starins, survey weber
                                                                                                                                                                                                                                                                                                                                                                                                                     Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention describes enzymatic nucleic acid molecules with RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome, and other syndromes and diseases related to the levels of ARNT, Tie-2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.0%; Score 15.4; DB 2; Length 17; 94.1%; Pred. No. 2e+04; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   integrin subunit alpha-6, or integrin subunit beta-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17 BP; 0 A; 13 C; 1 G; 0 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                      Coeshott C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 54; Page 226; 305pp; English.
                                                                                                                                                                                                                                                                                                                                      Jarvis T,
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                                                                                                                                                                                                              99WO-US006507.
                                                                                                                                                                                                                                                      98US-0079678P.
                                                                                                                                                                                                                                                                                               (RIBO-) RIBOZYME PHARM INC
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Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-591315/50.
                                                                                    Homo sapiens
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                                                                                                                                                                                                              24-MAR-1999;
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CC dequences ABZ43217-ABZ50887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates conceding enzymes associated with drug metabolism. The invention relates conceptoding and compositions for identifying individuals who have at least one polymorphisms may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from ABZ43217-ABZ50887 using a variety of detection assays, including hybridisation assays, nucleic acid arrays and PCR-based methods. The invention also encompasses methods of arrays and pCR-based methods. The invention also encompasses methods of arrays and excenting drugs using genetic polymorphism data. Genetic polymorphisms (SNPs), may be used in studying the relationship between DNA sequence variations and human diseases, conditions, and responses to drugs. SNPs are also useful as polymorphism markers for discovering genet that cause or exacerbate certain diseases. SNPs are particularly useful crugs. SNPs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. SNPs are particularly useful frequently, and have lower mutation rates than other genome variations such as repeating sequences. The detection and analysis of polymorphisms in genes encoding drug metabolising enzymes allows the customisation of drug therapeutic effect for a particular patient. Dut would also reduce the likelihood of adverse reactions, thereby increasing safety. Methods of the invention are also useful in the drug discovery and equate the invention are also useful in the drug discovery and conjunce the likelihood of adverse reactions, thereby individuals could be selected for clinical trials only if their generic profiles indicate that they are capable of responding to a particular drug or drug class, and previously falled drug candidates could be selected for clinical trials only if their generic profiles indicate that they are capable of responding to a particular drug or a drug c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying individuals having a polymorphism, useful for determining the effectiveness or side effect of a drug or treatment protocol, comprises detecting at least one polymorphism in the drug metabolizing enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       reactions, failed drug trials, the time taken for a drug to be approved, the length of time patients are on medication and the number of different medications a patient needs to take before finding an effective therapy
polymorphic site, drug evaluation, drug screening, genotyping, genetic profiling, therapeutic customisation, adverse reaction, clinical trial, drug approval, single nucleotide polymorphism, SNP, ds.
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/standard_name= "Single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saito S;
                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 23; Page 83; 2785pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Iida A,
                                                                                                                                                                        replace (21, A)
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02-MAY-2001; 2001JP-00135256.
27-AUG-2001; 2001JP-00256862.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nakamura Y, Sekine A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-583571/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (RIKE ) RIKEN KK.
                                                                                                                                                                                                                                                                         WO200252044-A2.
                                                                                                   Homo sapiens
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Gaps .; 0

77.0%; Score 15.4; DB 6; Length 41; 94.1%; Pred. No. 1.8e+04; ive 0; Mismatches 1; Indels

llarity 94.1%; Conservative

Query Match Best Local Similarity Matches 16; Conserv

Human; drug metabolising enzyme; gene; drug metabolism; chromosome 22;

Human catechol-O-methyltransferase COMT gene polymorphic site, #1181.

(first entry)

26-JUN-2003

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Identifying individuals having a polymorphism, useful for determining the effectiveness or side effect of a drug or treatment protocol, comprises detecting at least one polymorphism in the drug metabolizing enzyme
                                                                                                                                                                             clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
                                                                                                                                              Human, drug metabolising enzyme, gene, drug metabolism, chromosome 22, polymorphic site; drug evaluation; drug screening; genotyping; genetic profiling, therapeutic customisation; adverse reaction;
                                                                                                                                                                                                                                                /standard_name= "Single nucleotide polymorphism (SNP)"
                                                                                                                            Human catechol-O-methyltransferase COMT gene polymorphic site, #5376.
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replace(21,A)
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                                                                  ABZ48593 standard; DNA; 41 BP
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02-MAY-2001; 2001JP-00135256.
27-AUG-2001; 2001JP-00256862.
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Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates to methods and compositions for identifying individuals who have at least one polymorphism in such drug metabolising enzyme-encoding genes. The polymorphism may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from ABZ43217-ABZ60887 using a variety of detection assays, including hybridisation assays, nucleic acid arrays and PCR-based methods. The invention also encompasses methods of arrays and screening drugs using genetic polymorphism data, particularly that relating to single nucleotide polymorphism s(SNPs), may be used in studying the relationship between DNA sequence variations and human diseases, conditions, and responses to chuge sNNBs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur continue as repeating sequences. The detection and analysis of polymorphisms cuch as repeating sequences. The detection and analysis of polymorphisms in genes encoding drug metabolising enzymes allows the customisation of drug therapeutic effect for a particular patient. But would also reduce the likelihood of adverse reactions, thereby increasing safety.

Claim 23; Page 169; 2785pp; English.

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Methods of the invention are also useful in the drug discovery and approval processes. For example, individuals could be selected for clinical trials only if their genetic profiles indicate that they are capable of responding to a particular drug or drug class, and previously failed drug candidates could be revived if they were matched with more appropriate patient populations. The methods, data and compositions of the invention may therefore lead to a an increase in the range of possible drug targets and decreases in the number of adverse drug reactions, failed drug trials, the time taken for a drug to be approved, the length of time patients are on medication and the number of different medications a patient needs to take before finding an effective therapy
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BX004665 Arabidops
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ORGANISM Mus musculus  Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Mammalia; Eutheria; Euarchontcglires; Glires; Rodentia;  Sciurognathi; Muroidea; Muridae; Mus.  Sciurognathi; Muroidea; Muridae; Mus.  Sciurognathi; Muroidea; Muridae; Mus.  I (bases 1 to 20)  AUTHORS  Dunn,D., Aoyad,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  Reilly,M., Rose,M., Rose,R., Tingey,A., von  Niederhausern,A. and Wright,D., Weiss,R.  TITLE Mouse whole genome scaffolding with paired end reads from 10kb  plasmid inserts  JOURNAL Contact: Robert B. Weiss  University of Utah Genome Center  University of Utah Genome Center  University of Utah Genome Center  Hall; Usa Ses 500  Fax: 801 585 500  Fax: 801 585 5177  Email: ddunn@genetiss.utah.edu  Insert Length: 10000 Std Error: 0.00  Plate: 0177 row: I column: 20  Seg primer: CACACAGGAAACAGCTATGACC  Class: plasmide and  High quality sequence stop: 20.  FEATURES  Source  Location/Qualifiers  Source  Location/Qualifiers	ol_type="genomic DNA"  train="CS7BL/60"  Daw xef="taxon:10090"  av host="E. Coli strain XLIO-C  ab_host="E. Coli strain SLIO-C  ab_host="E. Coli strain SLIO-C  ab_host="E. Coli strain SLIO-C  ab_host="E. Coli strain SLIO-C  sculus CS7BL/60 (mala) was obtained by about cory  by dow, jax. org/resources/dc  ttp://www.jax.org/resources/dc  shydrodynamically sheared by  shydrodynamically sheared by  shut end-repaired with T4 Is  shut end-repaired with T4 Is  yrucleotide kinase. Adaptor of  gated to the blunt ends in hig  gated to the blunt ends in high  gated to the blu	Ouery Match Best Local Similarity 100.0%; Score 20; DB 9; Length 20; Best Local Similarity 100.0%; Pred. No. 6.38+03; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 AGGGAGGGAGGG 20	RESULT 2 AZ359724 LOCUS LOCUS LOCUS DEFINITION 1M0102M11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0102M11 R, genomic survey sequence. ACCESSION AZ359724 VERSION AZ359724.1 GI:10473424
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Euteleostomi;

5

SOURCE ORGANISM

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalvel [4] 4732114[gb] AF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XIIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0271G04R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0271G04 R, genomic survey sequence.
AZ462959
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84112, USA
                                                                                                                                                                                                                                                                                    Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Ielam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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//note="Vector: PMP42nv; Purified genomic DNA from M.musculus G57BL/6J (female) was obtained from the Ja Laboratory Mouse DNA Resource
                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eute
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Musinae, Mus.
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Ham
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
Email: dduun@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0225 row: G column: 02
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC2M0225G02"
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                                        Mus musculus (house mouse)
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/lab host="E.
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Matches 19;
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2M0225G02R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0225G02 R, genomic survey sequence.
                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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/note="Wector: PWB-ZIV; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                       1 (Dases II. 7) 
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0102 row: M Column: 11
Seg primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
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    .35
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"

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'clone="UUGC1M0102M11"
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Location/Qualifiers
musculus (house mouse)
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FEATURES

from the Jackson

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Gaps

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GSS 04-OCT-2000

DEFINITION

AZ958287

ACCESSION

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/clone lib="Mixed stage fosmid library of P. pacificus var. California"
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Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
AppabB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: 17
Class: foomid ends.
                                                                                       Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
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                                                                                                                                                                                                                                                                                                                                            Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Fax: 00497071601371

    .28
/organism="Pristionchus pacificus"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="California"
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Fax: 801 585 7177
  survey sequence.
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                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Wm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, '84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab host="B. Coli strain XLIO-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                              Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Keilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0271 row: G column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
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"mol type="genomic DNA"
'strain="C57BL/6J"
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clone="UUGC1M0271G04"
                                      Mus musculus (house mouse)
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Fax: 801 585 7177
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Length 28; Indels

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2M0244G20R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weises, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwalot (gilfa732114 [gb] AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-GGld (Stratagene) cells and selected for ampicillin resistance."
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An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics Plank Mol. Biol. 53 (1-2), 247-259 (2003)
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Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BX004665 11-noar GSS 01-APF
Arabidopsis thaliana T-DNA flanking sequence GK-400A12-017894
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA f.
musculus C57BL/6J (male) was obtained from th
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94.7%; Pred. No. 4.3e+04;
tive 0; Mismatches 1;
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Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0061 row: L column: 09

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 33.
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                                                                                                                                                                                                                                                        organism="Mus musculus"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                    /clone="UUGC2M0061L09"
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BX004665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114|gp|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XI10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
RM. 308, Binmedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
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                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC2M library"
hote="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/GJ (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
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2M0061L09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0061L09 F, genomic survey sequence.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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                                     Std Error: 0.00
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: C
Plate: 0244 row: G column: 20
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                   organism="Mus musculus"
                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                  'db_xref="taxon:10090"
'clone="UUGC2M0244G20"
                                                                                                                 Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers
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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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AZ375586/c
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                                                                                                                                                                                                                                                                     Direct Summission.

Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence has been recovered from the left border of the T-DNA. Details on the protocols used for generation of the sequence are described in References 1.3. Re-examination of the sequence from which this sequence has been produced indicates that the sequence is of low reliability. Therefore, no information on a potential insertion site is deduced. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jote-FPCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fromment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
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2M0093L16F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
|ecotype="Col-0"
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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                                                     Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A.
                                                                                          High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines BioTechniques 35 (6), 1164-1168 (2003)
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Pred. No. 4.3e+04;
0; Mismatches 1; Indels
                                                                                                                                                                                                  4 (bases 1 to 38)
Rosso, M.G., Strizhov, N., Li, Y. and Weisshaar, B.
Direct Submission
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University of Utah Genome Center
University of Utah
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/db_xref="taxon:3702"
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AZ820833.1 GI:12990741
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Best Local Similarity 94.7%;
Matches 18; Conservative
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMAD42 (gil 4732114 [gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll X110-GG1d (Stratagene) cells and selected for ampicillin resistance."
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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/clone l1b="Mouse 10kb plasmid UUGCNH library."
/note="Vector: PWD42nr; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Pred. No. 4.3e+04;
0; Mismatches 1;
                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0093 row: L column: 16
Seq primer: GTTGTAAAACGACGGCCAGT
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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University of Utah Genome Center
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/clone="UUGC2M0093L16"
                                                                                                                                                                                                                                                                           High quality sequence stop: 43.
Location/Qualifiers
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94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Male"
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                                84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
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Antirrhinum majus
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiids; Lamiales; Plantaginaceae; Antirrhineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. Coli strain XLIO-Gold, Ti-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCN library"
/note="Vector: PWD4ZIN; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Bey,M., Stueber,K., Fellenberg,K., Schwarz-Sommer,Z., Sommer,H.,
Saedler,H. and Zachgo,S.
Characterization of Antirrhium Petal Development and
Identification of Target Genes of the Class B MADS Box Gene
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC,
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                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0129 row: G column: 03
Seq primer: CGTTGTAAAACGACGACAGT
Class: plasmid ends
High quality sequence stop: 45.
Location/Qualifiers
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15539471
                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                       mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                           clone="UUGC1M0129G03"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      sex="Male"
                                                                      Tel: 801 585 5606
Fax: 801 585 7177
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was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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2M0058L20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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/clone lib="Mouse 10kb plasmid UGGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/60 (male) was obtained from the Jackson
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                                                                                                                                                                                                                                      /clone="018 3 02 k18"
/tissue type="whole plant"
/clone Tib="Antirrhinum majus whole plant"
Contact: Schwarz-Sommer Z
Molekulare Pflanzengenetik
MPI fuer Zuechtungsforschung
Carl-von-Linne Weg 10, D-50829, Germany.
Location/Qualifiers
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                                                                                                                                                                /organism="Antirrhinum majus"
/mol_type="mRNA"
/db_xref="taxon:4151"
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Class: plasmid ends
High quality sequence stop: 50.
Location/Qualifiers
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0058L20"
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Insert Length: 10000 Std Erro:
Plate: 0058 row: L column: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a
was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
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2M0017N06R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0017N06 R, genomic survey sequence.
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                                                                                                                                                                                                                                                                                         adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
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/clone lib="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G77BL/6J (male) was obtained from the Jackson
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Dunn,D., Acyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Waiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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84112, USA
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Insert Length: 10000 Std Error: 0.00
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Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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clone="UUGC2M0017N06"
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Fax: 801 585 7177
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TITLE

COMMENT

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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-GG1d (Stratagene) cells and selected for ampicillin resistance."
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Direct Submission

Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer

Direct Submission

Suchtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.

Details on the protocols used for generation of the sequence are described in References 1-3. Re-examination of the source from which this sequence has been produced indicates that the sequence is of low reliability. Therefore, no information on a potential insertion site is deduced. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project.

GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:
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An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
Elanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
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Arabidopsis thaliana T-DNA flanking sequence GK-009H02-016930,
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database the identification of T-DNA insertion mutants in Arabidopsis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines BioTechniques 35 (6), 1164-1168 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.0%; Score 16.8; DB 9; Length 25; 90.0%; Pred. No. 6.8e+04; ive 0; Mismatches 2; Indels
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GSS.
Arabidopsis thaliana (thale cress)
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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XI10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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1M0203B05R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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1 (bases 1 to 38)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Relam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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/note="Vector: PWD42nv; Purified genomic DNA from M.
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 38.
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/strain="C57BL/63"
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/clone="UUGC1M0203B05"
/sex="Male"
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Insert Length: 10000 Std Erro
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Fax: 801 585 7177
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1 (bases 1 to 33)

S Dum, D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Rallm,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R., Tingey,A., von Unpublished (2000)

L Ontact: Robert B. Weiss
University of Utah Genome Center
                                                                                                                                                                                                                                                 /note-rpcR was performed on DNA from Arabidopsis thaliana plants (TI) which were transformed with the T-DNA from vector pAC106 (GenBank accession number: AJ537513). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed.
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IM0525K06R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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/clone lib="Mouse 10kb plasmid UTGCIM library"
/note="Vector: PWD42Tv; Purified genomic DNA from M.
musculus C57BL/6J (wale) was obtained from the Jackson
                                                                                                                                                                                                   /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
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                                                                                      /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
     http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
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Fax: 801 585 7177
Email: ddunnegenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0525 row: K column: 06
Seq primer: CACACAGGAAACAGCTAATGACC
                                                                                                                                                                         /clone="GK-009H02-016930"
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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High quality sequence stop: 33.
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/clone="UUGC1M0525K06"
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Mus musculus
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Best Local Similarity
Matches 18; Conserva
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us-09-669-187a-906.sz1m50.rst

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10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114 |gh|APL97021), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XII.0-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                    (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Glires; Rodentia;
Sciurognathi; Muroidaa; Murinae; Mus:
(Dases 1 to 43)
Dunn, D., Aoyagi, B. Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Miderhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
      /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84.0%; Score 16.8; DB 9; Length 39; 90.0%; Pred. No. 6.7e+04; ive 0; Mismatches 2; Indels
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Insert Length: 10000 Std Error: 0.00
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Seg primer: CACAGGAAACAGCTATCACC
Class: plasmid ends
High quality sequence stop: 43.
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC2M0192L19"
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Fax: 801 585 7177
Email: ddunn@genet
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Best Local Similarity
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musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA DOLYMERSES and T4 polynuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
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Insert Length: 10000 Std Error: 0.00
Plate: 0100 row: J column: 14
Seg primer: CACACAGGAAACAGCTATGACC
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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Fax: 801 585 7177
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Matches 18; Conserv
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ts04f05.x1 NCI CGAP Pan1 Homo sapiens cDNA clone IMAGE:2227617 3' similar to SW:PRPB HUMAN P02814 PROLINE-RICH PEPTIDE P-B. ; contains TAR1.t2 MSR1 repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bmail: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing Dy: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LiNL at:
www-bio.llnl.gov/bbrp/image/image.html
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/note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.35 kb. Tumor types include: mixed Mullerian tumor, papillary scrous, clear cell, spindle cell. All are primary tumors, metastasis positive. Life Technologies catalog #: 11534-013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
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1 (Dass 1 to 400)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-GGAP ttp://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                    82.0%; Score 16.4; DB 1; Length 37; 94.4%; Pred. No. 9e+04; ive 0; Mismatches 1; Indels
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/lab_host="DH108"
/clone_lib="NCI_CGAP_pan1"
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
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Best Local Similarity 94.4%
....hes 17; Conservative
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                                                                                  indecratory Mouse DAR Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwM22 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clond distribution: NCI-GGAP clone distribution information can be
Gound through the I.M.A.G.E. Consortium/LiNL at:
www-bio.llnl.gov/bbrp/image/image.html
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1 (Dases 1 to 37)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
        /clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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/tissue type="tumor, 5 pooled (see description)"
/lab host="DH108"
/clone_lib="NCI_CGAP_Ov23"
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Seg primer: -400P from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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/db_xref="taxon:9606"
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AI800153.1 GI:5365625
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Homo sapiens
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Best Local Similarity 90.0
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                                                                                                                                                                                                                                                                                                                          E 1 (bases 1 to 19)
S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longarce, S., Mahmoud, M., Meenen, E., Pedersen, T., Railly, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
L Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                          AZ447248 1000 1000 110 DNA linear GSS 04-0CT-2000 1M0244H23F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0244H23 F, genomic survey sequence.
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
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.larity 89.5%; Pred. No. 1.4e+05;
Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0244 row: H column: 23
Seg primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
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Best Local Similarity
Matches 17; Consery
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                                                  LOCUS
                          AZ447248/C
                                                                                                                         ACCESSION
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AUTHORS
RESULT 21
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were lighted to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoreais. Vector DNA was prepared from a derivative of pWD42 (gij |4732114|gb|AFL29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
AZ512326 20 bp DNA linear GSS 05-0CT-2000 1M0357118R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0357118 R, genomic survey sequence.
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                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M.; Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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Pred. No. 1.4e+05;
0; Mismatches 2;
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Fax: 801 585 7177
Email: dduun@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0357 row: I column: 18
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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                                                                                                                                    AZ512326.1 GI:10693642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
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AZ772707 20 bp DNA linear GSS 16-FEB-2001 1M0583L18R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0583L18 R, genomic survey sequence.

19 GGGGGGGGGGGGGG 1

Mus musculus (house mouse)

Mus musculus

AZ772707.1 GI:12896303

GSS.

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VERSION
KEYWORDS
SOURCE
ORGANISM
                             RESULT 24
AZ772707/c
                                                                                                            DEFINITION
                                                                                                                                                                    ACCESSION
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Mus musculus

Mus macoulus

Muschoria; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Mus:

I (bases I to 20.

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
                                                    AZ645269
1M0510B10R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0510B10 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="B. Coli strain XL10-Gold, Tl-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCM library" /note="Wector: PWD4ZLY; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunm@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0510 row: B column: 10
Seq primer: CACACAGGAAAACAGCTAATGACC
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Location/Qualifiers
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RESULT 23
AZ645269/c
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwMD42 (gil#132114[gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-GG1d (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                            Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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                                                                                             1 (bases 1 to 20)
Dunn,D., Acyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
NiederAhausern,A. and Wright,D.,Waiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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Fax: 801 585 7177
Email: ddunn@qenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0583 row: L column: 18
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
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                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
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AUTHORS
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ö Gaps ö 79.0%; Score 15.8; DB 9; Length 20; ilarity 89.5%; Pred. No. 1.4e+05; Conservative 0; Mismatches 2; Indels Query Match Best Local Similarity Matches 17; Conserval

2 GGGGAGGGGAGGGG 20

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AZ653464 linear GSS 14-DEC-2000 IMO527G11F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0527G11 F, genomic survey sequence.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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2 GGGGAGGGAGGGGG 20
                              20 GGGGAGGGGGGGGGGG 2
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Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                     AZ653464
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KEYWORDS
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                                                                                                                                                   AZSB3408 13-DEC-200 21 bp DNA linear GSS 13-DEC-200 1M0378N23F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0378N23 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
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/clone_lib="Mouse 10kb plasmid UGCIM library"
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musculus C57BL/6J (Male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Duni, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Insert Length: 10000 Std Error: 0.00
Plate: 0378 row: N column: 23
Seg primer: CGTTGTAAAACGACGGCCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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High quality sequence stop: 21.
Location/Qualifiers
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clone="UUGC1M0378N23"
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                         20 GGGGGGGGAGGGGGGGG 2
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Fax: 801 585 7177
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Best Local Similarity
Matches 17; Conserva
                                                                                                      RESULT 25
AZ583408/c
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5

Euteleostomi;

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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Wector: PWD42nv; Purified genomic DNA from M.
musculus G75BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of out of the blunt end shall be adaptored the manahama of the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
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16

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Gaps

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Indels

5;

Mismatches

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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
17; Conservative
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KEYWORDS
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/clone_lib="Wouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note=="Weetor: PWD42nt, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa, Chordata, Craniata; Vertebrata; Eutheria; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Mus.

E 1 (bases 1 to 21)
S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Unpublished (2000)
L Unpublished (2000)
Context: Robert B. Weiss University of Utah
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84112, USA
                                                                                                                                                                                                                GSS 21-FEB-2001
                                                                                                                                                                                                             AZ871715
2M0184B13R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0184B13 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0184 row: B column: 13
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/strain="C57BL/6J"

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High quality sequence stop: 21.
Location/Qualifiers
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                              2 GGGGAGGGAGGGAGGGG 20
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Fax: 801 585 7177
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AZ871715/c
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SOURCE
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chamically-competent E. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                       AZ331988 29-SEP-2000 1M0060B11F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0060B11 F, genomic survey sequence.
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musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0060 row: B column: 11
Seq primer: CGTTGTAAACGACGCCCAGT
Class: plasmid ends
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC1M0060B11"
/sex="Male"
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Location/Qualifiers
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2 GGGGAGGGAGGGG 20
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DB 9; Length 22;

79.0%; Score 15.8;

Query Match

Score 15.8; DB 9; Length 21; Pred. No. 1.4e+05;

79.0%; 89.5%;

Query Match Best Local Similarity

Length 22;

ò g

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79.0%; Score 15.8; Dilarity 89.5%; Pred. No. 1.4e Conservative 0; Mismatches
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                                                                                                                                                21 GGGGGGGGGGGGGGGG 3
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                                                                                                    2 GGGGAGGGGAGGGGG
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Fax: 801 585 7177
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  Query Match
Best Local Similarity
Matches 17; Conser
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                                                                                                                                                                                                                              ALMANIATO GSS 04-OCT-2000 IND244E23F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0244E23 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308. Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria; Buarchontoglires, Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokee, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                               Gaps
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                               Indels
  89.5%; Pred. No. 1.4e+05;
tive 0; Mismatches 2;
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Fax: 801 585 7177
Email: ddunn@enetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0244 row: E column: 23
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
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clone="UUGC1M0244E23"
                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
                                                                             2 GGGGAGGGGAGGGGG 20
                                                                                                                    1 GGGGGGGGAGGGGGGGG 19
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                            17; Conservative
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  Best Local Similarity
Matches 17; Conserv
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ORIGIN

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muscular Cylabron (mare) was obcained from the backson laboratory Mouse DNR Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.05 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gol electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114 gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
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/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42rv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
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Score 15.8; DB 9;
Pred. No. 1.4e+05;
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Insert Length: 10000 Std Error: (
Plate: 0429 row: D column: 18
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                             17; Conservative
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Fax: 801 585 7177
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                           Query Match
Best Local Similarity
Matches 17; Conserv
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84112, US
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AZ488138/c
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
E Sciurognathi; Muroidea; Muridae; Mus.
E 1 (Dases 1 to 22)
S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacres,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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/clone lib="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G78L/6J (male) was obtained from the Jackson
                                                          Gaps
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Query Match 79.0%; Score 15.8; DB 9; Length 22; Best Local Similarity 89.5%; Pred. No. 1.4e+05; Matches 17; Conservative 0; Mismatches 2; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0511 row: C column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: plaemid ends
High quality sequence stop: 22.
Location/Qualifiers
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'strain="C57BL/6J"
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/clone="UUGC1M0511C07"
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                                                                                                            2 GGGGAGGGGAGGGG 20
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AZ645874.1 GI:11775791
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Fax: 801 585 7177
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AZ645874/c
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AP129072.1). a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells
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                                                                                                                                                                                                                                                                                                                                                                                                       AZ488138 100 Dorder GSS 05-0CT-2000 1M0318E13F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0318E13 F, genomic survey sequence.
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Sciurognathi; Muroidea; Muridae; Murinae; Mus.

I (bases 1 to 23)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Moderhausern, A. and Wright, D., Weiss, R.
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Score 15.8; DB 9; Length 22; Pred. No. 1.4e+05;
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Insert Length: 10000 Std Error:
Plate: 0318 row: E column: 13
Seq primer: CGTTGTAAAACGACGGCCAGT
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC1M0318E13"
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                                                                                                                                                    2 GGGGAGGGAGGGG 20
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Query Match
Best Local Similarity 89.5
Matches 17; Conservative
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AZ800632/c
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                                                                                                                                                                                                                                                                                                                                    AZ581259
1M0369N11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0369N11 R, genomic survey sequence.
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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/clone lib="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD42Iv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 23)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                         Gaps
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                                                                         Length 23;
                                                                                                                       Indels
and selected for ampicillin resistance."
                                                                       Score 15.8; DB 9; I
Pred. No. 1.4e+05;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0369 row: N column: 11
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory Mouse DNA Resource

    .23
    /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"

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clone="UUGC1M0369N11"
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High quality sequence stop: 23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
                                                                                                                                                                    2 GGGGAGGGAAGGGG 20
                                                                                                                                                                                                     22 GGGGGGGGAGGGGGGG 4
                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ581259.1 GI:11696092
                                                                       Query Match
Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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AZ581259/c
LOCUS
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KEYWORDS
SOURCE
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Laboratory Mouse DNA Resources documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifica at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
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240058E17R MOUSE 10kb plasmid UUGC1M library Mus musculus genomic
chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (basea 1 to 23)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Rally, M., Rose, M., Rose, M., Rose, Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                 Length 23
                                                                                                                                                                                                       2; Indels
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                                                                                                                                 Score 15.8; DB 9;
Pred. No. 1.4e+05;
0; Mismatches 2;
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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Location/Qualifiers
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Fax: 801 585 7177
Famil: ddunn@genetics.utah.edu
Insert Length: 10000 5td Err
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0
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GSS.
                                                                                                                                        79.0%;
89.5%;
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Mus musculus
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SOURCE
ORGANISM
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AZ640795/c
                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
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AUTHORS
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/67 (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-ealected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis Vector DNA was prepared from a derivative
of pWNA2 (gil 4772114 [gb] AFT25072.1), a copy number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
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adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                           AZ404465 1085 03-0CT-200 DNA linear GSS 03-0CT-200 DN0172P09R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0172P09 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria, Euarchontoglires, Glires; Rodentia;
Sclurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Waiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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                                                                                                                      Length 23;
                                                                                                                      Score 15.8; DB 9; Length 2
Pred. No. 1.4e+05;
0; Mismatches 2; Indels
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Fax: 801 585 7177
Email: ddunmagenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0172 row: P column: 09
Seg primer: CACACAGGAAACAGCTATGACC
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/mol type="genomic DNA"
/mol type="genomic DNA"
/mol type="genomic DNA"
/db xref="taxon:1009"
/clone="fugClM0172P09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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Mus musculus
                                                                                                                                                                      0;
                                                                                                                                                                                                                       2 GGGGAGGGAGGGG 20
                                                                                                                                                                                                                                                                        GGGGAGGGGGGGGGGGGG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ404465.1 GI:10528394
                                                                                                                        79.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Class: plasmid ends
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17; Conserva
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84112, USA
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                                                                                                                           Query Match
Best Local (
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ORGANISM
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AZ404465
                                                                                                                                                                      Matches
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KEYWORDS
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(http://www.jaxe.pun.esources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a co.05 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|472114|fg) RP12907211), a copy-number inducible derivative of plasmid R1. The vector was ligated
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purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli Xilo-Gold (Stratagene) and selected for ampicillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Ralm, I., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reily, M., Rose, M., Rose, M., Stokes, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Welse, R.
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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/clone lib="Mouse 10kb plasmid UUGCNM librazy"
/note="Vector: PWD4zny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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0
                                                                                                                                                                                                                         Length 24;
                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                             Query Match 79.0%; Score 15.8; DB 9; Best Local Similarity 89.5%; Pred. No. 1.4e+05; Matches 17; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0503 row: D column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory Mouse DNA Resource
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Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
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Unpublished (2000)
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Fax: 801 585 7177
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us-09-669-187a-906.szlm50.rst

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Laboratory Mouse Number, was obtained them the databoratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XLIO-GGOLd (Stratagene) cells and selected for ampicillin resistance."
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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                                                                                                                                                                                                 79.0%; Score 15.8; DB 9; Length 24;
larity 89.5%; Pred. No. 1.4e+05;
Conservative 0; Mismatches 2; Indels
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84112, USA
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Insert Length: 10000 Std Error: 0.00
Plate: 0036 row. a .....
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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Location/Qualifiers
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/clone="UUGC2M0036A15"
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Mus musculus
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunner
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Matches 17; Conserv
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inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0098F17F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0098F17 F, genomic survey sequence.
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Bukaryota, Metacaa, Chordata, Craniata, Vertebrata, Euteleostomi,

Bukaryota, Metacaa, Chordata, Craniata, Rodentia,

Sciurognathi, Muroidea, Muridae, Murinae, Mus.

(bases 1 to 24)

Dunn, D., Aoyagi, Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Miderhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42rry; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Pred. No. 1.4e+05;
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Insert Length: 10000 Std Brror: 0.00
Plate: 0098 row: F column: 17
Seq primer: CGTYGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
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Contact: Robert B. Weiss
University of Utah Genome Center
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/strain="C57BL/6J"
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/clone="UUGC2M0098F17"
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Fax: 801 585 7177
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of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sclurognathi; Muroidea; Muridae; Murinae; Mus.
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Pred. No. 1.4e+05;
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84112, USA
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0281 row: D column: 10
Seq primer: CACAGGAAACAGGTAATGACC
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
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/organism="Mus musculus"
/mol type="genomic DNA"
/db xref="textor:1090"
/clone="tutgClM0281D10"
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electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi]4732114 |gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XII.0-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZ602480
1M0421F16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic CODE UUGC1M0421F16 F, genomic survey sequence.
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Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Waiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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                                                                                                                                                                                                                                                                           Length 25;
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                                                                                                                                                                                                                                                                           79.0%; Score 15.8; DB 9;
llarity 89.5%; Pred. No. 1.4e+05;
Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0421 row: F column: 16
Seq primer: cGTTGTAAAACGACGCCAGT
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/clone="UUGC1M0421F16"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 17; Conserv
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84112, US
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/lab host="E. Gold DH108"
/lab host="E. Gold DH108"
/clone lib="WAP1"
/note="Vector: pT773D-Pac (Pharmacia); Site_1: NotI;
/note="Vector: pT773D-Pac (Pharmacia); Site_1: NotI;
Site_2: EcoRI; ESTS sequenced from the T7 prining site
that_reads from the 5' end of cDNA. The NAP1 is a
directionally cloned and normalized, oligo-T prinad cDNA
library constructed from a mixture of Anopheles gambiae
developmental stages according to: Bonaldo, Lennon &
Soarse (1996): Normalization and Subtraction: Two
Approaches To Facilitate Gene Discovery, Genome Research
6, 791-806."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ307654 29-SEP-2000 1M0009F22R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0009F22 R, genomic survey sequence.
     BX626114 BYP1 Anopheles gambiae cDNA clone ANGNP1181G08T7, mRNA
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae; Anopheliae; Anopheles.

1 (Sassa 1 to 26)

1 Lobo, N.L., Gardher, M., Romans, P. and Collins, F. H.

Anopheles gambiae EST, Center for Tropical Disease Research and
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Dunn, D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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'Unpublished (2003)

Contact: Frank H. Collins
Contact: Frank H. Collins
Contact: Frank H. Collins
Contact: Frank H. Collins
University of Notre Dame
Notre Dame, IN 46556, USA
Tel: 574-631-9245
Fax: 574-631-9246
Email: frank h.collins.75@nd.edu.
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                                                                                                                                                                Anopheles gambiae (African malaría mosquito)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Anopheles gambiae"
/mol_type="mRNA"
/db_xref="taxon:7165"
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Contact: Robert B. Weiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ307654.1 GI:10346867
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AZ307654/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Districted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 1SA, E-mail: barrell@sanger.ac.uk and nhi@sanger.ac.uk constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 duTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing projects. In Genome Sequencing projects. In Genome Sequencing projects. In Barrell, Oxford University Press, 1999).
10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD4 (gi|4732114 |gb|AF129072.11, a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptorebent B. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
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T. brucei sheared genomic DNA clone 33e11, forward sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 25)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Mel Ville, S. E., Rajandream, M.A. and Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                                                                             Query Match
Post Local Similarity 89.5%; Pred. No. 1.4e+05;
Matches 17; Conservative 0; Mismatches 2;
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/mol_type="genomic DNA"
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AL453376.1 GI:11854702
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RESULT 41 TA33E11P/c DEFINITION

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ORIGIN

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

FEATURES

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KEYWORDS

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Gaps

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COMMENT

RESULT 42 BX626114

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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
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DEFINITION
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          COMMENT
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AZ447254
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Mammalia; Buteria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 26)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
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                                                                                                                                                                                    Std Error: 0.00
                                                                                                                                                                                                      plate: 0009 row: F column: 22
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="UUGC1M0009F22"
                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunw@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0009 row: F column: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sex="Male"
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Best Local Similarity
Matches 17; Conserv
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AZ447254/c
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwh92 (gilfa732114[gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XIIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Mus.
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/lab host="B. Coli strain XL10-Gold, T1-resistant, F."
/lab host="Mouse 10kb plasmid UUGCIM library"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD4Znv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource And Mouse DNA Resource DNA Resou
Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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89.5%; Pred. No. 1.4e+05;
ative 0; Mismatches 2;
                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: CGTTGTAAAACGACGCCCAGT Class: plasmid ends
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/strain="C57BL/6J"
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/clone="UUGC1M0244020"
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/clone lib="Mouse 10kb plasmid UGGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G77BL/63 (male) was obtained from the Jackson
          Unpublished (2000)
Contact: Robert B. Weiss
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 318, Biomedical Polymers Research Bldg., 20
84112, USA
                                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0168 row: K column: 19
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
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/strain="C57BL/6J"
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/clone="UUGC2M0168K19"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Male"
                                                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
plasmid inserts
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Imboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adappored vector DNA, and transformed into
chemically-competent B. coli Xil0-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 S85 5606
Email: @dunn@genetics.utah.edu
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UTGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Nese, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0076 row: C column: 02
Seq primer: GGTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="taxon:10090"
clone="UUGC2M0076C02"
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Best Local Similarity 89.5'
Matches 17; Conservative
   Unpublished (2000)
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AZ604434 13-DEC-2000 1M0425118F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0425118 F, genomic survey sequence.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Murinae; Murinae; Mus.
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                                                                            Gaps
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Query Match 79.0%; Score 15.8; DB 9; Length 26; Best Local Similarity 89.5%; Pred. No. 1.4e+05; Matches 17; Conservative 0; Mismatches 2; Indels
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Laboratory without can describe the hotelous of the passage through was hydrodynamically sheared by repeated passage through was hydrodynamically sheared by repeated passage through of .005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose ggl electrophoresis. Vector DNA was prepared from a derivative of pwalp4 (ggl #4732114 [gb] AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                  Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 309, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="B. Coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse lokb plasmid UUGCIM library."
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
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Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0519 row: P column: 18
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db xref="taxon:10090"
/clone="UUGC1M0519P18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 27.
Location/Qualifiers
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Mus musculus
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Best Local Similarity 89.5
Matches 17; Conservative
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84112, US
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AZ327022
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                                 TITLE
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophorasis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|RR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                          Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Winversity of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT
84112, USA
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1M0519P18R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0519P18 R, genomic survey sequence.
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1 (bases 1 to 27)

1 (bases 1 to 27)

1 Norgai, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
      whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunmgenetics.utah.edu
bmart Length: 10000 5td Error: 0.00
Plate: 0425 row: I column: 18
                                                                                                                                                                                                                                                                                                                                                                                   Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 27.
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organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'db_xref="taxon:10090"
clone="UUGC1M0425118"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sex="Male"
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                                    plasmid inserts
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| Jab host="B. Coli strain XL10-Gold, T1-resistant, F-"
| Clone lib="whose 10kb plasmid UUGCIM library"
| / Clone lib="whose 10kb plasmid UUGCIM library"
| / Note="Wetcr: PWDAZIV; Purified genomic DNA from M.
| musculus C57BL/6J (male) was obtained from the Jackson
| Laboratory Mouse DNA Resource
| (http://www.jax.org/resources/documents/dnares/). The DNA
| was hydrodynamically sheared by repeated passage through a
| 0.005 inch orifice at constant velocity. The sheared DNA
| was blunt end-repaired with T4 DNA polymerase and T4
| polymucleotide kinase. Adaptor oligonucleotides were
| ligated to the blunt ends in high molar excess. The
| adaptored DNA was purified and size-selected for a 9.5 to
| 10.5 kb range using preparative agarose gol |
| electrophoresis. Vector DNA was prepared from a derivative
| of pWDAZ (gdi | 4732114| gbl AR129072.1); a copy-number
| inducible derivative of plasmid R1. The vector was ligated
| with adaptors complementary to the insert adaptors and
| purified. The sheared, adaptored mouse DNA was annealed to
| chanically-competent B. coli Xill0-Gold (Stratagene) cells
| and selected for ampicillin resistance."
                                                                   plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.

1 (bases 1 to 28)
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Length: 10000 Std Error: 0.00
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Plate: 0050 row: I column: 12
Seq primer: CGTTGTAAAACGACGGCCAGT
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Location/Qualifiers
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/clone_lib="Wouse lokb plasmid UUGCIM library"
/note="Vector: PWD42IV; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dhares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|Ar129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                                                                                 Unpublished (2000)
Contact: Robert B. Weiss
Contract: Yof Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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Pred. No. 1.4e+05;
); Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: G column: 02
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 28.
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
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US-09-1975-4508-6
US-09-1975-9518-6
US-09-1977-9518-6
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Sequence 9, Sequence 9, Sequence 67	3.8 69.0 47 3 US-09-422-978-285 Sequence 28	3.8 69.0 47 3 US-10-170-097-679 Sequence 67	3.8 69.0 50 3 US-10-131-827-5327 Sequence 53. 3.6 68.0 21 2 US-08-424-663-2	3.6 68.0 21 2 US-08-872-446-2 Sequence 2,	3.6 68.0 21 3 US-09-280-270A-2 Sequence 2,	3.6 68.0 24 3 US-08-729-598-7 Sequence 7,	3.6 68.0 24 3 US-09-894-799*ZI Sequence ZI	3.6 68.0 20 3 03-03-883-0435-6/ 3-4/4 Semience 3/	2 C CO::0 20 2 CC CC 24 11 CC CC 24 25 25 25 25 25 25 25 25 25 25 25 25 25	3.6 68.0 45.3 TS-08-931-220-36 Segmence 36	2 6 6 0 4 6 6 DCT-11202-1-2	2.0 00.0 4.1 0 FCI-0400-411/42.30 0044-0400000 30	3.0 00.0 4.0 0 FLI-US90-US99/-US90 0.00 0.00	3.6 68:0 4/ 3 03-09-6/1-5/9 Sequence 0.	3.6 68.0 48 2 US-U8-8/Z-446-12 Sequence 12	3.6 68.0 48 3 US-09-280-270A-12 Sequence 12	3.6 68.0 50 3 US-10-131-827-3003 Sequence 30	3.4 67.0 22 3 US-10-130-792A-3 Sequence 3,	3 4 67 0 34 2 HS-07-743-245-2 Segmence 2.		1.4 0/.0 4/.0 0.00-0/9-4ZZ-9/0-0ZJ SEQUENCE UK.	3.4 6/.0 50 3 05-10-131-82/-1882 sequence to	3.2 66.0 18 2 US-08-145-704-42 sequence 42	3.2 66.0 18 2 US-08-145-704-43 Sequence 43	2 2 66 0 18 2 TIS-08-358-5563-24 Semience 24	to company to the second of th	3.2 66.0 18 3 US-08-987-574-42 Sequence 42	3.2 66.0 18 3 US-08-987-574-43 Sequence 43	2 2 CE 0 10 2 HE-00-E2E-160-42 Commonded 42	ZE SOUTHER SET OF SET O	3.2 66.0 18 3 US-08-535-168-43 Sequence 43	3.2 66.0 18 3 US-09-437-076-3 Sequence 3,	2 2 5 6 0 10 1 115 00 117 00 00 00 00 00 00 00 00 00 00 00 00 00	3.2 do: 0 12 3 03-09-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20 03-01-14 20	3.2 66.0 18 3 US-09-017-974-43 Sequence 43	3 2 66 0 18 3 11S-08-682-255A-42 Segrence 42	1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1	3.2 66.0 18 3 US-08-682-255A-43 sequence 43	3.2 66.0 18 3 US-09-429-130-42 Sequence 42	3.2 66.0 18 3 US-09-429-130-43 Sequence 43	3.2 66.0 18 3 US-10-352-704-24 Sequence 24	2	( ) DOI DOI 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	3.2 66.0 18 3 US-09-09/-/91D-4 Sequence 4.	3.2 66.0 18 6 PCT-US96-11786-42 sequence 42	3.2 66.0 18 6 PCT-US96-11786-43 Sequence 43	3.2 66.0 19 3 US-09-109-663-31 Sequence 31	3.2 66.0 19 3 US-09-230-652-117 Sequence 11	3.2 66.0 21 2 US-08-424-663-3 Sequence 3.	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OTHER INFORMATION: "C" stands for 5-methylcytosine
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 613 West Fifth Street
STREET: 613 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-206
COMPUTER READABLE FORM:
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: PASLICATION DATA:
APPLICATION NUMBER: US/08/460,890A
FILING DATE: June 5, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/167,641
FILING DATE: March 19, 1993
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 20, 1993
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 20, 1993
APPLICATION NUMBER: 20, 1993
ATTORNEY/AGENT INFORMATION:
TELEFON: REFERENCE/OCKET NUMBER: 212/066
TELEFON: (213) 955-0440
TELEFON: (213) 955-0440
TELEFON: 77 has a nairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Sequence 10, Appl
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US-09-017-974-2
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US-08-682-255A-2
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US-09-429-130-2
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US-08-460-890A-15
; Sequence 15, Application US/08460890A
; Patent No. 5994109
; GENERAL INFORMATION:
; APPLICANT: Smith. Louis C.
; APPLICANT: Smith. Louis C.
; APPLICANT: Gottchalk, Stephen
; TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
; TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
    Length 27;
Query Match

87.0%; Score 17.4; DB 2;
Best Local Similarity 94.7%; Pred. No. 4.3e+02;
Matches 18; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
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                                                                                                                                             24 AAGGGAGGGAGGGAGGG
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RESULT 1
US-08-460-890A-14/c
Sequence 14, Application US/08460890A
Patent No. 5994109
GENERAL INFORMATION:
APPLICANT: WOO, Savio L.C.
APPLICANT: Gristiano, Richard J.
APPLICANT: Gristiano, Richard J.
TITLE OF INVENTION: METHODS OF USE
TITLE OF INVENTION: METHODS OF USE

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Patent No. 6033884

GENERAL INFORMATION:

APPLICANT: Woo, Savio L.C.

APPLICANT: Smith, Louis C.

APPLICANT: Smith, Louis C.

APPLICANT: Gristiano, Richard J.

APPLICANT: Sylvantion: Marthodos OF USE

NUMBER OF SEQUENCES: 65

CORRESPONDENCES: 65

CORRESPONDENCES: Lyon & Lyon

STREET: Suite 4700

STREET: Suite 4700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: "C" stands for 5-methylcytosine US-08-167-641C-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: LOS ANGELES
CTATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: STORAGE
COMPUTER: IBW COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTERN: IBM P.C. DOS 5.0
SOFTWARE: FASTERN: IBM P.C. DOS 5.0
SOFTWARE: DASTERNIAN DATA:
APPLICATION NUMBER: US/08/167,641C
FILING DATE: December 14, 1993
RILING DATE: MARCH 20, 1992
APPLICATION NUMBER: 07/855,389
FILING DATE: MARCH 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: MARCH 19, 1993
ATTORNEY AGENT INFORMATION:
                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 205/012
TELECOMMUNICATION INFORMATION:
TELECHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 205/012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: Other nucleic acid FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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WS-08-167-641C-14/C

Sequence 14, Application US/08167641C

Patent No. 6033804

GRNERAL INFORMATION:

APPLICANT: Woo, Savio L.C.

APPLICANT: Cristiano, Richard J.

APPLICANT: Cristiano, Richard J.

APPLICANT: Gottchalk, Stephen

TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND

TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND

TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND

TITLE OF INVENTION: RETHORS OF USE

NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: Suite 4700

CITY: Los Angeles

STREET: Suite 4700

CITY: Los Angeles

STATE: Galifornia

COUNTRY: U.S.A.

ZIPP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: SICORAGIE

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

CURRENT APPLICATION NUMBER: US/08/167,641C

* HILNG DATE: December 14, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 87.0%; Score 17.4; DB 2; Length 27; Best Local Similarity 94.7%; Pred. No. 4.3e+02; Matches 18; Conservative 0; Mismatches 1; Indels
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
COMPUTER: 1BM Compatible
SOFTWARE: FeatSEQ for Windows 2.0
CURRENT APPLICATION NUMBER: US/08/460,890A
FILING DATE: USCENDER: 4, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 19, 1993
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
APPLICATION NUMBER: 212/066
FILING DATE: Warch 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 21,2/06
TELEFRAN: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear;
; MOLECULE TYPE: CDNA
US-08-460-890A-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEPLICANT: WOO, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: MUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPENDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Galife Lyon & Lyon
STREET: Galife ATOO
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 17.4; DB 3; Length 27; Pred. No. 4.3e+02; 0; Mismatches 1; Indels
                                                                                                                                      Length 27;
                                                                                                                                                                                                 Indels
                                                    "C" stands for 5-methylcytosine
                                                                                                                                Query Match

87.0%; Score 17.4; DB 3;

Best Local Similarity 94.7%; Pred: No. 4.3e+02;

Matches 18; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM COMPAGIBLE
COMPUTER: TESTED (IBM P.C. DOS 5.0
SOFTWARE: FASTENCI IBM P.C. DOS 5.0
SOFTWARE: FASTENCI IBM P.C. DOS 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,971A
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION INTHER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: 07/855,389
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 212/063
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15, Application US/08460971A Patent No. 6150168 GENERAL INFORMATION:
MOLECULE TYPE: Other nucleic acid
                                                                                                                                                                                                                                                           1 AGGGGAGGGAGGG 19
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94.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (213) 55-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 94.73
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 67-3510 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
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                        FEATURE:
COTHER INFORMATION:
US-08-460-971A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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US-08-460-971A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-460-971A-15
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US-08-460-971A-14/C

Sequence 14, Application US/08460971A

Parent No. 6150168

GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: Suite 4700
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                            87.0%; Score 17.4; DB 3; Length 27; 94.7%; Pred. No. 4.3e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AGGGGAGGGGAGGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 AAGGGAGGGGAGGG 22
                     | TELEPHONE: (213) 489-1600 | TELEPAX: (213) 955-0440 | TELEX: (213) 955-0440 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,327
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 21 FLECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 94.73
Matches 18; Conservative
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: "C" stands for 5-methylcytosine
                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: Other nucleic acid FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
US-08-462-040-15
Sequence 15, Application US/08462040
Parent No. 6177554
1 AGGGGAGGGGAGGG 19
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Best Local Similarity 94.7
Matches 18; Conservative
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APPLICANT: Smith Louis C.
APPLICANT: Smith Louis C.
APPLICANT: Smith Louis C.
APPLICANT: Smith Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 613 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STREET: California
COUNTRY: U.S.A.
ZIP : 90011-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.0%; Score 17.4; DB 3; Length 27; 94.7%; Pred. No. 4.3e+02; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13. Application US/08460890A
Patent No. 5994109
GENERAL INFORMATION:
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gretchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage computer Storage computer: 1 the compatible computer: 1 the comput
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AGGGGAGGGAGGG 19
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 27 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 94.7
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-460-890A-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-462-040-15
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Gaps
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; Sequence 13, Application US/08460971A
; Sequence 13, Application US/08460971A
; Patent No. 6150168
; Patent No. 6150168
; APPLICANT: Woo, Savio L.C.; APPLICANT: Cristiano, Richard J. APPLICANT: Gritchalk, Stephen
; TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND TITLE OF INVENTION: METHODS OF USE NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
ADDRESSEE: Lyon & Lyon
; ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 87.0%; Score 17.4; DB 3; Length 39; Best Local Similarity 94.7%; Pred. No. 4.3e+02; Matches 18; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: 634 West Fifth Street
STREET: California
COUNTY: Los Angeles
CONTYN: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: STORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: STORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUGATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
                                  GOFTWARE: FastESE (For Windows 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,641C
FILING DATE: December 14, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US3/02725
APPLICATION NUMBER: PCT/US3/02725
ATTONNEY.AGENT INPORMATION:
NAME: WALDULG, RICHARD J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 205/012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
YSTEM: IBM P.C. DOS 5.0 FastSEQ for Windows 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 AAGGGAGGGGAGGGG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: CDNA US-08-167-641C-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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TELEX: 6'
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Sequence 13, Application US/08167641C

Batent No. 6033884

GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: MUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Smite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87.0%; Score 17.4; DB 2; Length 39;
94.7%; Pred. No. 4.3e+02;
tive 0; Mismatches 1; Indels
                                            CITY: Los Angeles
STATE: California
COUNTY: U.S.A.
ZIP: 90071-2066
ZOMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: STORAGE
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastESQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,890A
FILING DATE: June 5, 1995
CLASSIFICATION: 435
PRICA PAPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1993
APPLICATION NUMBER: PCT/US93/02725
RILING DATE: March 19, 1993
ATTORNEY, AGENT INFORMATION:
"NAME: Was-hurr" Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
  633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (213) 489-1600
TELEX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AGGGGAGGGGAGGG 19
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Best Local Similarity 94.79
"-rohes 18; Conservative
                       T: Suite 4700
Los Angeles
: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
US-08-167-641C-13
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/note= "Sticky single-stranded end
from base 1 to 4. Double stranded from base 5 to
43 to complementary strand, SEQ ID NO:3."
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                                                                                                                                                                                                                                                    87.0%; Score 17.4; DB 3; Length 39; 94.7%; Pred. No. 4.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application PC/TUS9302352

GENERAL INFORMATION:

APPLICANT: California Institute of Technology,

APPLICANT: Pasadena California 91125, U.S.A.

TITLE OF INVENTON: Triple helix recognition of DNA

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Richard F. Trecartin

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

CONNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02352
FILING DATE: 19930311
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 13-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: 31,801
REFERENCE/DOCKET NUMBER: 31,801
RELEPHONE: (415) 781-1989
TELEFRONE (415) 781-1989
TELEFRONE (415) 781-1899
TELEFRONE (415) 781-1899
TELEFRONE FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.0%; Score 16.4; DB 6;
89.5%; Pred. No. 9.8e+02;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                              1 AGGGGAGGGGAGGG 19
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLLGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_binding
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Best Local Similarity 89.5'
Matches 17; Conservative
                                                                                                                                                                                                                                                                                   Best Local Similarity 94.7
Matches 18; Conservative
            SEQUENCE CHARACTERISTICS
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) OTHER INFORMATION: /: / OTHER INFORMATION: £1
) CTHER INFORMATION: 43
PCT-US93-02352-2
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PCT-US93-02352-2
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US-08-462-040-13
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GENERAL OF INVENTION:
TITLE OF INVENTION:
METHODS OF USE
NUMBER OF SEQUENCES:
GENERAL LYON & LYON
STREET:
GADNESSES:
ADDRESSES:

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.0%; Score 17.4; DB 3; Length 39; 94.7%; Pred. No. 4.3e+02; tive 0; Mismatches 1; Indels
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Marburg, Richard J.
REGISTRATION NUMBER: 212,063
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
TELERAX: 67-3510
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REPERENCE/DOCKET NUMBER: 212/078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 13, Application US/08462040; Patent No. 6177554
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INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-460-971A-13
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US-08-462-040-13
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COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/781,986A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polymucleotides and Sequences
NUMBER OF SEQUENCES: 5256
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COTHER INFORMATION: /note= "Sticky single-stranded end oTHER INFORMATION: from base 1 to 4. Double-stranded from base 5 to OTHER INFORMATION: 37 to complementary strand, SEQ ID NO:2."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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0
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             GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: California Institute of Technology,
APPLICANT: Pasadena, California 91125, U.S.A.
TITLE OF INVENTION: Triple helix recognition of DNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard F. Trecartin
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02352
FILING DATE: 19930311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/850,503
FILING DATE: 13-MAR-1992
ATTONNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F
REGISTRATION NUMBER: 13,801
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 398-3249
INPORMATION FOR SEQ ID NO: 3:
ENGURACE CHARACTERISTICS:
LENGTH: 43 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
US-08-956-171E-2153/C
; Sequence 2153, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; GAPLICANT: Charles Kunsch
; Paterick S. Dillon
...? A ROSEN
                                                                                                                                                                                                                                                                                                                        ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AGGGGAGGGGAGGG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: NUCLEIC ACID
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: CDNA
PCT-US93-02352-3/c
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US-08-781-986A-2153/c

Sequence 2153 Application US/08781986A

Patent No. 6737248

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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0
                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: By Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
ATTORNEY/AGENT INFORMATION:
NAME: MARK J. Hyman
REGISTRATION NUMBER: 46,789
REGISTRATION NUMBER: 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
82.0%; Score 16.4; DB 3;
Best Local Similarity 89.5%; Pred. No. 9.8e+02;
Matches 17; Conservative 0; Mismatches 2;
                ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO: 2153:
US-08-956-171E-2153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (301) 309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 2153:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GGGGAGGGGAGGGG 20
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STRANDEDNESS: double
CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION NUMBER: PCT/SE00/00878
PRIOR FILING DATE: 2000-05-04
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.2
SEQ ID NO 21
LENGTH: 27
                                                                                                                                                                         ; OTHER INFORMATION: P R 1b GCVI Rev US-09-622-745B-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-118-752-2
; Sequence 2, Application US/09118752
; Patent No. 6114154
                                                                                                                                                                                                                                                                                                                   1 AGGGGAGGGAGGG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: primer bind
; LOCATION: (1)..(22)
US-09-118-752-2
                                                                                                                    TYPE: DNA
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DESIRED PROTEINS
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                                                                                                                                                          FEATURE:
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                                                                                                                                                                                                                                                                                               82.0%; Score 16.4; DB 3; Length 50;
89.5%; Pred. No. 9.8e+02;
iive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79.0%; Score 15.8; DB 3; Length 27; 89.5%; Pred. No. 1.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20, Application US/09622745B

Patent No. 6933124

GENERAL INFORMATION:
APPLICANT: AstraZencea AB
APPLICANT: Edund, Anders
APPLICANT: Estrand, Jonas
APPLICANT: Dohansson, Thore
APPLICANT: Johansson, Goran
TITLE OF INVENTION: HUMAN GABA B RECEPTOR 1 PROMOTERS
FILE REFERENCE: 1103326-0633
CURRENT APPLICATION NUMBER: US/09/622,745B
CURRENT FILING DATE: 2000-08-22
PRIOR PILING DATE: 2000-05-04
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.2
SEQ ID NO 20
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21, Application US/09622745B
Patent No. 6933124
| GENERAL INFORMATION
APPLICANT: Edlund, Anders
| APPLICANT: Estrand, Jonas
| APPLICANT: Estrand, Jonas
| APPLICANT: Lonardsson, Thore
| APPLICANT: Lonardsson, Goran
| TITLE OF INVENTION: HUMAN GABA B RECEPTOR 1 PROMOTERS
| CURRENT APPLICATION NUMBER: US/09/622,745B
| CURRENT FILING DATE: 2000-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                              NAME: BEHBOLL, BUCKET NUMBER: 30,446
REGISTRATION NUMBER: 30,446
REFERENCE/POCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 2153:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: P R 1b GCVI Fwd
US-09-622-745B-20
                                                                                                                                                                                                                                                                                                                                                                              2 GGGGAGGGAGGGGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                 28 GGGGGGGGNGGGGAGGGG 10
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      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                   Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial
                                                                                                                                                                                                                                          ; TOPOLOGY: 1;
US-08-781-986A-2153
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US-09-622-745B-20/c
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US-09-622-745B-21
                                                                                                                                                                                                                                                                                                   Query Match
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APPLICANT: Li, Huiwu
TITLE OF INVENTION: Direct Construction and Isolation Full Length Target
TITLE OF INVENTION: DIAM Molecule from an mRNA Population
TITLE OF INVENTION: CONST.
TITLE OF INVENTION: CONST.
TITLE OF INVENTION: CONST.
TITLE OF INVENTION: CONST.
TITLE OF INVENTION NUMBER: US/09/118,752
CURRENT FILING DATE: 1998-07-17
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 37
                                                              Gaps
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                                                           0
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;Patent No. 5182196
APPLICANT: ALLET, BERNARD;KAWASHIMA, ERIC H.
TITLE OF INVENTION: EXPRESSION SYSTEMS FOR OVERPRODUCTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: primer
Ouery Match 79.0%; Score 15.8; DB 3; Length 27; Best Local Similarity 89.5%; Pred. No. 1.6e+03; Matches 17; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 79.0%; Score 15.8; DB 9; Length 42; Best Local Similarity 89.5%; Pred. No. 1.6e+03; Matches 17; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 23
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/372,281
FILING DATE: 27-UW-1989
PRIOR APPLICATION NUMBER: 53,398
FILING DATE: 18-MAY-1987
APPLICATION NUMBER: 785,847
APPLICATION NUMBER: 785,847
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GENERAL INFORMATION:
APPLICANT: Meiji Seika Kaisha, Ltd.
APPLICANT: Meiji Seika Kaisha, Ltd.
APPLICANT: Meiji Seika Kaisha, Ltd.
APPLICANT: Moriya, Tatsuki
TITLE OF INVENTION: Systems for the Mass Production of Proteins or Peptides by Microo TITLE OF INVENTION: of the Genus Humicola
TITLE OF INVENTION: 0f the Genus Humicola
FILE REPERENCE: VX990054
CURRENT APPLICATION NUMBER: US/09/230,225B
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.1
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                     TITLE OF INVENTION: ENZYME ENDOGLUCANASE AND CELLULASE PREPARATIONS
TITLE OF INVENTION: CONTAINING THE SAME
FILE REFERENCE: 99-0055*/LC (WMC)/144
CURRENT APPLICATION NUMBER: US/09/230,222A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
LENGTH: 30
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                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 74.0%; Score 14.8; DB 3; Best Local Similarity 88.9%; Pred. No. 3.7e+03; Matches 16; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 31, Application US/09254352B
Patent No. 6365350
GENERAL INFORMATION:
TITLE OF INVENTION: METHOD OF DNA SEQUENCING
FILE REFERENCE: 024705-080
CURRENT APPLICATION NUMBER: US/09/254,352B
CURRENT APPLICATION NUMBER: PCT/JP98/03039
PRIOR FILING DATE: 1998-07-06
PRIOR FILING DATE: 1998-07-06
PRIOR FILING DATE: 1998-07-06
PRIOR APPLICATION NUMBER: UP 1-155847
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: UP 9-196478
PRIOR FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-230-225B-25/c
; Sequence 25, Application US/09230225B
; Patent No. 6403362
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SEQ ID NO 31
     APPLICANT: KONO, TOSHIAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 64
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                                                                                                                                                                                                                                                                TYPE: DNA
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Patent No. 5624803

GENERAL INFORMATION:
APPLICANT: HOND:
APPLICANT: HOND:
APPLICANT: HONDING:
APPLICANT: HOND:
APPLICANT: HOND:
APPLICANT: HOND:
APPLICANT: HOND:
APPLICANT: HOND:
AND TITLE OF INVENTION: OLIGONUCLEOTIDE GENERATOR, AND
TITLE OF INVENTION: OLIGONUCLEOTIDES DERIVED THEREFROM
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSES: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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76.0%; Score 15.2; DB 3; Length 37; 85.0%; Pred. No. 2.6e+03; ive 0; Mismatches 3; Indels
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/324,001

FILING DATE: 13-0CT-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MONDOY, GLADYS H.

REGISTRATION NUMBER: 22,430

REFERENCE/DOCKET NUMBER: 22,430

REFERENCE/DOCKET NUMBER: 22,600

TELLEPANINICATION NUMBER: 25,000

TELLEPANINICATION NO: 2: SEQUENCE CHARACTERISTICS:

LENGTH: 38 base pairs

LENGTH: 38 base pairs

TYPE: nucleic acid

TYPE: nucleic acid

TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18, Application US/09230222A
Patent No. 6159720
                                                                                                      1 AGGGAGGGAGGGGG 20
                                                                                                                                                         16 AGGGAAGGGGGGGGGGGGG 35
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APPLICANT: MORIAY, TATSUKI
APPLICANT: HAMAYA, TORU
APPLICANT: KOGA, JINICHIRO
APPLICANT: SUMIDA, NAOMI
APPLICANT: AOYAGI, KAORU
APPLICANT: MURAKAMI, TAKESHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 AGGGGAAGGGAAGGG 8
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Best Local Similarity 85.0
Matches 17; Conservative
                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
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                          Best Local Similarity
Matches 17; Conserv
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US-09-230-222-18/c
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  Query Match
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Gaps

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APPLICANT: LIN, SHI-LUNG
APPLICANT: LIN, SHI-LUNG
CHONG, CHENG-MING
YING, SHAO-YAO
TITLE OF INVENTION: Method for Generating Full-Length cDNA
Library from Single Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.0%; Score 14.4; DB 3; Length 25; 93.8%; Pred. No. 5.2e+03; Live 0; Mismatches 1; Indels
                                                                                                                                                  Query Match 72.0%; Score 14.4; DB 3; Length 20; Best Local Similarity 93.8%; Pred. No. 5.2e+03; Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Latour, Derek R.
APPLICANT: Thomas, Rite L.
APPLICANT: Kongachith, Ana
APPLICANT: Sheppard, Liana T.
APPLICANT: Lim, Moon Young
APPLICANT: Lim, Moon Young
APPLICANT: Bruice, Thomas W.
TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: David & Raymond Patent Firm
STREET: 108 N. Ynez Ave., Suite 128
CITY: Monterey Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 54600-8135.USO0
CURRENT APPLICATION NUMBER: US/09/875,453B
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/209,549
PRIOR PILING DATE: 2000-06-06
SUFURER OF SEQ ID NOS: 246
SOFTWARE: PartSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 66, Application US/09875453B Patent No. 6838556 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09197951; Patent No. 6197554; GENERAL INFORMATION:
                                                                                                                                                                                                                                                 5 GAGGGGAGGGGGGG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 93.8%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                  GAGGGGAGGTGAGGGG 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laurance, Megan E
Michelotti, Emil E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kim, Jungsuh P.
APPLICANT: Starr, Douglas B.
APPLICANT: Tam, Albert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  michelotti, Emil
Velligan, Mark D.
PatentIn Ver. 2.0
                                                               TYPE: DNA
CRGANISM: Rattus norvegicus
US-08-777-708C-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-875-453B-66
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US-09-197-951-2/C
                  SEQ ID NO 16
LENGTH: 20
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LENGTH: 25
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SOFTWARE:
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                                                                                OTHER INFORMATION: Description of Artificial Sequence: T7 RNA polymerase (WT)
NAME/KEY: misc_feature
LOCATION: (25)
LOCATION: (25)
CTHER INFORMATION: Nucleotide 25 is n wherein n = any nucleotide.
US-09-254-3528-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-011.77-708C-16/c

i Sequence 16, Application US/08777708C

j APPLICANT: Pescovitz, Ora H.

j TITLE OF INVENTION: USE OF GHRH-RP TO STIMULATE STEM CELL FACTOR PRODUCTION

j TITLE OF INVENTION: 1930-175/IU-62

j CURRENT APPLICATION NUMBER: US/08/777,708C

j CURRENT APPLICATION NUMBER: US 60/008,933

j PRIOR FILING DATE: 1995-12-20

j NUMBER OF SEQ ID NOS: 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (1)...(31)
OTHER INFORMATION: Mutant T7 RNA polymerase wild type.
NAME/KEY: misc. eature
LOCATION: (25)...(25)
OTHER INFORMATION: Nucleotide 25 is "n" wherein "n" = any nucleotide.
                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                            Score 14.8; DB 3; Length 31;
Pred. No. 3.7e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74.0%; Score 14.8; DB 3; Length 31; 88.9%; Pred. No. 3.7e+03; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-134-344-1); Sequence 17, Application US/09254344
Patent No. 6867027
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WATAHIKI, Masanori
ITILE OF INVENTION: RNA POlymerase
FILE REFERENCE: 024705-077
CURRENT APPLICATION NUMBER: US/09/254,344
CURRENT FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: UP 9/180883
PRIOR FILING DATE: 1998-07-06
PRIOR APPLICATION NUMBER: UP 9/180883
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: UP 10/155759
PRIOR PILING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.0
SEQ ID NO 17
                                                                                                                                                                                                                                                                         o;
                                                                                                                                                                                                                                                                                                                      50
                                                                                                                                                                                                                                                                                                                                                                  3 GGGAGGGAGGGGAGGGG 20
                  TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                            74.0%;
ilarity 88.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16; Conservative
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                                                                                                                                                                                                           Query Match
Best Local Similarity
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US-09-254-344-17
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  LENGTH: 31
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Gaps

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US-09-965-101-55/c
; Sequence 55, Application US/09965101
; Patent No. 6821957
  20 GGGGGGGGGGGGGGG 2
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US-09-082-649B-55/C

Sequence 55, Application US/09082649B

Patent No. 6330068

GENERAL INFORMATION:
APPLICANT: Davis, Heather L.
APPLICANT: Schorr, Joachim
APPLICANT: Wu, Tong

TITLE OF INVENTION: Vectors and Methods for Immunization or
TITLE OF INVENTION: Vectors and Methods for Immunization or
FILE REFERENCE: C1039/7009

CURRENT FALING DATE: 1998-05-20

PRIOR APPLICATION NUMBER: US 60/047,233

PRIOR APPLICATION NUMBER: US 60/047,233

PRIOR PLING DATE: 1997-05-20

NUMBER OF SEQ ID NOS: 85

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 20

LENGTH: 20

LENGTH: 20

LENGTH: 20
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ZIP: 91754

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/197,951

FILING DATE: 20-No. 6197554-1998

CLASSIFTCATION: <university | CLASSIFTCATION:

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                 NAME: Chan, Raymond Y.C.
RRGISTRATION NUMBER: 37,484
REFERENCE/DOCKET NUMBER: USP8462A-SL(3)
TELECOMMUNICATION INFORMATION:
TELEPONE: (626) 571-9812
TELEFAX: (626) 571-9813
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: synthetic oligonucleotide US-09-082-649B-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DESCRIPTION: /desc = "synthetic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGGGAGGGAGGGGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 84.2
Matches 16; Conservative
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Exieg, Arthur M.
APPLICANT: Krieg, Arthur M.
APPLICANT: Krieg, Arthur M.
APPLICANT: Schort, Joachim
APPLICANT: General Methods for Immunization or
TITLE OF INVENTION: Vectors and Methods for Immunization or
TITLE OF INVENTION: Therapeutic Protocols
TITLE OF INVENTION: Therapeutic Protocols
FILE REFERENCE: Clo39/7057 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/965,101
CURRENT FILING DATE: 1998-05-20
PRIOR PILING DATE: 1998-05-20
PRIOR FILING DATE: 1997-05-20
PRIOR FILING DATE: 1997-05-20
PRIOR FILING DATE: 1997-05-20
PRIOR FILING DATE: 1997-05-20
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 71.0%; Score 14.2; DB 3; Length 20; Best Local Similarity 84.2%; Pred. No. 6.1e+03; Matches 16; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Harmann, Gunther
APPLICANT: Brazaler, Robert L.
APPLICANT: Rrieg, Arthur
TITLE OF INVENTION: Methods Related to Immunostimulatory
TITLE OF INVENTION: Mucleic Acid-Induced Interferon
TITLE OF INVENTION: Mucleic Acid-Induced Interferon
TITLE OF INVENTION: Mucleic Acid-Induced Interferon
CURRENT APPLICATION NUMBER: US/09/672,126B
CURRENT FILING DATE: 2000-09-27
PRIOR FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 169
SEQ ID NOS: 169
SEQ ID NOS: 169
SEQ ID NOS: 184
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ), OTHER INFORMATION: Synthetic Oligonucleotide US-09-672-126B-134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , OTHER INFORMATION: synthetic oligonucleotide US-09-965-101-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-672-126B-134
; Sequence 134, Application US/09672126B
; Patent No. 6949520
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GGGGAGGGGAGGGG 20
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ORGANISM: Artificial Sequence
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Sequence 42, Application US/08403888A

| Patent No. 5952490
| GENERAL INFORMATION:
| APPLICANT: Henecak et al.
| TITLE OF INVENTION: Oligonucleotides Having A Conserved G4 Core
| TITLE OF INVENTION: Sequence
| NUMBER OF SEQUENCES: 146
| CORRESPONDENCE ADDRESS.
| ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP
| STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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Pred. No. 6.1e+03;
0; Mismatches 3; Indels
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CUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb

COMPUTER: 1BM FC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1

CURERY PAPLICATION DATA:
APPLICATION NUMBER: US/08/403,888A
FILING DATE: 12-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/954,185
FILING DATE: 29-SEP-1992
ATTONNEY/AGENT INFORMATION:
NAME: PAUL K. LEGGARA
REGISTRATION NUMBER: 38,534
                                                                                                                                                                                                                         COMPUTER: IBM
COMPUTER: IBM
COMPUTER: Wordberfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,964
FILING DATE: June 8, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C.
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 128D-1175A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 bases
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 1.44 Mb
                        2500 Harbor Boulevard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GGGGAGGGGAGGGG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 84.2%;
Matches 16; Conservative
STREET: 25vc
CITY: Pullerton
STATE: California
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US-08-257-964-3
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                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Reddy, Parameswara M.
APPLICANT: Reddy, Parameswara M.
APPLICANT: Hanna, Naeem B.
TITLE OF INVENTION: Methods and Reagents
TITLE OF INVENTION: Deprotecting
TITLE OF INVENTION: Oligonuclectides
COURSESPONDENCE BECKman Instruments, Inc.
STREFT: 2500 Harbor Boulevard
CUTY: Fullerton
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08257964

Patent No. 5518651

GENERAL INFORMATION:

APPLICANT: Reddy, Parameswara M.
APPLICANT: Hanna, Naeem B.

TITLE OF INVENTION: Methods and Reagents
TITLE OF INVENTION: Deprotecting
TITLE OF INVENTION: Oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTEX: COLUMER: COUNTEX: CONTEX: CONTEX: COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 1.44 Mb
COMPUTER: IBM
COMPUTER: INFORMATION:
FILING DATE: 19920424
CLASSIFICATION NUMBER: 34,787
REPERENCE/DOCKET NUMBER: 128D-111
TELECOMMUTATION NIFORMATION:
TELEPAX: (714) 773-7610
TELEPAX: (714) 773-7610
TELEPAX: (714) 773-7936
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beckman Instruments, Inc.
                                                                                                                                               Sequence 3, Application US/07873915A
Patent No. 5348868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GGGGAGGGGAGGGG 20
                           1 GGGGGGGGGGGGGGG 19
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , ANTI-SENSE: no
US-07-873-915A-3
                                                                                                                               US-07-873-915A-3
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US-08-257-964-3
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                                                                                                                                                                                                                              Score 14.2; DB 2; Length 21;
Pred. No. 6.1e+03;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 91101
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: COTEL WordPerfect 8 version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Matson, Robert S.
APPLICANT: Matson, Peter J.
APPLICANT: Coassin, Peter J.
APPLICANT: Cassin, Peter J.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABALdon & Mak
STREET: 225 South Lake Avenue, 9th Floor
    ISIS-1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/863,639A FILING DATE: May 28, 1997 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 35
US-08-863-639A-11/c

; Sequence 11, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: Other nucleic acid
REFERENCE/DOCKET NUMBER: ISIE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CARACTERISTICS:
                                                                                                                                                                                                                                                                                                              2 GGGAGGGAGGGGGG 20
                                                                                                                                                                                                                                                                                                                                                     2 GGGAGGGAGGGAGGGG 20
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REGISTRATION NUMBER: 20,532
REFERENCE/DOCKET NUMBER: 111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (626) 795-6321
INFORMATION FOR SEQ ID NO: 11
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
creanDEDNESS: single
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 84.2%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 84.2
Matches 16, Conservative
                                                                                                                                                           single
                                                                                                                             TYPE: nucleic STRANDEDNESS: sing
                                                                                                                                     nucleic acid
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Sequence 4484, Application US/09696791

| Sequence 4484, Application US/09696791
| Patent No. 6770633
| GENERAL INFORMATION:
| APPLICANT: Robbins, Joan M. |
| APPLICANT: Tritz, Richard |
| TITLE OF INVENTION: SKIN AND EYE DISEASES |
| TITLE OF INVENTION: SKIN AND EYE DISEASES |
| TITLE OF INVENTION: WINNER: US/09/696, 791 |
| CURRENT APPLICATION NUMBER: US/09/696, 791 |
| CURRENT FILING DATE: 2000-10-25 |
| NUMBER OF SEQ ID NOS: 4523 |
| SSQ ID NO 4484 |
| LENGTH: 21
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         Sequence 12, Application US/08863639A

Patent No. 5981185

GENERAL INFORMATION:
APPLICANT: Matson, Robert S.
APPLICANT: Rampal, Jang B.
APPLICANT: Coassin, Peter J.
APPLICANT: Cassin, Peter J.
APPLICANT: Cassin, Deter J.
APPLICANT: Cassin, Deter J.
APPLICANT: Cassin, Deter J.
APPLICANT: Cassin, Deter J.
APPLICANT: Cassin, Peter J.
APPLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: PDGF A ribozyme recognition site US-09-696-791-4484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 14.2; DB 2;
Pred. No. 6.1e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: Windows 95
SOFTWARE: COTE! WordPerfect 8 version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,639A
FILING DATE: May 28, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435.
ATORNEY/AGENT INFORMATION:
NAME: JOSEPH E. Mueth
REGISTRATION NUMBER: 20,532
REFERENCE/POCKET NUMBER: 118
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGGGAGGGAGGGG 20
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Best Local Similarity 84.2%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (626) 795-6321
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 base pairs
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EDNESS: single
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ORGANISM: Homo sapien
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US-08-863-639A-12
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Query Match 71.0%; Score 14.2; DB 6; Length 23; Best Local Similarity 84.2%; Pred. No. 6.1e+03; Matches 16; Conservative 0; Mismatches 3; Indels
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: 19921211

CLASSIFICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 05 07/808,452

FILING DATE: 13-DEC-1991

ATTOMNEY/AGENT INFORMATION:

NAME: Fabian, Cary R.

REGISTRATION NUMBER: 33,875

REFRENCE/DOCKET NUMBER: 32,875

REFRENCE/DOCKET NUMBER: 92,962

TELEPHONE: (415) 89-3880

TELEFAN: (415) 89-3880

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LEMOTH: 23 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INDIVIDUAL ISOLATE: SINGLE STRAND OLIGONUCLEOTIDE, INDIVIDUAL ISOLATE: 12/C-1
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10792
FILING DATE: 19921211
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Sequence 13, Application PC/TUS9210792
SERNERAL INFORMATION:
APPLICANT: Jayasena, Sumedha D.
APPLICANT: Johnston, Brian H.
TITLE OF INVENTION: Triple Helix Formation at TITLE OF INVENTION: (PuNPyN) - (PuNPyN) Tracts
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSED:
ADDRESSED:
STREET: 333 Ravenswood Avenue
CITY: Menlo Park
                                                                                                                                                                                                                                                                                                        IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                          ADDRESSEE: SRI International
STREET: 333 Ravenswood Avenue
CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GGGGAGGGAGGGG 20
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                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                   ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC OPERATING SYSTEM:
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                                                                                                                                                                                      COUNTRY:
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                          71.0%; Score 14.2; DB 3; Length 21; 84.2%; Pred. No. 6.1e+03; Live 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

SUSTRANES: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/808,452

FLING DATE: 19911213

CLASSIFICATION: 514

ATTORNEY AGENT INFORMATION:

NAME: Fabian, Gary R.

REFERENCE/DOCKET NUMBER: 8255-008

TELEPHONE: (415) 324-0880

TELEPHONE: (415) 324-0960

INFORMATION FOR SEQ ID NO: 15:

SEQUINCE CHARACTERISTICS:

LENGTH: 23 base pairs

TYPE: NUCLEIC ACID

TYPE: NUCLEIC ACID

TYPE: NUCLEIC ACID

TYPE: ACID

TYPE: NUCLEIC ACID

TYPE: NUCLEIC ACID

TO THE TYPE: T
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                                                                                                                                                                                                                                                                                                    RESULT 38
US-07-806-452-15
Jeguence 15, Application US/07808452
Patent No. 6063612
GENERAL INFORMATION:
APPLICANT: Jayasena, Sumedha D.
TITLE OF INVENTION: Antiviral Reagents Based on TITLE OF INVENTION: RNA-Binding Proteins
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 39
PCT-US92-10770-15
Sequence 15, Application PC/TUS9210770
SERVERAL INFORMATION:
APPLICANT: Jayasena, Sumedha D.
APPLICANT: Johnston, Brian H.
TITLE OF INVENTION: Antivixal Reagents Based on TITLE OF INVENTION: RNA-Binding Proteins
                                                                                                                                                        2 GGGGAGGGAGGGGG 20
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             Query Match
Best Local Similarity 84.29
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16; Conservative
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Matches 16; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 49, Application US/08486421
| Patent No. 5672479
| GENERAL INFORMATION:
| APPLICANT: JOHNSON, Edward M. APPLICANT: JOHNSON, CLONING AND EXPRESSION OF PUR PROTEIN INTERPRESSION OF PUR PROTEIN CORRESPONDENCES: 51
| CORRESPONDENCES: 51
| CORRESPONDENCES: 61
| ADDRESSEE: Pennie & Edmonds |
| STREET: 1155 Avenue of the Americas |
| CITY: New York
                                                                                                        Length 24;
                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,421
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION WHERE: WS 08/470,911
FILING DATE: 06-JUN-1995
ATPONENTAGEN OF JUN-1995
ATPONENTAGENT INFORMATION:
                                                                                                  Query Match 71.0%; Score 14.2; DB 2; Best Local Similarity 84.2%; Pred. No. 6.1e+03; Matches 16; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 71.0%; Score 14.2; DB 2; Best Local Similarity 84.2%; Pred. No. 6.1e+03; Matches 16; Conservative 0; Mismatches 3;
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TELEPAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-470-911-49
; Sequence 49, Application US/08470911
; Patent No. 5756684
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GGGGAGGGAGGGGG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742 REFERENCE/DOCKET NUMBER: 69,742 TELECOMMUNICATION INFORMATION:
                       MOLECULE TYPE: DNA (genomic) US-08-014-943A-7
unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA
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TOPOLOGY:
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US-08-014-943A-7

Eaquence No. 554551

GENERAL INFORMATION.

APPLICANT: Johnson, Edward M.

APPLICANT: Johnson, Edward M.

APPLICANT: Bergemann, Andrew D.

TITLE OF INVENTION: Cloning And Expression Of PUR Protein NUMBER OF SEQUENCES: 26

CORRESPONDENCES: 26

CORRESPONDENCES: 26

CORRESPONDENCES: Aborne of the Americas

CITY: New York

STATE: New York

COMPUTR: IN S.A.

ZIP: 10036-2711

COMPUTR: READABLE FORM:

MEDIUM TYPE: Flopyy disk

COMPUTR: Patentin Release #1.0, Version #1.25

CURENT APPLICATION DATA:

APPLICATION NUMBER: US/08/014,943A

FILING DATE: 02)FEB)1992

CLASSIFICATION NUMBER: US/08/014,943A

FILING DATE: 02)FEB)1992

CLASSIFICATION NUMBER: 0530-333

FELEFARAION NUMBER: 0530-333

TELEFANCE IN NUMBER: 0530-341

TELEFANCE IN NUMBER: 0530-341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 71.0%; Score 14.2; DB 6; Length 23; Best Local Similarity 84.2%; Pred. No. 6.1e+03; Matches 16; Conservative 0; Mismatches 3; Indels
                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/826,934
FILING DATE: 21-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,452
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pabian, Gary R.
REGISTRATION NUMBER: P-3141
TELEFONEY (415) 859-4550
TELEFONEY (415) 859-4560
TELEFONEY (415) 859-380
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: NUCLEIC ACID
STRANDENNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: FIGURE 10, C-1
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LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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NAME: COLUZZI, LAULA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6923-053
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
TELEX: 65141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 31, Application US/08960190A, Patent No. 6232445, GENERAL INFORMATION:
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CITY: Boston
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 84.2
Matches 16; Conservative
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TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA
US-08-486-809-49
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US-08-960-190A-31
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STATE:
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| Patent No. 5869622
| Patent No. 5869622
| Patent No. 5869622
| JOHNSON, Edward M. APPLICANT: Johnson, Edward M. APPLICANT: Bergemann, Andrew D. TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN NUMBER OF SEQUENCES: 51
| CORRESPONDENCE ADDRESS: ADDRESSE: Pennie & Edmonds STREET: 1155 Avenue of the Americas CITY: New York STREET: U.S.A. U.S.A. STREET: New York COUNTRY: U.S.A. STREET: New York COUNTRY: IN SALDABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER REALABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IR MP C compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
| CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/486,809
| FLING DATE: U-UTN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.0%; Score 14.2; DB 2; Length 24; 84.2%; Pred. No. 6.1e+03; Live 0; Mismatches 3; Indels
  Bergemann, Andrew D. VENTION: CLONING AND EXPRESSION OF PUR PROTEIN
  APPLICANT: Bergemaun, Anderson of PUR PROT ITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROT NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds STREET: 1155 Avenue of the Americas CITY: New York STATE: New York COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER: New York COMPUTER: IDOS COMPUTER: TRADABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: D6-101
FILING DATE: O6-JUN-1995
CLASSIFICATION NUMBER: 30,742
FILING DATE: CAPACITION: 435
ATTORNEY/AGENT INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9190
TELEPHONE: (212) 869-9741/8864
TTELERA: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 49: SEQUENCE CHARACTERISTICS: LENGTH: 24 base pairs TYPE: nucleic acid STRANDEDRESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,911
FILING DATE: 06-JUN-1995
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Best Local Similarity
Matches 16; Conserv?
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US-08-486-809-49
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71.0%; Score 14.2; DB 2; Length 24; 84.2%; Pred. No. 6.1e+03; Live 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastESEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,190A
FILING DATE: 29-OCT-1997
CLASSIFICATION NATA:
APPLICATION NUMBER:
ATTOMNEY/AGENT INFORMATION:
NAME: COLIGES, PETER F
REGISTRATION NUMBER: 33,860
REGISTRATION NUMBER: 48002
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rhode, Peter R.
APPLICANT: Acevedo, Jorge
APPLICANT: Burkhardt, Martin
APPLICANT: Burkhardt, Martin
APPLICANT: Wong, Hing C.
TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
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(602) 495-9475
                         JS-09-896-650C-26/c
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ZIP: 85016
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Fatent No. 6337188
GENERAL INFORMATION:
Head, Steven R.
APPLICANT: Head, Steven R.
APPLICANT: Goelet, Philip
APPLICANT: Goelet, Dathin
APPLICANT: Rarn, Jonathan
APPLICANT: Boye-Jacino, Michael
CURRENT PRILIG DATE: 2000-08-25
NUMBER OF SEQ ID NOS: 31
SOGTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 26
LENGTH: 25
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                                                                                                                                                                                                                                                                                                                  APPLICANT: Head, Steven R.
APPLICANT: Geolet, Philip
APPLICANT: Geolet, Philip
APPLICANT: Marn, Jonathan
APPLICANT: Marn, Jonathan
APPLICANT: Boyce-Jacino, Michael
TITLE OF INVENTION: De No. 63229680 or "Universal" Sequencing Array
FILE REFERENCE: 04990.0049
CURRENT APPLICATION NUMBER: US/08/976,427A
CURRENT FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PastSEQ for Windows Version 3.0
LENGTH: 25
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Query Match 71.0%; Score 14.2; DB 3; Length 24; Best Local Similarity 84.2%; Pred. No. 6.1e+03; Matches 16; Conservative 0; Mismatches 3; Indels
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84.2%; Pred. No. 6.1e+03;
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WS-00-976-427-26/c

Sequence 26, Application US/08976427A

Patent No. 6322968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FEATURE:
; OTHER INFORMATION: Synthetic primer
US-08-976-427-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) OTHER INFORMATION: Synthetic primer US-09-648-312-26
                                                                                            2 ggggagggagggagggg 20
                                                                                                                          3 GGGSGGGSGGGSGGG 21
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 84.23
Matches 16; Conservative
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Best Local Similarity
Matches 16; Conserv
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RESULT 48

RESULT 49

RESULT 40

RESULT 40
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                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 71.0%; Score 14.2; DB 2; Length 27; Best Local Similarity 84.2%; Pred. No. 6.1e+03; Matches 16; Conservative 0; Mismatches 3; Indels
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SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDDNESS: single
TOPOLOGY: linear
WOLECULE TYPE: Other nucleic acid (synthetic DNA)
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MEDIUM TYPE: Diskette, 5.25 inch, 1.2 Mb
COMPUTER: Packard Bell (IEM PC/AT compatible)
OPERATING SYSTEM: MS-Dos, Version 5.0
SOFTWARE: WordPerfect Version 5.1
APPLICATION DATA:
APPLICATION NUMBER: US/08/208,486
FILING DATE:
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PRIOR APPLICATION DATA:
PREDE APPLICATION DATA:
PREDICATION NUMBER: 07/869,916
FILING DATE: April 14, 1992
APPLICATION NUMBER: Japan 240525/91
FILING DATE: August 26, 1991
ATTORNEY/AGENT INPORMATION:
NAME: Janelle Faunce Raupp
REGISTRATION NUMBER: 30,485
REFERENCE/DOCKET NUMBER: #3954-A-7
TELECOMMINICATION INFORMATION:
TELEPAN: (602) 956-7000
TELEPAN: (602) 956-700
TELEPAN: (602) 956-700
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
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TYPE: nucleic acid
STRANDEDNESS: single
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Search completed: February 15, 2006, 21:14:25 Job time : 47.9587 secs

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               GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
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US-00-781-986A-2153
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Maximum Match 100%
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US-10-831-778-531  US-10-831-778-531  US-10-831-778-987  US-10-838-659-55  US-10-838-659-55  US-10-838-659-55  Sequence US-10-838-8128-13  US-10-661-402-13  SEQUENCE US-10-969-812A-13  SEQUENCE US-10-969-812A-13  SEQUENCE US-10-969-812A-13  SEQUENCE US-10-969-812A-13  SEQUENCE US-10-969-812A-13  SEQUENCE US-10-969-963  SEQUENCE US-10-969-963  SEQUENCE US-10-969-963  SEQUENCE US-10-112-653-91  SEQUENCE US-10-956-157-133-69  SEQUENCE US-10-96-157-133-69  SEQUENCE US-10-96-157-158-158  SEQUENCE US-10-96-157-1	6 US-10-314-578-1096 Sequence 1 US-10-433-899-9 Sequence 2 US-10-689-745-55 Sequence 9 US-10-6849-491-4 Sequence 9 US-10-6849-491-5 Sequence 3 US-09-88-326-172 Sequence 3 US-09-776-479-771 Sequence 5 US-10-017-995-771 Sequence 5 US-10-017-995-771 Sequence 5 US-10-017-995-771 Sequence 0 US-10-017-995-771 Sequence 0 US-10-017-995-771 Sequence 0 US-10-017-995-771 Sequence 0 US-10-034-578-771 Sequence 0 US-10-034-578-771 Sequence 0 US-10-034-578-771 Sequence 0 US-10-034-578-771 Sequence 0 US-10-405-158-1 Sequence 0 US-10-405-158-1 Sequence 0 US-10-66-088-21 Sequence 1 US-10-66-088-21 Sequence 1 US-10-66-088-21 Sequence 1 US-10-66-097-22 Sequence 1 US-10-66-097-21 S
71.0 20 8 US-10-831-778-931 Sequence 71.0 20 8 US-10-831-778-987 Sequence 71.0 20 8 US-10-831-778-987 Sequence 71.0 20 8 US-10-831-778-987 Sequence 71.0 20 9 US-10-661-402-14 Sequence 71.0 20 9 US-10-661-402-14 Sequence 71.0 20 9 US-10-661-403-14 Sequence 71.0 20 9 US-10-661-403-13 Sequence 71.0 24 3 US-9-76-479-428 Sequence 71.0 24 3 US-9-776-479-963 Sequence 71.0 24 3 US-9-776-479-963 Sequence 71.0 24 5 US-10-112-653-410 Sequence 71.0 25 3 US-9-9-86-650A-26 Sequence 71.0 25 3 US-9-9-86-86-650A-26 Sequence 71.0 25 3 US-9-9-86-86-650A-26 Sequence 71.0 25 3 US-9-9-86-86-86-86-86-86-86-86-86-86-86-86-86-	71.0 30 6 US-10-314-578-1096 Sequence 71.0 30 9 US-10-433-899-9 Sequence 71.0 30 9 US-10-433-899-9 Sequence 71.0 32 9 US-10-849-91-5 Sequence 71.0 32 9 US-10-849-491-5 Sequence 71.0 35 3 US-09-888-326-172 Sequence 71.0 35 3 US-09-776-479-771 Sequence 71.0 35 3 US-09-776-479-771 Sequence 71.0 35 5 US-10-112-653-744 Sequence 71.0 35 5 US-10-112-653-744 Sequence 71.0 35 5 US-10-112-653-744 Sequence 71.0 35 6 US-10-017-995-771 Sequence 71.0 35 6 US-10-017-995-771 Sequence 71.0 35 6 US-10-314-578-771 Sequence 71.0 35 6 US-10-314-578-771 Sequence 71.0 37 6 US-10-317-78-771 Sequence 71.0 37 6 US-10-405-158-4 Sequence 71.0 37 6 US-10-405-158-4 Sequence 71.0 37 6 US-10-795-667-124 Sequence 71.0 38 8 US-10-797-3133-52 Sequence 71.0 40 7 US-10-661-088-21 Sequence 71.0 40 7 US-10-661-098-21 Sequence 71.0 40 7 US-10-661-097-21 Sequence 71.0 40 7 US-10-661-097-21 Sequence 71.0 40 7 US-10-661-097-21 Sequence
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Gaps

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Query Match 100.0%; Score 20; DB 3; Length 20; Best Local Similarity 100.0%; Pred. No. 3e+02; Matches 20; Conservative 0; Mismatches 0; Indels

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; OTHER INFORMATION: Synthetic Sequence US-09-776-479-906

TYPE: DNA ORGANISM: Artificial Sequence

FEATURE:

FILE REFERENCE: C1037/7013 (HCL/WAT)
CURRENT APPLICATION NUMBER: US/09/776,479
CURRENT FILING DATE: 2001-02-02
FRIOR APPLICATION NUMBER: US 60/179,991
FRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
SERIOR NO 906
LENGTH: 20

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Sequence 3759, Ap Sequence 22, Appl Sequence 14, Appl Sequence 17, Appl Sequence 13541, Sequence 176142, Sequence 261177, Sequence 155953, Sequence 155953,
                                                                                                                                                                                                           23, Appl
26, Appl
26, Appl
34, Appl
3759, Ap
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Sequence 166862,
Sequence 198478,
Sequence 228006,
Sequence 250515,
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Sequence 240365,
Sequence 249309,
Sequence 279389,
Sequence 279353,
                                114, App
2, Appli
2, Appli
1882, Ap
3, Appli
2, Appli
24, Appl
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Sequence 26, Appl
                                                                                                        1085, Ap
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Sequence 183495,
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US-10-307-724-114

US-10-312-390-114

US-10-723-947-2

US-09-949-744-3

US-09-949-748-3

US-09-949-748-2

US-09-949-768-2

US-09-949-702-24

US-10-849-072-24

US-10-849-072-24

US-10-849-072-24

US-10-949-76-1086

US-10-949-76-1086

US-10-949-76-1086

US-10-949-76-1086

US-10-949-76-1086

US-10-98-919-38

US-09-932-300-31

US-10-9776-479-559

US-09-932-300-23

US-09-932-300-23

US-10-112-653-559

US-10-112-653-559

US-10-99-22-117

US-10-919-042-26

US-10-956-157-176142

US-10-956-157-176142

US-10-956-157-176142

US-11-036-317-155963

US-11-036-317-155963

US-11-036-317-1569159

US-11-060-756-249399

US-11-060-756-249399

US-11-060-756-229353

US-11-060-756-229353

US-11-060-756-229353
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## ALIGNMENTS

Sequence 906, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Brateler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immanostimulatory Nucleic Acids for the TITLE OF INVENTION: Treatment of Asthma and Allergy

US-09-776-479-906

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US-10-112-653-875
; Sequence 875, Application US/10112653
; Publication No. US2000050268A1
; Publication No. US2000050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Rerg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AMS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
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  Sequence 406, Application US/09776479
; Sequence 406, Application US/09776479
; Publication No. US2040067902A9
; Fublication No. US20400667902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Pouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acide for the
; TITLE OF INVENTION: Immunostimulatory Nucleic Acide for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: CLO37/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2000-02-03
; RIOR FILING DATE: 2000-02-03
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 906
; LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 20; DB 3; Length 20; 100.0%; Pred. No. 3e+02; ative 0; Mismatches 0; Indels
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Matches 20; Conserv
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TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
FILE REFERENCE: C1037/7025 (HCL/MAT)
CURRENT APPLICATION UNBER: US/10/017,995
CURRENT FILING DATE: 2001-12-18
PRIOR PELLANG DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 1093
SEG ID NO 906
LENGTH: 20
                                                                                                                                                                                      100.0%; Score 20; DB 5; Length 20; 100.0%; Pred. No. 3e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Krieg, Arthur M.
APPLICANT: Schetter, Christian
APPLICANT: Schetter, Christian
APPLICANT: Vollmer, Jones
TITLE OF INVENTION: Immunostimulatory Nucleic Acids
FILE REPERENCE: C1039/7035 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/10/314,578
CURRENT APPLICATION NUMBER: US 60/156,113
PRIOR FILING DATE: 1999-09-25
PRIOR FILING DATE: 1999-09-27
PRIOR FILING DATE: 1999-09-27
PRIOR FILING DATE: 2999-09-27
PRIOR FILING DATE: 2000-08-23
                                                                                                                         ; OTHER INFORMATION: Synthetic Oligonucleotide US-10-112-653-875
SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 875 LENGTH: 20
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SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 906
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Synthetic Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 906, Application US/10017995; Publication No. US20030055014A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 906, Application US/10314578 Publication No. US20030212026A1 GENERAL INFORMATION:
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                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Matches 20; Conservative
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Matches 20; Conservative
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US-10-010-920-43

| Sequence 43, Application US/10010920 |
| Publication No. US20030027165A1 |
| Publication No. US20030027165A1 |
| APPLICANT: Saus, Juan |
| TITLE OF INVENTION: Alternatively spliced polk nucleotide and amino acid sequences |
| TITLE OF INVENTION: and methods for using |
| FILE REFERENCE: 98,723-E3 |
| CURRENT APPLICATION NUMBER: US/10/010,920 |
| PRIOR FILING DATE: 2001-12-07 |
| PRIOR FILING DATE: 2000-12-08 |
| NUMBER OF SEQ ID NOS: 102 |
| SOFTWARE: PatentIn Ver. 2.0 |
| LENGTH: 30 |
| SEQ ID NO 43 |
| LENGTH: 2000-12-08 |
| LENGTH: 30 |
| LENGTH: 
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Sequence 906, Application US/10831778

Sequence 906, Application US/10831778

Publication No. US20040235774A1

GENERAL INFORMATION:

APPLICANT: Bratzler, Robert L.

APPLICANT: Fouron, Ves

TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the

TITLE OF INVENTION: Treatment of Asthma and Allergy

FILE REFERENCE: C1037/7013 (HCL/MAI)

CURRENT APPLICATION NUMBER: US/10/831,778

CURRENT FILING DATE: 2000-02-03

PRIOR FILING DATE: 2000-02-03

FRIOR FILING DATE: 2000-02-03

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 906

LENGTH: 20
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94.7%; Pred. No. 2.2e+03;
tive 0; Mismatches 1; Indels
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                                                                                                                                                                 Score 20; DB 6;
Pred. No. 3e+02;
                                                                                                                                                                 Query Match
100.0%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 3e+
Matches 20; Conservative 0; Mismatches
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Pred. No. 3
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Synthetic Sequence US-10-831-778-906
                                                                                                                                                                                                                                                                                                                                                                                                          1 AGGGGAGGGGAGGGG 20
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Best Local Similarity 100.0%;
Matches 20; Conservative 0
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ORGANISM: Artificial Sequence
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Best Local Similarity
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TYPE: DNA
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Sequence 159, Application US/10971736

Publication No. US20050227251A1

GENERAL INFORMATION:

APPLICANT: denen, kirk

APPLICANT: jeneen, kirk

TITLE OF INVENTION METHOD OF PURIFYING RNA BINDING PROTEIN-RNA COMPLEXES

TITLE OF INVENTION NUMBER: US/10/971,736

CURRENT APPLICATION NUMBER: US/10/971,736

CURRENT FILING DATE: 2004-10-25

NUMBER OF SEQ ID NOS: 509

SOFTWARE: Patentin version 3.2

SEQ ID NO 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: Primer ON-TATADE1
US-10-008-721-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                    APPLICANT: Saus, Juan
TITLE OF INVENTION: TNF-Inducible Promoters and Methods for Using
FILE REFERENCE: 98,723-E1
CURRENT APPLICATION NUMBER: US/10/008,721
CURRENT FILING DATE: 2001-12-07
PRIOR PILING DATE: 2001-12-08
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 43
LENGTH: 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.0%; Score 17.4; DB 5; Length 30;
94.7%; Pred. No. 2.2e+03;
tive 0; Mismatches 1; Indels
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Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Rowen, Lery E.
                                                                                                                            ; Sequence 43, Application US/10008721; Publication No. US20030082745A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 AGGGGAGGGAGGGGTGGG 20
1 AGGGGAGGGGAGGG 19
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Best Local Similarity 94.7°
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
US-09-263-959-699/c
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                                                                                                               US-10-008-721-43
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APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSER: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SSCTWARE: PatentIn version 3.2
LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.0%; Score 16.8; DB 3; Length 23; 90.0%; Pred. No. 3.9e+03; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 220152, Application US/11060756 Ubblication No. US20050221354A1 GENERAL INFORMATION:
APPLICANT: Wyeth
                                                                                                                                                                                                                                                                                                                                            FILING DATE: 05-MAR-1999
TORNEY PARENT OS-MAR-1999
TORNEY PARENT OS-MAR-1999
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NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFRENCE/DOCKET NUMBER: 9200
TELECOMMUNICATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 GGGAGGGAGGGAGGGG 20
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 90.0°
Matches 18, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
EDNESS: single
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: US
                                                                                                            STREET: 6300 COLUCITY: Seattle STATE: Washingtor COUNTRY: US ZIP: 98104-7092
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Matches 17; Conserv
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US-11-060-756-220152
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US-11-060-756-220152
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US-09-263-959-699
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Publication No. US20040043037A1
GENERAL INFORMATION:
GILH. Charles Kunsch
GILH. Choi
Patrick S. Dillon
Craig A. Rosen
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
  Sequence 2153, Application US/08781986A
Publication No. US20030054426A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
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ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCIT Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
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TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 2153:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB24
TELECOMMUNICATION INFORMATION:
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Best Local Similarity 89.5-
Thes 17; Conservative
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US-08-781-986A-2153/c
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US-10-329-624-2153/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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Sequence 923, Application US/09263959

Sequence 923, Application US/09263959

Sequence 923, Application US/09263959

Sequence 923, Application US/09263959

Sequence 923, Application US/0920163959

APPLICANT: Nowen, Lee

APPLICANT: Rowen, Lee

APPLICANT: Read and Berry LLP

CORRESPONDENCE ADDRESS:

ADDRESSES: Seed and Berry LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seatle

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seatle

STREET: 6300 Columbia Center, 701 Fifth Avenue

COUNTRY: US

COUNTRY: US

COUNTRY: US

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC COMPUT
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR.1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MOMBAGERE, David D.
REGISTRATION NUMBER: 33,963
REGISTRATION NUMBER: 920010.426C2
TELEPHONE: (206) 622-4900
                                 SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Mark J. Hyman
REGISTRATION NOWBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear SEQ ID NO: 2153: US-10-329-624-2153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 2153:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GGGGAGGGAGGGGG 20
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STRANDEDNESS: double
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
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Sequence 41, Application US/10407449
Publication No. US20040005601A1
GENERAL INFORMATION:
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METHYLTRANSFERASE AND METHODS FOR USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSE: Merchant, Gould, Smith, Edell, Welter & Schmidt STREET: 11150 Santa Monica Boulevard, Suite 400 CITY: Los Angeles STATE: CA
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                                                                                                            Query Match 79.0%; Score 15.8; DB 3; Length 19; Best Local Similarity 89.5%; Pred. No. 9.3e+03; Matches 17; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.0%; Score 15.8; DB 5; Length 26; 89.5%; Pred. No. 8.4e+03; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIE: 90025

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: DISKETS
SOFTWARE: FASTEM: DOS
SOFTWARE: FASTESE for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/10/010,476
FILING DATE: 07-Dec-2001
CLASSIFICATION CURROWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/485,071
FILING DATE: 12-Jun-1998
APPLICATION NUMBER: 60/057,411
FILING DATE: 29-AUG-1997
ATTORNEY/AGRAT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 Sequence 38, Application US/10010476
Publication No. US20030114402A1
GENERAL INFORMATION:
APPLICANT: Flynn, James
Flynn, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Canady, Karen S
REGISTRATION UNDRER: 39,927
REFERENCE/DOCKET NUMBER: 30794.30W001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 38:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 310 445-1140
TELEFAX: 310 445-9031
                                                                                                                                                                                                                                1 GGGCGGGGAGGGCGGGG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 38: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 89.5:
Matches 17; Conservative
    ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                          RESULT 15
US-10-010-476-38
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RESULT 16 US-10-407-449-41

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US-10-407-449-44

Sequence 44, Application US/10407449

Publication No. US20040005601A1

GENERAL INFORMATION:
APPLICANT: Hutley, Laurence
APPLICANT: Farrell, Thomas
APPLICANT: Beares, David
TITLE OF INVENTION: METHODS FOR TARGETING QUADRUPLEX DNA
FILE REPERENCE: 53223-20004.00
CURRENT APPLICATION NUMBER: US/10/407,449

CURRENT PILING DATE: 2003-04-04

PRIOR PELICATION NUMBER: US 60/404,966

PRIOR PELICATION NUMBER: US 60/370,358

PRIOR PILING DATE: 2002-08-04

PRIOR FILING DATE: 2002-08-05

PRIOR FILING DATE: 2002-08-05

PRIOR FILING DATE: 2003-03-20

NUMBER: OF SEQ ID NOS: 64

SOFTWARE: FSALSEQ for Windows Version 4.0

SEQ ID NO 44

LENGENT NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.0%; Score 15.2; DB 6; Length 22; llarity 85.0%; Pred. No. 1.4e+04; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 76.0%; Score 15.2; DB 6; Length 22; Best Local Similarity 85.0%; Pred. No. 1.4e+04; Matches 17; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Generalized quadruplex structure for RET
US-10-407-449-41
APPLICANT: Siddiqui-Jain, Adam
APPLICANT: Hurley, Laurence
APPLICANT: Farrell, Thomas
APPLICANT: Farrell, Thomas
APPLICANT: Farrell, Thomas
APPLICANT: Bearse, David
TITLE OF INVENTION: METHODS FOR TARGETING QUADRUPLEX DNA
FILE REFERENCE: 53223-20004,00
CURRENT APPLICATION NUMBER: US/10/407,449
CURRENT APPLICATION NUMBER: US 60/404,966
PRIOR APPLICATION NUMBER: US 60/404,966
PRIOR FILING DATE: 2002-08-04
PRIOR PLILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: US 60/370,358
PRIOR PLILING DATE: 2003-03-04
PRIOR PLILING DATE: 2003-03-04
NUMBER OF SEQ ID NOS: 64
SOPTWARE: FeatsEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 17; Conserv
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1 Accedecedecedecedes 20
TYPE: DNA
ORGANISM: Zea mays
US-10-931-077-28
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                                                                                                                            US-10-12/248/-5

Sequence 5, Application US/10820487

Fublication No. US20050004160A1

GENERAL INFORMATION:

APPLICANT: WHITTEN, Jeffrey P.

APPLICANT: WHITTEN, TETRANCE

ITILE OF INVENTION: 1,4-DIMYDRO-4-OXO-1,8-NAPTHTHYRIDINE ANALOGS

TITLE OF INVENTION: 1,4-DIMYDRO-4-OXO-1,8-NAPTHTHYRIDINE ANALOGS

FILE REFERENCE: 5322320001200

TITLE OF INVENTION: 1,6-DIMYDRO-4-OXO-1,8-NAPTHTHYRIDINE ANALOGS

FILE REFERENCE: 5322320001200

CURRENT APPLICATION NUMBER: US 60/461,205

PRIOR APPLICATION NUMBER: US 60/461,205

PRIOR APPLICATION NUMBER: US 60/519,569

PRIOR PILING DATE: 2003-04-07

PRIOR PILING DATE: 2003-11-12

NUMBER OF SEQ ID NOS: 20

SOFTWARE FABELSEQ for Windows Version 4.0

SEQ ID NO 5

LENGTH: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 15.2; DB 8; Length 22; Pred. No. 1.4e+04; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ### Sequence 5, Application US/10903975
### Sequence 5, Application US/10903975
### Publication No. US20050085468A1
### GENERAL INFORMATION:
### APPLICANT: WHITTEN, Jeffrey P.
### APPLICANT: SCHWAEBE, Michael
### APPLICANT: SIDDIQUI-JAIN, Adam
### APPLICANT: MORAN, Terrance
### TILE OF INVENITON: SUBSTITUTED QUINOBENZOXOZINE ANALOGS
### TILE REFERENCE: 532132001120
### CURRENT APPLICATION NUMBER: US/10/903,975
### CURRENT PILING DATE: 2004-07-07
### PRIOR PILING DATE: 2003-04-07
### PRIOR PILING DATE: 2003-04-15
### PRIOR PILING DATE: 2003-11-12
### PRIOR PILING DATE: 2003-12-23
### WUMBER OF SEQ ID NOS: 20
### WUMBER OF SEQ ID Windows Version 4.0
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        1 AGGGGGGGGGGGGGGG 20
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85.0%;
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Best Local Similarity 85.0%;
Matches 17; Conservative (
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Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA; ORGANISM: Homo sapiens US-10-820-487-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
CRGANISM: Homo sapiens
US-10-903-975-5
                                                                                    RESULT 18
US-10-820-487-5
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APPLICANT: Multani, Dilbag
APPLICANT: Multani, Dilbag
APPLICANT: Multani, Dilbag
APPLICANT: Niu, Xiaomu
APPLICANT: Niu, Xiaomu
APPLICANT: Tomes, Dwight T
APPLICANT: Wang, Halvin
APPLICANT: Xu, Deping
TITLE OF INVENTION: BRZ AND DW3 PROMOTERS AND METHODS OF USE
FILE REFERBNCE: 035718/281933
CURRENT APPLICATION NUMBER: US/10/931,077
CURRENT FILING DATE: 2004-08-31
PRIOR APPLICATION NUMBER: 60/499,580
PRIOR FILING DATE: 2003-09-02
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: RET quadruplex-forming nucleotide sequence US-10-407-449-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 15.2; DB 9; Length 27;
Pred. No. 1.4e+04;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 76.0%; Score 15.2; DB 6; Length 24; Best Local Similarity 85.0%; Pred. No. 1.4e+04; Matches 17; Conservative 0; Mismatches 3; Indels
                                                                     GENERAL INFORMATION:

APPLICANT: Siddiqui-Jain, Adam
APPLICANT: Siddiqui-Jain, Adam
APPLICANT: Starell, Thomas
APPLICANT: Farrell, Thomas
APPLICANT: Farrell, Thomas
APPLICANT: Barned, Cory,
APPLICANT: Bersels, David
TITLE OF INVENTION: METHODS FOR TARGETING QUADRUPLEX DNA
FILE REFERENCE: 5323-20004.00
CURRENT APPLICATION NUMBER: US 60/404,966
PRIOR FILING DATE: 2002-04-05
PRIOR FILING DATE: 2002-06-04
PRIOR FILING DATE: 2002-06-05
PRIOR PLING DATE: 2002-04-05
PRIOR PLING DATE: 2003-03-20
NUMBER OF SEQ ID NOS: 64
SEQ ID NOS: 64
LENGTH: 24
Sequence 43, Application US/10407449
Publication No. US20040005601A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 28, Application US/10931077
Publication No. US20050204432A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AGGGGAGGGGAGGGG 20
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85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 85.01
Matches 17; Conservative
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US-10-239-176-4/c

| US-10-239-176-4/c
| Sequence 4, Application US/10239176
| Sequence 4, Application No. US20040086856A1
| Sequence 4, Application No. US2004008685A1
| Sequence 4, Application No. US2004008685A1
| GENERAL INFORMATION:
| APPLICANT: TAKAHASHI, MASAYOSHI
| APPLICANT: HASHIMANO', KOJI
| TITLE OF INVENTION: NUCLEIC ACID PROBE-IMMOBILIZED SUBSTRATE AND METHOD OF
| TITLE OF INVENTION: DETECTING THE PRESENCE OF TARGET NUCLEIC ACID BY USING THE SAME
| TITLE OF INVENTION: NUMBER: US/10/239,176
| CURRENT FILING DATE: 2003-03-19
| PRIOR FILING DATE: 2002-03-69
| PRIOR APPLICATION NUMBER: PCT/JP02/08670
| PRIOR APPLICATION NUMBER: DET/JP02/08670
| PRIOR PILING DATE: 2002-07-26
| PRIOR PILING DATE: 2002-07-26
| PRIOR FILING DATE: 2002-07-26
| SOFTWARE: Patentin version 3.1
| SEQ ID NO 4
| LENGTH: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 443, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Rowen, Leroy E.
APPLICANT: Rowen, Leroy E.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PATENTIN Release #1.0, Version #1.25
GURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 76.0%; Score 15.2; DB 7; Best Local Similarity 85.0%; Pred. No. 1.1e+04; Matches 17; Conservative 0; Mismatches 3;
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NAME: McMateers, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 AGGGGGGGGGGGGGGGG 11
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        21 AGGGGGGGGGGGGGGG 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Seattle
STATE: Washingt
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 0:
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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Sequence 3, Application US/10239176

Publication No. US2004008686A1

GENERAL INFORMATION:
APPLICANT: TAKAHASHI, MASAYOSHI

APPLICANT: OKADA, JUN

APPLICANT: OKADA, JUN

TITLE OF INVENTION: NUCLEIC ACID PROBE-IMMOBILIZED SUBSTRATE AND METHOD OF

TITLE OF INVENTION: DETECTING THE PRESENCE OF TARGET NUCLEIC ACID BY USING THE SAME

FILE REPERENCE: 228763USOSRDPCT

CURRENT FILING DATE: 2003-03-19

PRIOR APPLICATION NUMBER: DCT/JP02/08670

PRIOR APPLICATION NUMBER: DCT/JP02/08670

PRIOR FILING DATE: 2002-07-26

NUMBER OF SEQ ID NOS: 18

SEQ ID NO 3

LENGTHA: 39

LENGTH: 39
                                                                                                                                                                                                                                                    APPLICANT: ANALYSINA FACALOSIII
APPLICANT: ANALYSINA FACALOSIII
APPLICANT: ASHIMOTO, KOJI
TITLE OP INVENTION: NUCLBIC ACID PROBE-IMMOBILIZED SUBSTRATE AND METHOD OF
TITLE OP INVENTION: DETECTING THE PRESENCE OF TARGET NUCLEIC ACID BY USING THE SAME
FILE REPERENCE: 228763USOSRDPCT
CURRENT APPLICATION NUMBER: US/10/239,176
CURRENT PLING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: PCT/JP02/08670
PRIOR APPLICATION NUMBER: PCT/JP02/08670
PRIOR APPLICATION NUMBER: DC1/266
NUMBER OF SEQ ID NOS: 18
SEQ ID NOS: 18
SEQ ID NO 13
SEQ ID NO 13
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                                                                                                                                                   Sequence 13, Application US/10239176; Publication No. US20040086856A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AGGGAGGGGAGGGGG 20
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26 AGGGAGAGGAGGAGGGG 7
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                      RESULT 22
US-10-239-176-13/c
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US-10-239-176-3/c
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TITLE OF INVENTION: MODULATORS OF DNA CYTOSINE-5
METHYLTRANSFERASE AND METHODS FOR USE THEREOF
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METHYLTRANSFERASE AND METHODS FOR USE THEREOF
NUMBER OF SEQUENCES: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 11150 Santa Monica Boulevard, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 11150 Santa Monica Boulevard, Suite 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATIOR SYSTEM: DOS
OPERATURE SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/010,476
FILING DATE: 07-Dec-2001
CLASSIFICATION: <UNKnown>
                                                                                                            ; Sequence 55, Application US/10010476
; Publication No. US20030114402A1
; GENERAL INFORMATION:
APPLICANT: Reich, No. US20030114402Albert O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74.0%; Score 14.8; DB 5; 88.9%; Pred. No. 1.9e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Reich, No. US20030114402Albert O. Plynn, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 39,927
REFERENCE/DOCKET NUMBER: 30794.30W001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/485,071
FILING DATE: 12-Jun-1998
APPLICATION NUMBER: 60/057,411
FILING DATE: 29-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 310 445-1140
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10 GGAAGGGAGGGRAGGGG 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: <UNKNOWNY INFORMATION FOR SEQ ID NO: 55: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 110
                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diske
                                                                                                                                                                                                                                                                                                                                                                  CITY: Los Angeles
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                                                                                                                                                                                                                                                                                                                                                                                     STATE: CA
COUNTRY: USA
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Best Local Simi
Matches 16;
                                                                  RESULT 28
US-10-010-476-55
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                                                                                                                                                         ore 15; DB 3; Length 15;
red. No. 1.9e+04;
Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1181, Application US/10035833A

Publication No. U520040072156A1

GENERAL INFORMATION:

APPLICANT: Nakamura, Yuho

APPLICANT: Sexine, Akihiro

APPLICANT: Ida, Aritoshi

APPLICANT: Saito, Osamu

ITLE NEFERRICE: FORS-06904

CURRENT APPLICATION NUMBER: US/10/035,833A

CURRENT FILING DATE: 2001-12-27

NUMBER OF SEQ ID NOS: 7669

SOFTWARE: Patentin version 3.2

SEQ ID NO 1181

LENTH: 41
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Sequence 5376, Application US/10035833A

Publication No. US20040072156A1

GENERAL INFORMATION:

APPLICANT: Nakamura. Yuho

APPLICANT: Saito, Osamu

TITLE OF INVENTION: Detection of Genetic Polymorphisms

TITLE OF INVENTION: Detection of Genetic Polymorphisms

TITLE OF INVENTION: Detection OF Genetic Polymorphisms

CURRENT APPLICATION NUMBER: US/10/035,833A

CURRENT APPLICATION NUMBER: 2001-12-27

NUMBER OF SEQ ID NOS: 7669

SOFTWARE: PatentIn version 3.2

SECTUMENT 32160

SOFTWARE: PatentIn version 3.2
                                                                                                                                         75.0%; Scu-
100.0%; Pre
0; 1
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                                                                                                                                                                                                                                                   5 GAGGGGAGGGAGGG 19
                                                                                                                                                                                                                                                                                             15 GAGGGGAGGGAGGG 1
                                                                                                                                                       Query Match 75.0
Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 88.2
Matches 15; Conservative
                  LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-10-035-833A-1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
                                                                                         linear
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Best Local Similarity
Matches 15; Conserv
                                                           STRANDEDNESS:
TOPOLOGY: lin
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                                                                                                            US-09-263-959-443
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APPLICANT: Socos, John
APPLICANT: Rienhoff, Jr., Hugh
APPLICANT: Rienhoff, Jr., Hugh
APPLICANT: Guida, Marco
APPLICANT: Guida, Marco
APPLICANT: Curran, Mark
TITLE OF INVENTION: Polymorphisms Associated with Ion-Channel Disease
FILE REFERENCE: DNA-33US2
CURRENT APPLICATION NUMBER: US/10/942,561A
CURRENT FILING DATE: 2004-09-15
PRIOR PLILING DATE: 2002-08-20
PRIOR PLILING DATE: 2002-08-20
PRIOR PLILING DATE: 2001-08-20
PRIOR PLILING DATE: 2001-05-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Nakamura, Yuho
APPLICANT: Sekine, Akihiro
APPLICANT: 11da, Aritoshi
APPLICANT: 11da, Aritoshi
APPLICANT: 31da, Aritoshi
APPLICANT: 31da, Osamu
TITLE OF INVENTION: Detection of Genetic Polymorphisms
FILE REFERENCE: FORS-06904
CURRENT APPLICATION NUMBER: US/10/035,833A
CURRENT FILING DATE: 2001-12-27
NUMBER OF SEQ ID NOS: 7669
SOFTWARE: Patentin version 3.2
SEQ ID NO 6318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 74.0%; Score 14.8; DB 9; Best Local Similarity 88.9%; Pred. No. 1.7e+04; Matches 16; Conservative 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: misc_feature
; LOCATION: (21)...(21)
; OTHER INFORMATION: c is present or absent.
US-10-035-833A-6318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6318, Application US/10035833A Publication No. US20040072156A1 GENERAL INFORMATION:
                                                                                                                                                     Sequence 93, Application US/10942561A Publication No. US20050089905A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GGGGAGGGGAGGG 19
2 GGGAGGGAGGGAGGG 19
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Best Local Similarity 88.9%;
Matches 16; Conservative (
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SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-10-942-561A-93
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ORGANISM: Homo sapiens
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                                                                                                                                    US-10-942-561A-93
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LENGTH: 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 93, Application US/10224683
Publication No. US20030162192A1
GRNERAL INFORMATION:
GRNERAL INFORMATION:
Sotos, John
APPLICANT: Sienhoff, Jr., Hugh
APPLICANT: Guida, Marco
APPLICANT: Curran, Mark
TITLE OF INVENTION: Polymorphisms Associated with Ion-Channel Disease
FILE REFERENCE: 4389-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Pred. No. 1.7e+04;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74.0%; Score 14.8; DB 5; Length 26; 88.9%; Pred. No. 1.9e+04; Live 0; Mismatches 2; Indels
                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compartible
COMPUTER: IBM Compartible
COMPUTER: IBM Compartible
COPERATING SYSTEM: DOS
SOFTWARE: Fast680 for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/010,476
FILING DATE: 07-Dec-2001
CLASSIFTCATION: «Unknown»
PRIOR APPLICATION NUMBER: US/09/485,071
FILING DATE: 12-Jun-1998
APPLICATION NUMBER: 60/057,411
FILING DATE: 29-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Canady, Karen S
REGISTRATION NUMBER: 39,927
REFERENCE/DOCKET NUMBER: 30794.30W001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310 445-1140
TELEPHONE: 310 445-9031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/224,683
CURRENT FILING DATE: 2002-01-06
FRIOR APPLICATION NUMBER: 60/314,331
PRIOR PILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 60/378,521
PRIOR FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 185
SOFTWARE: Patentin version 3.1
SEQ ID NO 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 107:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGGGGGAGCGGAGGGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GGGAGGGGAGGGGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 107: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.0%;
88.9%;
  CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: <Unknown>
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Best Local Similarity 88.5
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CORGANISM: Homo sapiens
US-10-224-683-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-010-476-107
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US-10-224-683-93
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APPLICANT: Sheppadd.Liana T.
APPLICANT: Lim, Moon Young
APPLICANT: Lim, Moon Young
APPLICANT: Lim, Moon Young
ITILE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
FILE REPERENCE: 4600-0135.30
CURRENT APPLICATION NUMBER: U$/09/875,453
CURRENT APPLICATION NUMBER: U$ 60/209,549
PRIOR PILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 66
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 72.0%; Score 14.4; DB 3; Length 25; Best Local Similarity 93.8%; Pred. No. 2.7e+04; Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72.0%; Score 14.4; DB 7; Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Neville, Matt
APPLICANT: de Arrdda Indig, Monika
APPLICANT: Cao, Feng
APPLICANT: Oldenburg, Mary C.
APPLICANT: Koelbl, Jim C.
APPLICANT: Aizenstein, Brian D.
APPLICANT: Davey, Keith
TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: FORS-08195
CURRENT APPLICATION NUMBER: US/10/617,070
CURRENT FILING DATE: 2003-07-10
PRIOR PELING DATE: 2003-04-11
PRIOR PLING DATE: 2003-04-11
PRIOR PLING DATE: 2003-04-11
PRIOR PLING DATE: 2002-04-11
NUMBER OF SEQ ID NOS: 529
SOFTWARE: Patentin version 3.2
SEQ ID NO 431
LENGTH: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 431, Application US/10617070 Publication No. US20040096874A1 GENERAL INFORMATION:
       Sequence 66, Application US/09875453
Publication No. US20030027320A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GGGGAGGGGAGGGAG 17
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                                                                                                                                                    Laurance, Megan E
Michelotti, Emil
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                                                                             APPLICANT: Kim, Jungsuh P.
APPLICANT: Starr, Douglas B.
APPLICANT: Tam, Albert W.
                                                                                                                                                                                                    Velligan, Mark D.
                                                                                                                                                                                                                          Latour, Derek R.
Thomas, Rita L.
Kongpachith, Ana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
CORGANISM: Homo sapiens
US-09-875-453-66
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US-09-943-944E-100/c

Sequence 100, Application US/09943944E

Publication No. US20040014036A1

GENERAL INFORMATION:

APPLICANT: Petashne, et al.,

TITLE OF INVENTION: Therefor

FILE REFERENCE: 0342941-0065

CURRENT APPLICATION NUMBER: US/09/943,944E

CURRENT APPLICATION NUMBER: US/09/943,944E

SOFTWARE: PAGE 100 NOS: 238

SOFTWARE: PAGE 100 NOS: 238

SOFTWARE: PAGE 100 NOS: 238

LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.0%; Score 14.8; DB 7; Length 43; 84.2%; Pred. No. 1.6e+04; Live 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: Description of Artificial Sequence:Random; OTHER INFORMATION: nucleotide sequences.
US-09-943-944E-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 72.0%; Score 14.4; DB 3; Length 18; Best Local Similarity 93.8%; Pred. No. 3e+04; Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (32) ... (32)
OTHER INFORMATION: This residue is a non-paired base.
Sequence 9, Application US/10397943;
Publication No. US20040053876A1
GENERAL INFORMATION:
APPLICANT: Turner, David L.
APPLICANT: Yu, Jenn-Yah
TITLE OF INVENTION: SIRNAA and Uses Thereof
FILE REFERENCE: UM-7885
CURRENT APPLICATION NUMBER: US/10/397,943
CURRENT FILING DATE: 2003-03-26
NUMBER OF SEQ ID NOS: 169
SEQ ID NO 9
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(22)
OTHER INFORMATION: n is a, c, g, or u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (42); (43); OTHER INFORMATION: n is a, c, g, or u US-10-397-943-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGGAGGGAGGGAGGGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 dedecedencedecede 23
                                                                                                                                                                                                                                                                                                                       TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GGGAGGGAGGGAGG 18
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                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Synthetic
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Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
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Gaps

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PRIOR APPLICATION NUMBER: US 09/627,249
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 432, Application US/10956507
Publication No. US20050196771A1
GENERAL INFORMATION:
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-956-507-431
                                                                                                                                                                                                                                                                                                                                                     5 GAGGGGAGGGGGG 20
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                              23 GTGGGGAGGGGGGG 38
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                                                                                                                                                                                                                                             Best Local Similarity 93.8 Matches 15; Conservative
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US-10-956-507-432
                                                                                                                                                                                                                Query Match
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                                           Gaps
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                                                                                                                                                                                                                                                                                                                                   Sequence 472.43.4pplication US/10617070
Sequence 472.43.pplication US/10617070
GENERAL INPORMATION:
APPLICANT: Neville, Matt
APPLICANT: de Arruda Indig, Monika
APPLICANT: Geo. Feng
APPLICANT: Cao, Feng
APPLICANT: Cao, Feng
APPLICANT: Cao, Feng
APPLICANT: Aizenstein, Brian D.
AIXENT: Aizenstein, Brian D.
AIXENT: Aizenstein, Brian D.
AIXENSTEING DATE: 2002-04-11
APPLICANT: Aizenstein, Brian D.
AIXENSTEING DATE: 2002-04-11
APPLICANT: Aizenstein, Brian D.
AIXENSTEING DATE: Aixenstein, Brian D.
AIXENSTEING DATE: Ai
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Sequence 431, Application US/10956507
Sequence 431, Application No. US20050196711A1
GENERAL INFORMATION:
APPLICANT: Neville, Matt
APPLICANT: Gao, Feng
APPLICANT: Cao, Feng
APPLICANT: Maizenstein, Brian D.
APPLICANT: Davey, Keith
ITILE OF INVENTION: Characterization of CYP2D6 Genotypes
FILE REFERENCE: FORS-08195
CURRENT APPLICATION NUMBER: US/10/956,507
CURRENT FILING DATE: 2004-10-01
PRIOR APPLICATION NUMBER: 10/411,954
PRIOR PILING DATE: 2003-04-11
PRIOR PLILING DATE: 2003-04-11
PRIOR PLILING DATE: 2003-04-11
PRIOR PLILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 529
SOFTWARE: PatentIn version 3.2
SOFTWARE: PatentIn version 3.2
                                           1; Indels
       93.8%; Pred. No. 2.3e+04; tive 0; Mismatches 1
                                                                                                           5 GAGGGGAGGGGGG 20
                                                                                                                                                      23 GTGGGGAGGGAAGGG 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Synthetic US-10-617-070-432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 93.89
Matches 15; Conservative
       Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                RESULT 37
US-10-617-070-432
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US-10-956-507-431
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Sequence 2, Application US/09916369A
Publication No. US20020058802A1
Publication No. US20020058802A1
Publication No. US20020058802A1
APPLICANT: Dellinger, Douglas J
APPLICANT: Perbost, Michael GM
APPLICANT: Caruthers, Marvin H
APPLICANT: Betley, Jason R
TITLE OF INVENTION: Chemistry
FILE NFERENCE: 10003866-1
CURRENT APPLICATION NUMBER: US/09/916,369A
CURRENT FILING DATE: 2001-07-21
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72.0%; Score 14.4; DB 9; Length 39; 93.8%; Pred. No. 2.3e+04; cive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Nevillo, Matt
APPLICANT: de Arruda Indig, Monika
APPLICANT: Cao, Feng
APPLICANT: Cao, Peng
APPLICANT: Cao, Peng
APPLICANT: Oldenburg, Mary C.
APPLICANT: Koelbl, Jim C.
APPLICANT: Azenstein, Brian D.
APPLICANT: Azenstein, Brian D.
APPLICANT: Davey, Keith
TITLE OF INVENTION: Characterization of CYP2D6 Genotypes
FILE REFERENCE: FORS-08195
CURRENT PELLORITON NUMBER: US/10/956,507
CURRENT FILING DATE: 2004-10-01
PRIOR FILING DATE: 2003-07-10
PRIOR FILING DATE: 2003-04-11
PRIOR FILING DATE: 2003-04-11
PRIOR FILING DATE: 2003-04-11
PRIOR PLILING DATE: 2003-04-11
PRIOR PLILING DATE: 2003-04-11
SROFTWARE: PatentIn version 3.2
SOFTWARE: PatentIn version 3.2
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; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-895-007A-133
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Best Local Similarity
Matches 16; Conserv
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US-09-920-313-133
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APPLICANT: Brailly.
APPLICANT: Betersen, Deanna M.
TITLE OF INVENTION: Immunostimulatory Nucleic Acids and
TITLE OF INVENTION: Cancer Medicament Combination Therapy for the Treatment of
TITLE OF INVENTION: Cancer Medicament Combination Therapy for the Treatment of
TITLE OF INVENTION: Cancer Medicament Combination Therapy for the Treatment of
TITLE OF INVENTION: Cancer Medicament Combination Therapy for the Treatment of
TITLE OF INVENTION: Cancer Medicament Combination Therapy for 103-05
CURRENT APPLICATION NUMBER: US/09/800,266A
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 146
SEQ ID NOS: 146
SEQ ID NO 133
LENGTH: 20
LENGTH: 20
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Sequence 133, Application US/09895007A
Sequence 133, Application US/09895007A
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Scheter: Christian
APPLICANT: Petersen, Deanna M.
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS FOR THE
TITLE OF INVENTION: TREATMENT OF ANEMIA, THROMBOCYTOPENIA, AND NEUTROPENIA
FILE REFERENCE: C1041/7014 (AMS)
CURRENT APPLICATION NUMBER: US/09/895,007A
CURRENT APPLICATION NUMBER: US/09/895,007A
CURRENT APPLICATION NUMBER: US/02/214,368
PRIOR APPLICATION NUMBER: US/02/214,368
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 133
LENGTH: 20
                                                                                                                                                         CTHER INFORMATION: synthetic sequence US-09-916-369A-2
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SOFTWARE: PatentIn version 3.1
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ORGANISM: Artificial Sequence
                                                                           TYPE: DNA ORGANISM: artificial sequence
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ORGANISM: Artificial Sequence
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                      SEQ ID NO 2
LENGTH: 20
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Best Local S:
Matches 16
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| Sequence 168, Application US/0988326
| Sequence 168, Application US/0988326
| Publication No. US20030026801A1
| GENERAL INFORMATION:
| APPLICANT: Weiner, George
| APPLICANT: Hartman, Gunther
| TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
| TITLE OF INVENTION: Methods for Enhancing Cancer
| TITLE OF INVENTION: Methods for Enhancing Cancer
| FILE REFERENCE: C1039/7052 (AMS)
| CURRENT APPLICATION NUMBER: US/09/888,326
| CURRENT FILING DATE: 2001-06-22
| PRIOR APPLICATION NUMBER: US 60/213,346
| PRIOR FILING DATE: 2000-06-22
| NUMBER OF SEQ ID NOS: 848
| SOFTWARE: FSECSEQ for Windows Version 3.0
| SEQ ID NO 168
| LENTER OF USER OF WINDOWS WERSION 3.0
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Sequence 133, Application US/09920313

Publication No. US20020198165A1

GENERAL INFORMATION:

APPLICANT: Bratzler, Robert L.

APPLICANT: Petersen, Deanna M.

TITLE OF INVENTION: Treatment of Gastric Ulcers

TITLE OF INVENTION: Treatment of Gastric Ulcers

FILE REFERENCE: C1037/7019 (HCL/MAT)

CURRENT APPLICATION NUMBER: US/09/920,313

CURRENT FILING DATE: 2001-08-08

PRIOR PILING DATE: 2001-08-08

NUMBER OF SEQ ID NOS: 148

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 20
                                                                 3; Indels
      DB 3;
Ouery Match
71.0%; Score 14.2; DB 3;
Best Local Similarity 84.2%; Pred. No. 3.4e+04;
Matches 16; Conservative 0; Mismatches 3
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NAMEKEY: misc feature
LOCATION: (0)...(0)
LOCATION: (0)...(0)
US-09-888-326-168
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NAME/KEY: misc_feature
LOCATION: (0) ...(0)
OTHER INFORMATION: chimeric phosphorothioate/phosphodiester backbone
OTHER INFORMATION: with phosphorothioate at 5' and 3' ends
US-09-888-326-169
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LOCATION: (0)...(0)
OTHER INFORMATION: chimeric phosphorothioate/phosphodiester backbone
OTHER INFORMATION: with phosphorothioate at 5' and 3' ends
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71.0%; Score 14.2; DB 3; Length 20; 84.2%; Pred. No. 3.4e+04; ive 0; Mismatches 3; Indels
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APPLICANT: Weiner, George
APPLICANT: Hartmann, Gunther
TITLE OF INVENTION: Wethods for Enhancing Antibody-Induced
TITLE OF INVENTION: October of Street of Stree
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APPLICANT: Weiner, George
APPLICANT: Hartmann, Gunther
TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
TITLE OF INVENTION: Cell Lysis and Treating Cancer
FILE REFERENCE: C1039/7052 (AWS)
CURRENT APPLICATION NUMBER: US/09/888,326
CURRENT PILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: US 60/213,346
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 848
SOFTWARE: FRSESO for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 169, Application US/0988326; Publication No. US20030026801A1; GENERAL INFORMATION:
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. Sequence 429, Application US/0988326
. Publication No. US20030026801A1
. GENERAL INFORMATION:
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                                                   Best Local Similarity 84.2
Matches 16; Conservative
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LENGTH: 20
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LENGTH: 20
         Query Match
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; Bublication No. US20030087848A1
; GENERAL INNORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
APPLICANT: FOURDN Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
                                                                                                                                                                                                                                                                                                                             APPLICANT: Weiner, George
APPLICANT: Weiner, George
APPLICANT: Hartmann, Gunther
TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
TITLE OF INVENTION: Cell Lysis and Treating Cancer
TITLE OF INVENTION: Cell Lysis and Treating Cancer
CURRENT APPLICATION NUMBER: US/09/888,326
CURRENT APPLICATION NUMBER: US 60/213,346
PRIOR FILING DATE: 2000-06-22
NUMBER: OF SEQ ID NOS: 848
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 430
LENGTH: 20
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Length 20;
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Pred. No. 3.4e+04;
  Score 14.2; DB 3;
Pred. No. 3.4e+04;
0; Mismatches 3;
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; LOCATION: (0)...(0)
; OTHER INFORMATION: phosphodiester backbone
US-09-888-326-430
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SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                             Sequence 430, Application US/09888326 Publication No. US20030026801A1 GENERAL INFORMATION:
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84.2%;
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  Query Match 71.0%;
Best Local Similarity 84.2%;
Matches 16; Conservative
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Best Local Similarity
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LENGTH: 20
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US-09-776-479-530/c

$ Sequence 530, Application US/09776479

$ Sequence 530, Application US/09776479

$ Publication No. US20030097848A1

$ GENERAL INFORMATION:

$ APPLICANT: Petersen, Deanna M.

$ APPLICANT: Pouron, Yves

$ TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Tractment of Asthma and Allergy

$ TITLE OF INVENTION: Tractment Of Asthma and Allergy

FILE REFERENCE: Clo3777013 (HCL/MAT)

$ CURRENT APPLICATION NUMBER: US/09/776,479

$ PRIOR PILING DATE: 2000-02-03

$ NUMBER OF SEQ ID NOS: 1093

$ SOFTWARE: FastSEQ for Windows Version 3.0

$ SEQ ID NO 530
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US-09-776-479-531

i Sequence 531, Application US/09776479

i Sequence 531, Application US/09776479

i Publication No. US20030087848A1

i GENERAL INFORMATION:

i APPLICANT: Betersen, Deanna M.

APPLICANT: Petersen, Deanna M.

APPLICANT: Pouron, Yves

ITILE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Tractment of Asthma and Allergy

FILE REFERENCE: C1037/7013 (HCL/MAT)

CURRENT APPLICATION NUMBER: US/09/776,479

CURRENT APPLICATION NUMBER: US 60/179,991

PRIOR FILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 1093

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 20
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Best Local Similarity 84.2%; Pred. No. 3.4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels
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3; Indels
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Sequence 1295111. Application US/10310914A

Publication No. US/0060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich. Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: uses thereof
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US-10-914A-776151/ Application US/10310914A

Subjuction No. US20060003322A1

GENERAL INFORMATION.

GENERAL INFORMATION.

APPLICANT: Bentwich, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

TITLE OF INVENTION: uses thereof

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: Patentin version 3.3

SEQ ID NO 776151

LENGTH: 19
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TITLE OF INVENTION: INFLAMMATORY DISEASES
FILE REFERENCE: C1039.70060US01
CURRENT APPLICATION NUMBER: US/11/127,654
CURRENT FILING DATE: 2005-03-29
FRIOR APPLICATION NUMBER: US 10/112,653
FRIOR FILING DATE: 2002-03-29
FRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 1040
SOFTWARE: PACENTIN VERSION 3.2
LENGTH: 20
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Matches 20; Conservative
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ORGANISM: Human
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; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
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TYPE: RNA

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Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REPERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1162719
LENGTH: 20
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Fublicate 10 US20660003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Bentwich, Isaac

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

TITLE OF INVENTION: Uses thereof

TITLE OF INVENTION: Uses thereof

TITLE OF INVENTION: Uses thereof

CURRENT APPLICATION NUMBER: US/10/310, 914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 1162726

LENGHE: 21
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Fublication No. US20060003322A1
Fublication No. US2006000332A1
Fublication No. US2006000332A1
Fublication No. US2006000332A1
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION WINGHER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
LENGTH: 21
LENGTH: 21
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Pred. No. 1.3e+02;
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100.0%; Pred. No. ...
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Best Local Similarity 100.
Matches 19; Conservative
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Best Local Similarity
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US-10-310-914A-1295143
                                                                                                                                                                                                                                                                                                                                          ORGANISM: Human
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ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                 TYPE: RNA
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; Sequence 776152/c
; Sequence 776152, Application US/10310914A
; Sequence 776152, Application US/10310914A
; Publication No. US20060003322A1
; Publication No. US2006000332A1
; Publication No. US200600032A1
; APPLICANT: Shiler, Kvuzat
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: uses thereof
; TITLE OF INVENTION: uses thereof
; TITLE OF INVENTION: USES thereof
; CURRENT APPLICATION VMBER: US/10/310, 914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 776152
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Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
APPLICANTON: uses thereof
FILE REFERENCE: 06097.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 739686
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                                                                       Score 19; DB 7; Length 19; Pred. No. 1.3e+02;
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                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 1.3
Matches 19; Conservative 0; Mismatches
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Live 0; Mismatches
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Best Local Similarity 100.
Matches 19; Conservative
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Best Local Similarity
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; ORGANISM: Human
US-10-310-914A-739686
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US-10-310-914A-739686
  ; ORGANISM: Human
US-10-310-914A-776151
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ORGANISM: Human
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APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kuuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.cUPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-112-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE PATENTING OFFER PATENTIAL SEQ ID NO 1295149
LENGTH: 23
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Publication No. US20060003322A1
Publication No. US20060003322A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
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GENERAL SHILE OF INVENTION:
TITLE OF INVENTION:
USES Thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 739676
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Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
APPLICANTON: uses thereof
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION VUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOGTWARE: ParentIn version 3.3
SEQ ID NO 1162727
LENGTH: 27
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Pred. No. 1.3e+02;
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Best Local Similarity 100.0
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Best Local Similarity 100.
Matches 19; Conservative
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US-10-310-914A-1162727/c
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Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Benewich, Isaac
APPLICANT: Shiler, Wuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1295144
LENGTH: 21
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Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Kvuzat
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PATENTIN version 3.3
SEQ ID NO 1295148
LENGTH: 23
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                                       95.0%; Score 19; DB 7; Length 21; 100.0%; Pred. No. 1.3e+02; ive 0; Mismatches 0; Indels
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Mismatches 0; Indels
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                                            Query Match
Best Local Similarity 100.
Matches 19; Conservative
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Matches 19; Conservative
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Matches 19; Conservative
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US-10-310-914A-1295149
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US-10-310-914A-1295143
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ORGANISM: Human
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ORGANISM: Human
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Sequence 16294, Application US/10310914A
Publication No. US20060003322A1
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bhiler, Kvuzat
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 162974
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 066087.0200.CPUSOI.
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER: Patentin version 3.3
SEQ ID NO 162906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 24;
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Pred. No. 2.1e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.0%;
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Best Local Similarity 95.0°
Matches 19; Conservative
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Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                 TYPE: RNA
ORGANISM: Human
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Sequence 1162700, Application US/10310914A

Fublication No. US2060003322A1

Sequence 1162700, Application US/10310914A

Fublicantion No. US206000332A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Bentwich, Isaac

APPLICANT: Bentwich, Isaac

APPLICANT: Briller Kruzat

TITLE OF INVENTION: uses thereof

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION WUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SEQ ID NO 1162700

LENGTH: 28

LENGTH: 28
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Publication No. US20060003322A1
GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
APPLICATION NUMBER:
APPLICATION NUMBER:
AUS/10/310,914A
CURRENT FILING DATE:
AD02-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1155402
LENGTH: 20
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   Length 27;
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   DB 7; Le
1.3e+02;
Query Match 95.0%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 1.3 Matches 19; Conservative 0; Mismatches
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US-10-310-914A-162906
; Sequence 162906, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
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Best Local Similarity 95.0°
Matches 19; Conservative
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Matches 19; Conservative
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; ORGANISM: Human
US-10-310-914A-1155402
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ORGANISM: Human
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Page 7

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereoff TITLE OF INVENTION: uses thereoff FILE REPERENCE: 06087.0200.CPUS01; CURRENT APPLICATION NUMBER: US/10/310,914A; CURRENT APPLICATION NUMBER: US/10/310,914A; NUMBER OF SEQ ID NOS: 1388402 SOFTWARE: PatentIn version 3.3 SEQ ID NOS: 1388402 INGCTH: 22

TYPE: DATE OF THE OFFICE OFFICE
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APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Biller, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 739675
LENGTH: 23
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Publication No. US20060003322A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Uses thereof
CURRENT PELING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOOTWARE: Patentin version 3.3
SEQ ID NO 1047386
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Pred. No. 2.9e+02;
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.06;
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Best Local Similarity 100..
Best Local 18; Conservative
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Best Local Similarity
Matches 18; Conserv
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US-10-310-914A-739675
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Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bloinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION WUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 282266
LENGTH: 28
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APPLICANT: Shiler, Kwizat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087,0200, CPUS01
CURRENT APPLICATION WUMBER: uS/10/310,914A
CURRENT PILLNG DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 905589
LENGTH: 19
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Pred. No. 2.1e+02;
                                                                                                                                                                                           92.0%; Score 18.4; DB 7; Length 24; 95.0%; Pred. No. 2.1e+02;
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Pred. No. 2.9e+02;
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Best Local Similarity 95.0%; Pred. No. 2.1e
Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                    0; Mismatches
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; Publication No. US20060003322A1
; GENERAL INFORMATION:
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Conservative 0;
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Matches 19, Conservative
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Best Local Similarity
Matches 18; Conserv
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US-10-310-914A-282266
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US-10-310-914A-906589
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US-10-310-914A-906589
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TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION VNDBER: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 152912
LENGTH: 19
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Sequence 386825, Application US/10310914A

Sequence 386825, Application US/10310914A

Publication No. US20060003322A1

Sequence 386825

Publication No. US2006000332A1

SEPLICANT: Bentwich, Isaac

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: uses thereof

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION UNDER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SEQ ID NO 386825

LENGTH: 19
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bloinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 66087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
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Pred. No. 4.6e+02;
0; Mismatches 1; Indels
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Pred. No. 4.6e+02;
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Pred. No. 4.6e+02;
                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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94.7%;
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Best Local Similarity 94.7%
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Best Local Similarity 94.7
Matches 18; Conservative
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Best Local Similarity
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US-10-310-914A-386824
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US-10-310-914A-386825
                                                                                                                                                                                                        TYPE: RNA
ORGANISM: Human
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ORGANISM: Human
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                                                                                                                                                                                                             Sequence 100302, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Baioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 100302
LENGTH: 19
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Sequence 148888, Application US/10310914A

Sequence 148888, Application US/10310914A

Publication No. US20060003322A1

GRNERAL INFORMATION: Bentwich, Isaac

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: USES thereof

FILE REFERENCE: 0687.0200.CPUS01

FULE REFERENCE: 0687.0200.CPUS01

CURRENT APPLICATION WNBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SEQ ID NO 148888

LENGTH: 19
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Pred. No. 4.6e+02;
0; Mismatches 1; Indels
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                           Indels
  Pred. No. 2.9e+02;
Hismatches 0;
    l Similarity 100.0%; Pred. No. 2.9
18; Conservative 0; Mismatches
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US-10-310-914A-162912
US-10-310-914A-162912
Sequence 162912, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
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Best Local Similarity 94.7
Matches 18; Conservative
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Matches 18, Conserv
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US-10-310-914A-148888
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ORGANISM: Human
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    Best Local
Matches 1
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Sequence 1155411, Application US/10310914A
Publication No. US20060003322A1
Publication No. US2006000322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
FILE REFERENCE: 06087.0200.CPUS01
CURRENT PELING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1155411
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TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REPREBUCE: 06.097.02.00. CPUSOI.
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 628864
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Pred. No. 4.6e+02;
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llarity 94.7%; Pred. No. 4.6e+02;
Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                      0; Mismatches
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TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 588532
LENGTH: 20
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94.7%;
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Best Local Similarity 94.7<sup>3</sup>
Matches 18; Conservative
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Matches 18, Conservative
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Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                       TYPE: RNA
ORGANISM: Human
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Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: Uses thereof
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 288225
LENGTH: 20
                                                                                                                                                                                                                                                                                            APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REPERBACE: 06.087_0208 thereof
FILE REFERBACE: 06.087_0208 thereof
FILE REFERBACE: 06.087_0208 thereof
CURRENT APPLICATION NUMBER: US/10/310, 914A
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 386850
LENGTH: 19
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TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
       Gaps
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Pred. No. 4.6e+02;
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         1; Indels
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94.7%; Pred. No. ...
0; Mismatches
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         0; Mismatches
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; Sequence 386850, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
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Matches 18; Conservative
       18; Conservative
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US-10-310-914A-288225
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ORGANISM: Human
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ORGANISM: Human
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Publication No. US2006000332A1

Publication No. US2006000332A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
TITLE REFERENCE: 06087,0200.CPUS01
FILE REFERENCE: 06087,0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SSEQ ID 0386839
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Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: USES thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOCTWARE: PatentIn version 3.3
SEQ ID NO 386841
LENGTH: 21
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                                                                                                                                                                                                                                                                                     Mismatches
                CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SEQ TWARE: PatentIn version 3.3
SEQ ID NO 288227
LENGTH: 21
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FILE REFERENCE: 06087.0200.CPUS01
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Best Local Similarity 94.7%;
Matches 18; Conservative
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Matches 18, Conservative
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US-10-310-914A-288227
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ORGANISM: Human
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                                                                                                                                                        TYPE: RNA
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Best Local 9
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                                                                                                                                                               Sequence 100342, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION: BENEWICH, Isaac
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: USES TO COUSOI
CURRENT APPLICATION UNBER: US/10/310, 914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SEQ ID NO 10342
LENGTH: 21
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Publication No. US20060003322A1
GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
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APPLICATION NOWBER:
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NOWBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SOFTWARE: PatentIn version 3.3
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US-10-310-914A-288227
US-10-310-914A-288227, Application US/10310914A

Sequence 288227, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof
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Best Local Similarity 94.7
Matches 18; Conservative
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Matches 18; Conservative
                                                                                                                          RESULT 34
US-10-310-914A-100342/c
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US-10-310-914A-100342
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; ORGANISM: Human
US-10-310-914A-288226
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Sequence 282307, Application US/10310914A
Publication No. US/0060003322A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich. Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: uses thereof
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Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac

APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: Patentin version 3.3
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                                                                                                                                                                                                                                                                               Score 17.4; DB 7; Length 21;
Pred. No. 4.6e+02;
0; Mismatches 1; Indels
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Pred. No. 4.6e+02;
0; Mismatches 1; Indels
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Pred. No. 4.6e+02;
0; Mismatches 1;
CURRENT APPLICATION NUMBER: US/10/310,914A CURRENT FILING DATE: 2002-12-06 NUMBER OF SEQ ID NOS: 1388402 SOFTWARE: Patentin version 3.3 SEQ ID NO 1345469 LENGTH: 21
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Best Local Similarity 94.7%;
Matches 18; Conservative
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Best Local Similarity 94.7
Matches 18; Conservative
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Best Local Similarity 94.7
Matches 18; Conservative
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US-10-310-914A-282307
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ORGANISM: Human
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                                                                                                                                                                                   Sequence 386851, Application US/10310914A
| Publication No. US2066003322A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Bentwich, Isaac
| TITLE OF INVENTION: Uses thereof
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Publication No. US20660003322A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 0609'.0200.CPUS01
CURRENT PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 659280
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Sequence 1345469, Application US/10310914A
Sequence 1345469, Application US/10310914A
Sequence 1345469, Application US/10310914A
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
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Pred. No. 4.6e+02;
0; Mismatches 1; Indels
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     1 AGGGGAGGGAGGGGG 19
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Best Local Similarity 94.7
Matches 18; Conservative
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Best Local Similarity 94.7
Matches 18; Conservative
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; ORGANISM: Human
US-10-310-914A-659280
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US-10-310-914A-386851
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US-10-310-914A-1345363/C

Sequence 1345363, Application US/10310914A

Publication No. US2060003322A1

Sequence 1345363, Application US/10310914A

Publication No. US2060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Bentwich, Isaac

APPLICANT: Bentwich, Isaac

TITLE OF INVENTION: Uses thereof

TITLE OF INVENTION: Uses thereof

TITLE OF INVENTION: Uses thereof

TITLE OF INVENTION: Uses (18/10/310, 914A)

CURRENT APPLICATION VUMBER: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE PATENTIN VERSION 3.3

SEQ ID NO 1345363

LENGTH: 22

LENGTH: 22
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Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Youzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Uses thereof
FILE REPREMENT: 06097,0200, CCPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1384402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1345365
LENGTH: 22
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                                                                                                                                                                                              Score 17.4; DB 7; Length 22;
Pred. No. 4.6e+02;
0; Mismatches 1; Indels
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87.0%; Score 17.4; DB 7;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 1;
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  CURRENT FILING DATE: 2002-12-0
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 659284
LENGTH: 22
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94.7%;
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Best Local Similarity 94.7
Matches 18; Conservative
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US-10-310-914A-1345365/c
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US-10-310-914A-1345363
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                                                                                                                                    ; ORGANISM: Human
US-10-310-914A-659284
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ORGANISM: Human
                                                                                                                    TYPE: RNA
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                                                                                                                         Sequence 560684, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT PAPLICATION NUMBER: US/10/310,914A
CURRENT PAPLICATION NUMBER: Second NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NOS: 22
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US-10-310-914A-659284

US-10-310-914A-659284, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Benewich, Isaac

APPLICANT: Shiler, Kvuzac

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: Uses thereof

TITLE REFERENCE: 06087.0200.CPDUS01;

CURRENT APPLICATION NUMBER: US/10/310,914A
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Best Local Similarity 94.77
Matches 18; Conservative
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Best Local Similarity 94.7
Matches 18; Conservative
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US-10-310-914A-560684
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; ORGANISM: Human
US-10-310-914A-628966
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US-10-914A-162972

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US-10-910-914A-162972

US-10-914A-162972

US-10-914A-162972

US-10-914A-162972

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Benewich, Maaac

APPLICANT: Benewich, Kevaac

APPLICANT: Benewich, Kevaac

APPLICANT: Benewich, Towas

APPLICANT: Benewich, 18aac

APPLICANT: Benewich, 19aac

APPLICANT: Benewich, 19aac

TITLE OF INVENTION: uses thereof

TITLE OF INVENTION: uses

TITLE OF INVENTION
US-10-914A-100318/c
Sequence 100318, Application US/10310914A
Sequence 100318, Application US/10310914A
Sequence 100318, Application US/10310914A
Sequence 100318, Application US/10310914A
GENERAL INFORMATION:
APPLICANT: Shiler, Kuzat
APPLICANT: Shiler, Kuzat
TITLE OF INVENTION: uses thereof
FILE REFRENCE: 06097.0200.CPUS01
CURRENT APPLICATION WHOBER: US/10/310,914A
CURRENT APPLIANG DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SOFTWARE: PatentIn version 3.3
LENGTH: 23
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Best Local Similarity 94.7
Matches 18; Conservative
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Best Local Similarity 94.7
Matches 18; Conservative
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; ORGANISM: Human
US-10-310-914A-162972
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; ORGANISM: Human
US-10-310-914A-100318
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